

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 21.2583 Seconds

(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-1

perfect score: 3522

Sequence: 1 EVQLQQSGPDLVKPGASVKI.....EATHKTSTSPVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

```
Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1107	31.4	257	2	A29179	enterotoxin E prec
2	1036.5	29.4	225	2	S37484	Ig kappa chain - m
3	973	27.6	446	2	S40295	Ig gamma-2a chain
4	952	27.0	220	2	S31790	Ig kappa chain v r
5	951.5	27.0	469	2	S37483	Ig gamma-2a chain
6	948	26.9	257	2	A28664	enterotoxin A prec
7	931	26.4	548	2	S38864	Ig epsilon chain C
8	929	26.4	246	2	S38950	Ig gamma chain - m
9	926	26.3	214	2	S68212	Ig kappa chain (Ma
10	918	26.1	260	2	S89984	enterotoxin p [imp
11	914.5	26.0	219	2	S52028	Ig kappa chain - m
12	914	26.0	214	2	PC4202	monoclonal antibod
13	910.5	25.9	219	2	PC4320	Ig kappa chain (mo
14	903.5	25.7	219	2	S14112	Ig kappa chain v r
15	900.5	25.6	474	1	G2MS11	Ig kappa chain - m
16	896.5	25.5	219	2	S38865	Ig kappa chain - m
17	892	25.3	218	2	JC5810	monoclonal antibod
18	890.5	25.3	221	2	S49220	Ig gamma-1 chain -
19	886.5	25.2	217	2	S42772	Ig kappa chain - m
20	880	25.0	218	2	S68241	Ig kappa chain v r
21	878.5	24.9	235	2	S25058	Ig kappa chain - m
22	876.5	24.9	225	2	UL0029	Ig kappa chain pre
23	875	24.8	234	2	S14237	Ig kappa chain pre
24	874	24.8	234	2	S01320	Ig kappa chain pre
25	873	24.8	475	2	S01321	Ig gamma-2b chain
26	870	24.7	444	2	PC4436	monoclonal antibod
27	857	24.3	210	2	A56169	Ig kappa chain v r
28	853	24.2	240	2	S64084	Ig kappa chain pre
29	808	22.9	220	2	S68211	Ig heavy chain (Ma

ALIGNMENTS

RESULT 1

A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1993
C:Accession: A28179
R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; PMID:88257005; PMID:3384800
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: GB:M21319; NID:g153001; PID:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.4e-50;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSLQGTALGNLQIYYYNKSAITSEKSAQDFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSLQGTALGNLQIYYYNKSAITSEKSAQDFLNTLLFKGFFTG 84
QY 286 HPVYNDLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 345
DB 85 HPVYNDLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
QY 346 EEEKVPINLMDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGGKQV 405
DB 145 EEEKVPINLMDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGGKQV 204
QY 406 RGLIVHSSSGSVSYDLFPAQGYPTLLRIYRDNTTISLSLSLYLYTT 458
DB 205 RGLIVHSSSGSVSYDLFPAQGYPTLLRIYRDNTTISLSLSLYLYTT 257

RESULT 2

S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PID:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.4%; Score 1036.5; DB 2; Length 225;
Best Local Similarity 93.9%; Pred. No. 5.1e-47;
Matches 200; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 459 SIYVTPQPTSLIYVAGDRVITTCASQSVNDVAVYQKQKQSPKLLISVTSRYAGVDP 518
DB 13 SIYVTPQPTSLIYVAGDRVITTCASQSVNDVAVYQKQKQSPKLLISVTSRYAGVDP 72
QY 519 RFSGSGYGTDTLTISVQAEAAVFCQDYNKSPPTFGGKTKLEIKRADAAPTWSIFPP 578
DB 73 RFSGSGYGTDTLTISVQAEAAVFCQDYNKSPPTFGGKTKLEIKRADAAPTWSIFPP 131
QY 579 SSELQTSGGASVVCFLNNFVKDINVKWKIDGSEKQNGVLSNWTDDSKDSTYSMSLT 638
DB 132 SSELQTSGGASVVCFLNNFVKDINVKWKIDGSEKQNGVLSNWTDDSKDSTYSMSLT 191

QY 639 LTKDEYERHNSYTCEATHKTSTSPVKSFNRE 671
DB 192 LTKDEYERHNSYTCEATHKTSTSPVKSFNRE 224

RESULT 3

S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-17/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96/144-195,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 27.6%; Score 973; DB 2; Length 446;
Best Local Similarity 34.9%; Pred. No. 2.3e-43;
Matches 241; Conservative 57; Mismatches 123; Indels 270; Gaps 14;
QY 1 EVQLQQSGPDLVPGASVKISCKASGYFTGYVHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QIQQLQQSGPELVPGASVKISCKASGYFTDYIHWVKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKPKQKATLVDSSTAYNMLSLTSEDSAVYICARSTMTNYVMDYQGQTSVTSS 120
DB 61 NEKPKKATLVDSSTAYNMLSLTSEDSAVYICARSTMTNYVMDYQGQTSVTSS 117
QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPTVTWNSGSLSSGVHTFPVQLQSD 180
DB 118 AKTTPSVYPLAPVCGDTTGSSTVLGCLVKGYPEPTVTWNSGSLSSGVHTFPVQLQSD 177
QY 181 LYTSSSVTPSSWTPSETVTCNVNHPASSTKVDKIVPRDSGGSPSEKSEINEKDLRKK 240
DB 178 LYTSSSVTPSSWTPSETVTCNVNHPASSTKVDKIVPRDSGGSPSEKSEINEKDLRKK 225
QY 241 SELQGTALGNLQIYYYNKSAITSEKSAQDFLNTLLFKGFFGHPWYNDLVLDGSTA 300
DB 226 -----PCKCPAPN-----LLGGPSVF----- 241
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 226 -----PCKCPAPN-----LLGGPSVF----- 241
QY 361 TTVIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGGKQVORGLIYVHSGSGTSS 420
DB 242 -----IPFKIKQVLM----- 260
QY 421 YDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLYTTISVMTQTPTSLLSVAGDRVTIT 480
DB 261 CVVVDVSEDDFD-----VQLSMFVNNEVLTAQT----- 291
QY 481 CKASQSVNDVAVYQKQKQSPKLLISVTSRYAGVDPDFSGSGYGTDTLTISVQAEAD 540

Db 292 -----HREDNSTLRV----- 303
QY 541 AAVYFCQDYNPPPTFGGKLEIKRAD-----AAPTVPSPSSQOLT 584
Db 304 SALPIQHODMWSGKEF-----KCKVNNKDLPAPIERTISKPRGSRAPQVYVLPPEBEEMT 359
QY 585 SGGASVWCFLNFPKIDNVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSVSLTL 639
Db 360 KQVTLTCMVDTFMPEDIVYVWNTNGKTELNYKTEFVLDS-----DGSYFMYSLRV 412
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFNR 669
Db 413 EKKWVERNYSYCSVVHEGLNHHHTKSFNR 443

RESULT 4
A1790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1998
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an antibody that recognizes the immunoglobulin V region; immunoglobulin homology
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M03626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 952; DB 2; Length 220;
Best Local Similarity 82.6%; Pred No. 1.2e-42;
Matches 180; Conservative 19; Mismatches 13; Indels 6; Gaps 1;
QY 460 IVMTQPTSLVSAAGRVITCKASQVSND-----VAVYQKPGQPKLLISYTSRY 513
Db 2 IVMTQPSLSLTVAGEKVTMSCTSSQSLFNSQKQKWLTVQKPGQPKVLIWASRE 61
QY 514 AGVPRFSGSGVGTFTLTISVQAEADAANVFCQDYNPPPTFGGKLEIKRADAAPT 573
Db 62 SGVPRFTSGSGGTFTLTISVQAEADLAIVYQNDYNSNPLTFGGGKLEIKRADAAPT 121
QY 574 SIFPPSSQLTSGGASVVCFLNFPKIDNVKWKIDGSRQNGVLSNWTQDQSKDSTYSM 633
Db 122 SIFPPSSQLTSGGASVVCFLNFPKIDNVKWKIDGSRQNGVLSNWTQDQSKDSTYSM 181
QY 634 SSTLTLTDEYERHNSYTCEATHK-TSTSPIVKSFNR 671
Db 182 SSTLTLTDEYERHNSYTCEATHK-TSTSPIVKSFNR 219

RESULT 5
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 951.5; DB 2; Length 469;
Best Local Similarity 34.2%; Pred No. 3.2e-42;
Matches 236; Conservative 62; Mismatches 126; Indels 267; Gaps 13;
QY 1 EVLOQSGPDLVKPGASVKISKAGSYSTGYTHVHWKQSPKGLWIGRIINPNNGVTL 60
Db 20 QILOQSGPELVKPGASVKISKAGSYSTGYTHVHWKQSPKGLWIGRIINPNNGVTL 79
QY 61 NQKFKDKATLVTDKSTTAYMELRSITSDSAVYVCARSTMTLNTVYMDYKGGTSTVVS 120
Db 80 NENFKKATLVTDKSTTAYMELRSITSDSAVYVCARSTMTLNTVYMDYKGGTSTVVS 139
QY 121 AKTTPSVVPLAPGSAATNSMTVLGCLVKGYFPEPTVTVNSGSLSSGVHFPAYLQSD 180
Db 140 AKTTPSVVPLAPGSAATNSMTVLGCLVKGYFPEPTVTVNSGSLSSGVHFPAYLQSD 199
QY 181 LYTLLSSVTVPSSTWPESETVTCNVAHPASSTVDKIVPRDGGPSEKSEENKDLRKK 240
Db 200 LYTLLSSVTVPSSTWPESETVTCNVAHPASSTVDKIVPRDGGPSEKSEENKDLRKK 247
QY 241 SELQGTALGNLKQIYYNYSKAITSEKSAQDLTNTLLEKFFTGHPWYNDLLVLDLSTA 300
Db 248 ----- 247
QY 301 ATSEYEGSSVDLYGAVYQCAGGTGNKTCAMVGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 248 -----PKCPAPN-----LLGSPSVF----- 263
QY 361 TTVPIDKVKTSKEVTVQELDLQARHLHGKFLYNSDSFGGKVGQVGLIVFHSSEGSTVS 420
Db 264 -----LFPKIKDVLMI-----SLSPVIT 282
QY 421 YDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTTISVMTQTPTSLLSAGDVTIT 480
Db 283 CVVVDVSEDDPD-----VQISFVANNVEVHTAQQT----- 313
QY 481 CKASQSVSNDVAVYQKPGQPKLLISYTSRYAGVPRDFSGSGYGTDFLTLTISVQAE 540
Db 314 -----HREDNSTLRV----- 325
QY 541 AAVYFCQDYNPPPTFGGKLEIKRAD-----AAPTVPSPSSQOLT 584
Db 326 SALPIQHODMWSGKEF-----KCKVNNKDLPAPIERTISKPRGSRAPQVYVLPPEBEEMT 381
QY 585 SGGASVVCFLNFPKIDNVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSVSLTL 639
Db 382 KQVTLTCMVDTFMPEDIVYVWNTNGKTELNYKTEFVLDS-----DGSYFMYSLRV 434
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFNR 669
Db 435 EKKWVERNYSYCSVVHEGLNHHHTKSFNR 465

RESULT 6
A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:88086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: GB:M18970; NID:gi53120; PIDN:AAA26681.1; PID:gi53121
A:Experimental source: strain FR1337
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293; PMID:3584106
A:Accession: A29566

A:Molecule type: protein
A:Residues: 25-241,'S',243-257 <HUA>
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

Query Match 26.4%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 2.3e-42;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEETNEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQLNTLLKGFFTG 285
DB 25 SEKSEETNEKDLRKSELOQTALGNLKOIYYNEKAKTNSKSHDQFLQTLKGFFTD 84
QY 286 HPWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCAGMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSDKIDVYKKGKVDLYGAYGYOCAGGTPNKTCAGMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWDGKQTPIDKVTSKKEVTVQELDQARHYLHGKFLYNSDSGCKVQ 405
DB 145 BEKKVPINLWDGKQNTVPLETKNKNVTVQELDQARHYLQEKYNYNSDVFGRVQ 204
QY 406 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNTTISSTSLSLSLYLTT 458
DB 205 RGLIVHSTSTPSVNYDLFDAQOQYNTLLRIYRDNTKNTSENMHIDILYTS 257

RESULT 7
S38864
Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38864
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <KIP>
A:Cross-references: EMBL:Z27397; NID:G416537; PIDN:CAA81788.1; PID:G940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 931; DB 2; Length 548;
Best Local Similarity 35.0%; Pred. No. 4.5e-41;
Matches 241; Conservative 83; Mismatches 186; Indels 178; Gaps 19;

QY 1 EVQLQQSGDPLVKPGASVKISKASGYSFTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 1 QVXLESGLDVKPGGSLKLSCAASGLTSSYGMVNRQIPDKLEWVATISSGGTYTY 60
QY 61 NQKFKKATLTVDKSTTAYMELRSLTSEDSAVYICARSTMTINYVDYWGQGTSTVSS 120
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSKSDTAMYYCARQGVSTMRFPAYWGQGLTVTSA 120
QY 121 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPPTVTVNSGSLSSGVTHTFPVQLQSD 180
DB 121 GKTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPPTVTVNSGSLSSGVTHTFPVQLQSD 180
QY 181 LYTLLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIKIVPRDSG-----GPSKSEEEI--- 232
DB 181 LYTLLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIKIVPRDCGCKPCIVPEVSSVFIFPP 240
QY 233 NEXDLRKSELO-----GVALGNLKOIYYNSKAITSEKSDAQLNTLLKGFFTGH 286
DB 241 KPQDLVTRSTIQLYCFYGHILNDVSVWMLDREITDR-----LAQTVLK----- 287
QY 287 PWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCAGMYGGVTLHNNRLTE 346
DB 288 -----BEGLASTCKLNITEQQWMSSESTFTCK-----VTSGQVDYLAH 326

QY 347 EKKVPINLWDGKQTV-----PIDKVKTSKKEVTVQELDQARHYLHGKFLYNSD 398
DB 327 TRRCF-----DHEPRGVITVLLIPSPDLQYQNGAPKLTCLVWDLSEKYN----- 372
QY 399 SFGGKVGRLIVPHSSSGSVSYDLFDAQOQYPTLLRIYRDNTTISSTSLSLYLTT 458
DB 373 -----VTNQEKKTSSVS-----ASQWYTK-----HNNATTSITS----- 403
QY 459 SIWMTQTPSLLVSAGRVTITCKASQSVSNDAVYQKQSPKLLIYSSTRYAGVDP 518
DB 404 -----LPVAKD-----WIE----- 413
QY 519 RFSSGSGTDTLTITSSVQAEADAIFYCQODYNS--PPTFGGCTKLEIKRAADAAPTYSIF 576
DB 414 -----GYG-----YQICVDHPDFPKPIVRSITKTPGQR--SAPEYVVF 449
QY 577 PPSSEQLTSGGASVVCFLNNFYKIDINVKWKIDGSEKQNGVLSWTDQDSKDS--YSMS 634
DB 450 PPPEEE--SEDKRTLTCLIQNFFPEDISQWMLGDGKLLSNQSHSTTTPKXNGSNRGFFIF 508
QY 635 STLTLTKDEVERHNSYTCETHTKTSTSP 662
DB 509 SRLEVAKTLTQRKQFTCQVHEALQKP 536

RESULT 8
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Weisgetber, C.; Bit
Biol.Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(G
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
A:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 929; DB 2; Length 246;
Best Local Similarity 78.5%; Pred. No. 2.1e-41;
Matches 179; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLQQSGDPLVKPGASVKISKASGYSFTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 1 QIQLQQSGPELVRFPGASVKISKASGYFTDYIHWYKQRPGEGLWIGWYFGSGNTKY 60
QY 61 NQKFKKATLTVDKSTTAYMELRSLTSEDSAVYICARSTMTINYVDYWGQGTSTVSS 120
DB 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARG--GKFANDYWGQGTSTVSS 117
QY 121 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPPTVTVNSGSLSSGVTHTFPVQLQSD 180
DB 118 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYPEPPTVTLWNSGSLSSGVTHTFPVQLQSD 177
QY 181 LYTLLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIKIVPRDSGSPSEK 228
DB 178 LYTLLSSSVTVPSSTWSPSQSITCNVAHPASSTKVDKIKIEPR---GPTIK 222

RESULT 9
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
 A;Reference number: S68211; MUID:95085223; PMID:7498516
 A;Accession: S68212
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-214 <TAK>
 A;Cross-references: EMBL:D29668
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.3%; Score 926; DB 2; Length 214;
 Best Local Similarity 83.1%; Pred. No. 2.5e-41;
 Matches 177; Conservative 16; Mismatches 14; Indels 6; Gaps 1;
 QY 460 IVMTQTPTSLVSGADRVITTCASQSVND-----VAVYQKPGQSPKLLISYTSRY 513
 Db 2 IVMTQSPSLAVSGQKVTMSCKSSQLLNQKVLAWYQKPGQSPKLLVYFASTRE 61
 QY 514 AGVDRFSGSGYGDFTLTITSSVQAEADAAVYFCQDYNSTPTFGGKLEIKRADAAPT 573
 Db 62 SGVDRFSGSGYGDFTLTITVQAEADLAADYFCQCHYSTPTFGGKLEIKRADAAPT 121
 QY 574 SIFPPSSQQLTSGGASVVCFLNNFPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYS 633
 Db 122 SIFPPSSQQLTSGGASVVCFLNNFPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYS 181
 QY 634 SSTLTLTDEYERHNSYTCEATHKTSPIVKS 666
 Db 182 SSTLTLTDEYERHNSYTCEATHKTSPIVKS 214

RESULT 10
 C89984
 enterotoxin P [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: C89984
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.;
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: C89984
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-260 <KUR>
 A;Cross-references: GB:BA000018; PID:g13701743; PIDN:BA043036.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: sep
 C;Superfamily: enterotoxin B

Query Match 26.1%; Score 918; DB 2; Length 260;
 Best Local Similarity 73.0%; Pred. No. 8.3e-41;
 Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKATTSSEKSDAQFLTNLLPKGFTG 285
 Db 28 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKATTSSEKSDAQFLTNLLPKGFTG 87
 QY 286 HPVNDLLVDLSTAAATSEYSGSSVDLYGAYGYQCAGTPTNKACMYGGVTLHDNNRLT 345
 Db 88 HPVNDLLVDLSTAAATSEYSGSSVDLYGAYGYQCAGTPTNKACMYGGVTLHDNNRLT 147
 QY 346 BEKKVPINLWDGKQTTPIDPKVTSKEVTVQELDLQARHLYLHGKGLYNSDFGKQV 405
 Db 148 BEKKVPINLWDGKQTTPIDPKVTSKEVTVQELDLQARHLYLHGKGLYNSDFGKQV 207
 QY 406 RGLIVFHSSSEGSTVSDYDLFDQAGQVPTDLLRIYRNTTISSTLSISLYLTT 458
 Db 208 RGLIVFHSSSEGSTVSDYDLFDQAGQVPTDLLRIYRNTTISSTLSISLYLTT 260

RESULT 11
 S52028
 Ig kappa chain - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C;Accession: S52028
 R;Van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; F
 submitted to the EMBL Data Library, August 1994
 A;Description: Coordinate expression of antibody subunit genes yields high levels of func
 A;Reference number: S52028
 A;Accession: S52028
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-219 <VAN>
 A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IMW>

Query Match 26.0%; Score 914.5; DB 2; Length 219;
 Best Local Similarity 81.6%; Pred. No. 1e-40;
 Matches 177; Conservative 15; Mismatches 20; Indels 5; Gaps 2;
 QY 460 IVMTQTPTSLVSGADRVITTCASQSV--SND---VAVYQKPGQSPKLLISYTSRYA 514
 Db 2 IVMTQSPSLPVLGQASISCRSSQSVHSGNTVLEWYLOKPGQSPKLLIKVSNRFS 61
 QY 515 GVPDRFSGSGYGDFTLTITSSVQAEADAAVYFCQDYNSTPTFGGKLEIKRADAAPT 574
 Db 62 GVPDRFSGSGYGDFTLTITKISRVEADLVYVYFCQSHVPTFGGKLEIKRADAAPT 121
 QY 575 IPPPSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYS 634
 Db 122 IPPPSSEQLTSGGASVVCFLNNFPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYS 181
 QY 635 STLTLTDEYERHNSYTCEATHKTSPIVKSFNRE 671
 Db 182 STLTLTDEYERHNSYTCEATHKTSPIVKSFNRE 218

RESULT 12
 PC4202
 monoclonal antibody MABA34 gammal heavy chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 21-Jan-2000
 C;Accession: PC4202
 R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
 Gene 173, 257-259, 1996
 A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mo
 A;Reference number: PC4202; MUID:97082978; PMID:8964510
 A;Accession: PC4202
 A;Molecule type: mRNA
 A;Residues: 1-214 <KWA>
 A;Cross-references: GB:U29146; NID:g1594223; PIDN:AA052820.1; PID:g1594224
 C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 F;1-112/Domain: V region #status predicted <VRG>
 F;113-214/Domain: C region #status predicted <CRG>
 F;132-136/Domain: immunoglobulin homology <IMW>

Query Match 26.0%; Score 914; DB 2; Length 214;
 Best Local Similarity 80.1%; Pred. No. 1e-40;
 Matches 177; Conservative 14; Mismatches 22; Indels 8; Gaps 1;
 QY 1 EVLOQSGDPLVKGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVLOQSGDPLVKGASVKISCKATDYRFSYVWIKVQKPGHLEWIGDILPGSNTNY 60
 QY 61 NQFKDKKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNYMDYWGQGTSTVSS 120
 Db 61 NQFKDKKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNYMDYWGQGTSTVSS 112
 QY 121 AKTTPSVPLAPGSAQAQNSWTLGCLVKGTFPEVTVWNSGSLSSGSHVTFPAVLQSD 180

Db 113 AKTTPTSVYELAPGSAATNSMTVTLGLKVGYPEPVTWNSGSLSSGVHTFPVAVLQSD 172
 QY 181 LYTLLSSVTPSWPSETVTCNVAHPASSTKVDKIVPRD 221
 Db 173 LYTLLSSVTPSWPSPRSETVTCNVAHPASSTKVDKIVPRD 213

RESULT 13
 PC4203
 Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
 C:Accession: PC4203
 R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
 Gene 173, 257-259, 1996
 A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mAb
 A:Reference number: PC4202; MUID:97082978; PMID:8964510
 A:Accession: PC4203
 A:Molecule type: mRNA
 A:Residues: 1-219 <KWA>
 A:Cross-references: GB:U29147; NID:G1594225; PID:AA052821.1; PID:G1594226
 A:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-112/Domain: V region #status predicted <VRG>
 F:113-219/Domain: C region #status predicted <CRG>

Query Match 25.9%; Score 910.5; DB 2; Length 219;
 Best Local Similarity 80.6%; Pred. No. 1.6e+40;
 Matches 175; Conservative 16; Mismatches 21; Indels 5; Gaps 1;

QY 460 IVMTQPTSLVVSAGDRVTITCKASQSV-----SNDVAVQKPGQSPKLLISYSSRYA 514
 Db 2 VLMTQPTSLVPSLGDQASISCRSSQSVHTNGNTVLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 515 GVPDRFSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGGTKLEIKRAADAAPTVS 574
 Db 62 GVPDRFSGSGYGTDFLTIKSRVEAEDLVGYVFCQSHVPTFGGGTKLEIKRAADAAPTVS 121

QY 575 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 634
 Db 122 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 181

QY 635 STLTLTKDEYERNSTCEATHKTSPIVKSFNNE 671
 Db 182 STLTLTKDEYERNSTCEATHKTSPIVKSFNNE 218

RESULT 14
 S16112
 Ig kappa chain V region (G2a) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16112
 R:Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
 Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
 A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
 A:Reference number: S16112; MUID:92000313; PMID:1910583
 A:Accession: S16112
 A:Molecule type: protein
 A:Status: preliminary
 A:Residues: 1-219 <BIT>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-95/Domain: immunoglobulin homology <INW>

Query Match 25.7%; Score 903.5; DB 2; Length 219;
 Best Local Similarity 81.6%; Pred. No. 3.8e+40;
 Matches 177; Conservative 14; Mismatches 21; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVVSAGDRVTITCKASQSV-----SNDVAVQKPGQSPKLLISYSSRYA 514
 Db 2 VVMTQPTSLVPSLGDQASISCRSSQSVHTNGNTVLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 515 GVPDRFSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGGTKLEIKRAADAAPTVS 574
 Db 62 GVPDRFSGSGYGTDFLTIKSRVEAEDLVGYVFCQSHVPTFGGGTKLEIKRAADAAPTVS 121

QY 575 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 634
 Db 122 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 181

QY 635 STLTLTKDEYERNSTCEATHKTSPIVKSFNNE 671
 Db 182 STLTLTKDEYERNSTCEATHKTSPIVKSFNNE 218

RESULT 15
 G2MS11
 Ig gamma-2b chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 Submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific mAb
 A:Reference number: S25057
 A:Accession: S25057
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-474 <FIS>
 A:Cross-references: EMBL:X67210; NID:G54826; PID:CAA47649.1; PID:G54827
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from ne
 A:Reference number: A02157; MUID:80120716; PMID:6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A:Note: the sequence was determined from the germline gene
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heav
 A:Reference number: A26235; MUID:80081501; PMID:117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 A:Note: Lys-474 is probably removed posttranslationally
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
 A:Reference number: A26232; MUID:80081502; PMID:117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
 R:Ollio, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
 A:Reference number: A26233; MUID:82173203; PMID:6803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359; PMID:7512967
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.

C;Genetics: 138/1: 236/1: 258/1: 368/1
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a trimeric complex. In some cases, such as IgG and IgE, the subunits associate into a dimeric complex.
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 900.5; DB 1: Length 474;
Best Local Similarity 35.4%; Pred. No. 1.4e-39;
Matches 238; Conservative 55; Mismatches 130; Indels 249; Gaps 17;

QY 1 EVLOQSGPDLVKGASVYKISKAGSYFTGYMHVWQSPGKLEWIGRINPNNGVLY 60
DB 20 EVLOQSGPDLVKGASVYKISKAGSYFTGYMHVWQSPGKLEWIGRINPNNGVLY 60
QY 61 NQKFKDQKATLVDRKSTTAYMELSLSEDSAVVYCARSTWITNVVD---YWGQTSVT 117
DB 80 NEKFKGKATLVDRKSTTAYMELSLSEDSAVVYCARSTWITNVVD---YWGQTSVT 117
QY 118 VSSAKTTTPSVPLAPGAAQTNSMVTGLCLVKGYPFPPVTVTWNSGSLSGVHTF-PAV 176
DB 135 VSAKTTTPSVPLAPGCGDTGSSVTSGCLVKGYPFPPVTVTWNSGSLSGVHTF-PAV 176
QY 177 LOSDLITLSSSVTPSSVTPSETVTCNVAPASSTKDKIVPRDSDGSPSEKSEINE-- 234
DB 195 LOSGLYTWSSSVTPSSVTPSETVTCNVAPASSTKDKIVPRDSDGSPSEKSEINE-- 234
QY 235 --KDLRK--KSELQGTALGNLQVYVNSKAITSSKSAQDLNTLLFKGFFTGHPWYN 290
DB 249 PKCKZKCPANLEG---GPSVFIPPNIKV--- 277
QY 291 DLLVDLGSTAAATSEYEGSSVDLYGAYGYQACAGTTPNKACMYGGVTLHDNRLTEKKV 350
DB 278 -LMTSL---TP--- 284
QY 351 PINLWIDGKQTVPIDKVTKSKKEVTVQELDLQARVHLHKGFLYNSDSFGKVGQRLIV 410
DB 285 -----KVTCVVVD-----VSEDDPQVQISWFVNN-----VE 310
QY 411 FHSSEGSTVSYDLFDAQQYPTLLRIYRDNMTTSSLSLSLYLYTTSIWMQTPTSL 470
DB 311 VHTAQTHREDY-----NSTIRVVS----- 331
QY 471 VSAGRVITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTFT 530
DB 332 -----T 332
QY 531 LTISVQAEADAAYVFCODYNSPPTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASV 590
DB 333 LPIQHODWMSKEFKCKVNNKDLSPERTISKLGVRAPQVILPPEAEQLSRKDVSL 392
QY 591 VCFNNFYPKDVNWKIDGSRQNV-----GVLSNWTDDQSDKSTYSMSPTLTLDKDEYE 645
DB 393 TCLVVGFPNGDISVEWTSNGHTTEENYKDTAPVLDSE-----DGSYFIYKLNKMTKWE 445
QY 646 RHNSYTCETHK 657
DB 446 KIDSFSQNVNRE 457

RESULT 16
S38865
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001

C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
Submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an antibody gene into a heterotetramer.
A;Reference number: S38865
A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.5%; Score 896.5; DB 2: Length 219;
Best Local Similarity 80.2%; Pred. No. 8.7e-40;
Matches 174; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

QY 460 IYMTQPTSLVAGDRVITCKASQSV-----SNDVAVYQKPGQPKLLISYTSRYA 514
DB 2 LVMTQSPFLSVSLGDAQISCRSSQSLVHTNGNTVYLHWYLOKPLSPKLLIYVSNRFS 61
QY 515 GVPDRFSGSGYGTFTLTITSSVQAEADAAYVFCODYNSPPTFGGTTKLEIKRADAAPTYS 574
DB 62 GVPDRFSGSGYGTFTLTITSSVQAEADAAYVFCODYNSPPTFGGTTKLEIKRADAAPTYS 574
QY 575 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSRQNVLSNWTDDQSDKSTYSMS 634
DB 122 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSRQNVLSNWTDDQSDKSTYSMS 181
QY 635 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRE 671
DB 182 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRE 671

RESULT 17
JC5810
monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
A;Accession: JC5810
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.; Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: JC5810
A;Molecule type: protein
A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase activity. It is directed against a porphyrin
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-94/Domain: immunoglobulin homology <IM>

Query Match 25.3%; Score 892; DB 2: Length 218;
Best Local Similarity 79.7%; Pred. No. 1.5e-39;
Matches 173; Conservative 12; Mismatches 28; Indels 4; Gaps 1;

QY 459 SIYMTQPTSLVAGDRVITCKASQSVND---VAVYQKPGQPKLLISYTSRYA 514
DB 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIMHWYQKPGQPKLLISLASNLES 60
QY 515 GVPDRFSGSGYGTFTLTITSSVQAEADAAYVFCODYNSPPTFGGTTKLEIKRADAAPTYS 574
DB 61 GVPDRFSGSGYGTFTLTITSSVQAEADAAYVFCODYNSPPTFGGTTKLEIKRADAAPTYS 574
QY 575 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSRQNVLSNWTDDQSDKSTYSMS 634
DB 121 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSRQNVLSNWTDDQSDKSTYSMS 180
QY 635 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRE 671
DB 181 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRE 671

RESULT 18

S49220

IG gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R:Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:D237502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A:Experimental source: strain Balb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 25.3%; Score 890.5; DB 2; Length 221;
Best Local Similarity 77.4%; Pred. No. 1.8e-39;
Matches 171; Conservative 20; Mismatches 29; Indels 1; Gaps 1;
QY 1 EVOLQSGDPLVKPGASVKISCKASYFTGYMHVWKQSPGKLEWIGRIINPNNGVTLY 60
DB 1 QVQLKESGAEIVKSGASVXLSTPAGFNKIDYMHVKORPEQGLEWIGRIDPANGEIKY 60
QY 61 NQKFKDKATLVDSKSTTAYMELRLTSDSAVYICARSTMTNYYMDYWGQTSVTYSS 120
DB 61 DPRFQGTATITADTSTNTAYLQLSLTSDTAVYICVRGYSQSPQEPYWGQGTTLTVSS 119
QY 121 AKTPPSVPLAPGSAATNSMTLCLVKGYPPEPTVTNNSGLSSGVHTFPAVLQSD 180
DB 120 AKTPPSVPLAPGSAATNSMTLCLVKGYPPEPTVTNNSGLSSGVHTFPAVLQSD 179
QY 181 LYTLLSSSVTPSWTSEITVCNVAHPASSTKVDKKIVPRD 221
DB 180 LYTLLSSSVTPSWTSEITVCNVAHPASSTKVDKKIVPRD 220

RESULT 19

S42772
IG kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:9414143; PIDN:CAA53226.1; PID:9414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 25.2%; Score 886.5; DB 2; Length 217;
Best Local Similarity 79.6%; Pred. No. 2.8e-39;
Matches 172; Conservative 14; Mismatches 25; Indels 5; Gaps 1;
QY 461 VMTQTPTSLVSGAGDRVTITCKASQSV-----SNDVAVYQOKPGQSPKLLISYTSRYAG 515
DB 1 VMTQSPSLFSLVSLGDAQSISCRSSQSLVHNGNTYLHWYLRQPGQSPKLLYKVSITRPSG 60
QY 516 VDRFSGSGVGTFTLTITSSVQAEADAAYFCQDYNPPTFGGKLEIKRAADAAPTYSI 575
DB 61 VDRFSGSGSGTFTFKISRVEAEDLGIVFCSQSTVPTFTFGSGTKLEIKRAADAAPTYSI 120
QY 576 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 635

Db 121 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 180

QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 671

Db 181 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRGE 216

RESULT 20

S68241
IG kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:9473962; PIDN:BAA06141.1; PID:9473963
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'N', 3-212 <TAM>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 25.0%; Score 880; DB 2; Length 218;
Best Local Similarity 78.7%; Pred. No. 6.2e-39;
Matches 170; Conservative 13; Mismatches 29; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGAGDRVTITCKASQSVND----VAVYQOKPGQSPKLLISYTSRYAG 515

Db 2 LVLTQSPASLAVSLGQRTATISCRASKSVASGVYIMHWYQOKPGQSPKLLISLATNLESG 61

QY 516 VDRFSGSGVGTFTLTITSSVQAEADAAYFCQDYNPPTFGGKLEIKRAADAAPTYSI 575

Db 62 VPARFSGSGSGTFTLNIHPVEBEDVATYYCQHSRELPLTFGAGTKLEIKRAADAAPTYSI 121

QY 576 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 635

Db 122 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 181

QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 671

Db 182 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRGE 217

RESULT 21

S25058
IG kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S25058
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25058
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <FIS>
A:Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:38-111/Domain: immunoglobulin homology <IMM>

```
Query Match      24.9%; Score 878.5; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 8.1e-39;
Matches 171; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSIISLYLTTISVMTQTPTSLVSGADRVITCKASQSVNDVAVYQKQSPKLLISY 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 ISASVIRSGQVLVLCSPAIMASASPEKVTWTCSSASSVSK-MQWYQKSGTSPKRWYD 71

QY 509 TSSRYAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRAD 568
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 TSKLASGVPRFSGSGSYSLTSSAEADAATYICQWSSNPLTFGAGTKLEIKRAD 131

QY 569 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 628
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 191

QY 629 SNYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 STYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 234

RESULT 22
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JUR>
F:120-225/Domain: C region #status predicted <COR>

Query Match      24.9%; Score 876.5; DB 2; Length 225;
Best Local Similarity 76.4%; Pred. No. 9.8e-39;
Matches 168; Conservative 21; Mismatches 26; Indels 5; Gaps 1;

QY 457 TTSIVMTQTPTSLVSGADRVITCKASQSVND-----VAVYQKQSPKLLISYTS 511
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 SSDVLMTQIPSLPVSLGDAQASICRSCQNIHVHSTGNTYLEWYLQKQSPNLLIYKISN 64

QY 512 RVAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAA 571
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 RFGVPDRFSGSGGTDFTLSISRVEADLGVYCFQSHVWTFGGQTKLEIKRADAA 124

QY 572 TVSIFFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKSTY 631
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 TVSIFFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKSTY 184

QY 632 SMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 SMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 224

RESULT 23
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
```

```
R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody di
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBL:X56394; NID:G51622; PIDN:CAA319805.1; PID:G51623
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>
```

```
Query Match      24.8%; Score 875; DB 2; Length 234;
Best Local Similarity 78.8%; Pred. No. 1.2e-38;
Matches 167; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSGADRVITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 IKMTQSPSSMYASLGERVTVTCKASQDINSYLSIQKPKSPKTLIYRGNLAVGVPGR 81

QY 520 FSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAAPTVSIFPPS 579
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 FSGSGGQDYSLTSSLEVEDGVYCYLAYDEPPTFGGQTKLEIKRADAAPTVSIFPPS 141

QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 639
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 201

QY 640 TKDEYERHNSYTCEATHKTSTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 TKDEYERHNSYTCEATHKTSTSPIVKSFNNE 233
```

```
RESULT 24
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed as
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DE1>
A:Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
```

```
Query Match      24.8%; Score 874; DB 2; Length 234;
Best Local Similarity 74.9%; Pred. No. 1.4e-38;
Matches 167; Conservative 24; Mismatches 28; Indels 4; Gaps 1;

QY 453 LYLTYT-----SIWMTQTPTSLVSGADRVITCKASQSVNDVAVYQKQSPKLLISY 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LLLWLTDARCDIQMTQSPASLSVSGESVTITCRASENIYSLAWYQKQKSPQLLVVY 70

QY 509 TSSRYAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRAD 568
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 ATKLVDPSPRFGSGSGYQYSLKINSLOSEDFGSYCFQFWDPTPTFGSGTKLEMKRAD 130

QY 569 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 628
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 190

QY 629 STYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 STYSMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNNE 233
```



```

RESULT 27
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeltdt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
J. Biol. Chem. 270, 6628-6638, 1995
A:Title: Recombinant antibodies in bioactive peptide design.
A:Reference number: A56169; MUID:95204454; PMID:7896802
A:Accession: A56169
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-210 <MON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.3%; Score 857; DB 2; Length 210;
Best Local Similarity 79.4%; Pred. No. 9.1e-38;
Matches 166; Conservative 13; Mismatches 26; Indels 4; Gaps 1;

Qy 460 IVMTQTPTSLVAGDRVTITCKASQVND----VAMTQQKPGSPKLLISYTSRYAG 515
Db 2 IVLTQSPASLTSLGQRATISCRASXSVSSGYSYMHWTQQKPGPPKVLIIASNLMSG 61

Qy 516 VPRFSGSGYGTFTLTIISSVQAEADAAVFCQDYNSTPTFGGTYKLEIKRADAAPTYSI 575
Db 62 VPRFSGSGSGTDTLTNIHPVEEDAATYCYQHSRELPTFGGTRLEIKRADAAPTYSI 121

Qy 576 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNSTDQDSKDSYSSMS 635
Db 122 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNSTDQDSKDSYSSMS 181

Qy 636 TLTLTKDEYERHNSYCEATHKTSTSPIV 664
Db 182 TLTLTKDEYERHNSYCEATHKTSTSPIV 210

RESULT 28
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of V3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 853; DB 2; Length 240;
Best Local Similarity 69.6%; Pred. No. 1.7e-37;
Matches 165; Conservative 31; Mismatches 31; Indels 10; Gaps 2;

Qy 445 SSTSLSISLYIT---SIWMTQTPTSLVAGDRVTITCKASQV-----SNDVAVY 494
Db 3 SQTQVLSMLLLISGTCGDFWMTQSPSSSLAVSAGETVTINCKSSQSLFVSGNKNYLAWY 62

Qy 495 QOKPGOSPILLISYTSRYAGVDPDRSGSGYGTDTFTLTIISSVQAEADAAVFCQDYNSTP 554
Db 63 QOKPGOSPILLIYASSTQSGVDPDRIGSGSGTDTFTLTIISSVQAEADAIYICLYETPY 122

Qy 555 TFGGGTYKLEIKRADAAPTYSIIFPPSSEQLTSGASVVCFLNFPKIDINVKWKIDGSRQ 614

```

QY 62 QKPKKATLTVDKSSTAYWELASLTSSESAVYICARSTMITNYVMDYWGQSTSVTVSSA 121
 Db 62 DTWKGRTISDRPNKNTLFLQMTSLSESDTAMVYICARSWLLP---FDYWGQSTTVTVSSA 118
 QY 122 KTTTPPSVYPLAPGSAAGTSMVTLGCLVKGYFPEPVTVTWNSGSLSSGSHVHTFPVAVLQSDL 181
 Db 119 KTTTPPSVYPLAPGCGDTTGSSTVTLGCLVKGYFPEPVTVTWNSGSLSSGSHVHTFPVAVLQSL 178
 QY 182 YTLSSSVTVPSSTWPSSTVTCNVAPASSTKVDKK 216
 Db 179 YTMSSSVTVPSSTWPSSTVTCNVAPASSTKVDKK 213
 RESULT 31
 PC4155
 Ig gamma-2b chain V-C region Mabb23 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
 C:Accession: PC4155
 R:Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
 Gene 169, 237-239, 1996
 A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
 A:Reference number: PC4155; MUID:96194809; PMID:8647454
 A:Accession: PC4155
 A:Molecule type: mRNA
 A:Residues: 1-231 <KWA>
 A:Cross-references: GB:U28970; NID:G1262180; PIDN:AA052489.1; PID:G1262181
 A:Note: This protein has unusual amino acid compared with the conserved sequences of mou
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:1-231/Product: heavy chain #status predicted <Mat>
 F:98-102/Region: unique D sequence
 F:103-119/Region: V region
 F:119-203/Domain: immunoglobulin homology <IMM>
 Query Match 20.3%; Score 715; DB 2; Length 231;
 Best Local Similarity 60.9%; Pred. No. 2.3e-30;
 Matches 137; Conservative 29; Mismatches 55; Indels 4; Gaps 2;
 QY 1 EVOLQSGDPLVKGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
 Db 1 EVOLVESGGLVAPQSLSITCTVSGFSLTDYGVSWIRQPPGKGLWGLVIWA-GGSITF 59
 QY 61 NQKFKKATLTVDKSSTAYWELASLTSSESAVYICARSTMITNYVMDYWGQSTSVTVSS 120
 Db 60 NSALKSRSLNSKNSKQVFLKMSLHTDITAMYYCVKHEHDYDFVWAGATTVTVSS 119
 QY 121 AKTTPPSVYPLAPGSAAGTSMVTLGCLVKGYFPEPVTVTWNSGSLSSGSHVHTFPVAVLQSD 180
 Db 120 AKTTPPSVYPLAPGCGDTTGSSTVTLGCLVKGYFPEPVTVTWNSGSLSSGSHVHTFPVAVLQSG 179
 QY 181 YTLSSSVTVPSSTWPSSTVTCNVAPASSTKVDKXIVPRDSGCP 225
 Db 180 LYTMSSSVTVPSSTWPSSTVTCNVAPASSTKVDKXIVPRDSGCP 221
 RESULT 32
 JE0244
 Ig kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0244
 R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
 A:Reference number: JE0243
 A:Accession: JE0244
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>
 Query Match 19.9%; Score 702.5; DB 2; Length 215;

Best Local Similarity 62.1%; Pred. No. 9.3e-30;
 Matches 133; Conservative 36; Mismatches 42; Indels 3; Gaps 2;
 QY 460 IVMTQTTSLLVSGADRVTTTCASQSVNDVAMVYQKPGSKLLISYTSRYAGVPDR 519
 Db 2 VVLTSQSPATLVSFGERATLSCASQSVHNLAWYQKPGAPRLLIYRATKATGIPAR 61
 QY 520 FSGSGYGTDFTLTISSVQAEADAAVYFCQDYNS--PTFGGKTLEIKRAAAPTYSIFP 577
 Db 62 FSGSGGTDFLTISSVQAEADAAVYFCQDYNS--PTFGGKTLEIKRAAAPTYSIFP 577
 QY 578 PSSEQLTSGGASVYVFLNNFYPKDINVKWIDGSRQNGVNLNWTDDSDKDYSSSTL 637
 Db 121 PSDEQLASGTASVVCLLNFFYPREKQVQVMDNALQSGNSQESVTEQDSKDYSSSTL 180
 QY 638 TLTDEYERHNSYTCEATHKTSTSPIVKSFRNE 671
 Db 181 TLTADYERHNSYTCEATHKTSTSPIVKSFRNE 671
 RESULT 33
 S04845
 Ig heavy chain precursor - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
 C:Accession: S04845; S05695
 R:Amemiya, C.T.; Haire, R.N.; Litman, G.W.
 Nucleic Acids Res. 17, 5388, 1989
 A:Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
 A:Reference number: S04845; MUID:89345103; PMID:2503814
 A:Accession: S04845
 A:Molecule type: mRNA
 A:Residues: 1-549 <AME>
 A:Cross-references: EMBL:X15114
 R:Litman, G.W.
 submitted to the EMBL Data Library, April 1989
 A:Reference number: S05695
 A:Accession: S05695
 A:Molecule type: mRNA
 A:Residues: 'LC', 3-308, 'H', 310-549 <LIT>
 A:Cross-references: EMBL:X15114; NID:G64799; PID:G763031
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotrimer; immunoglobulin
 F:26-109/Domain: immunoglobulin homology <IMM>
 F:281,294/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 19.9%; Score 700.5; DB 2; Length 549;
 Best Local Similarity 28.0%; Pred. No. 3.8e-29;
 Matches 194; Conservative 107; Mismatches 214; Indels 179; Gaps 23;
 QY 1 EVOLQSGDPLVKGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
 Db 12 DIELVQPSSEIKSPGESIKUSCKTSGTFTNYLHWLQQVPGKGLWIGRIPGADTDY 71
 QY 61 NQKFKKATLTVDKSSTAYWELASLTSSESAVYICARSTMITNYVMDYWGQSTSVTVSS 120
 Db 72 SSSVQGRCHISTDNPQSTTFLQNLNKLVEDTAIYICAREGV--GVYFDYWGQGTMTVTS 129
 QY 121 AKTTPPSVYPLAP--GSAATNSMTVTLGCLVKGYFPEPVTVTWNSGSLSSGSHVHTFPVAVL- 177
 Db 130 ATLHAPSVPFPLPCGSSS--SDSHVTTCGLSTGLPAPVDVKNWNSGSHITGLKNFPVAVLQ 188
 QY 178 QSLDYTLSSSVTVPSSTWPS--ETVTCNVAPASSTKVDKXIVPRDSGSGPSEINEKD 236
 Db 189 QSGFPASSQQTFLPSDWKAKSECEVHKPTSTKTKIECODEPEIEPTVEL--- 244
 QY 237 LRKSEIQGTALGNLQIYYNKAITSSEKSAADQFTNTLLFKGFTGHPWINDLLVDL 296
 Db 245 -----LQ----- 247
 QY 297 GSTAATSEYSGSSVDLYGAYYQACAGTGNKTKACMYGGVTLHDNRLTEBKVPINLWI 356
 Db 248 -----PCASSKVELLCITGYA-----PSEIKVHLL 275

QY 357 DGKOTTVPIDKVTSKKE-----VTVQELDLQARHYLHGKFGLYNS-DSFGGKVQR 406
Db 276 NGQVTNISPNSKPKCKENGTFSSRSKVSFKPKD-----WNSEDSYTCKVTH 322
QY 407 GLIVFHS-SEGSTVSYDLFDQAQQPDTLLRIYRDNNTTISSTLSLSLYLTTSI-VMTQ 464
Db 323 P--ASHTKTEASTKKC-----DETAI-----TPKDVLPP 350
QY 465 TPTSLYSAGDRVTITCKASQSVSDNVANVQOKPGQSPKLLIYSTSRYAGVDPRSGSG 524
Db 351 SPKDLLVT--KEAKVYCVISRMASDTDLTVQWSSSDGKKAL-----AFDSAPEKAYDGT 402
QY 525 YGTDFTLTITISSVOAEDAAVFCQ---QDVNSPPTFGGKTLEIKRAD---AAPTVSIFPP 578
Db 403 FTVKSTLKISPGDWENKKQFNCKVVHEDLSP-----IEKSICKSQDPGTETFIILLPP 456
QY 579 SSEOLTGGGASVVCFLNFYPMKINVKWKIDGERQGVNLNSWTD-QDSKDSYSTMSSTL 637
Db 457 SDDELRLDFSLICMLKNFRPDQIVYFWFKDGVTLEEDYYMNTTPVLEEEEGFISPSKL 516
QY 638 TLTKDYERHNSYTCETHATKTSTSPIVKSFNRE 671
Db 517 TIARSDMWGATGYSCIAAHNTISQDIKK-NRGK 549

RESULT 34
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C/Accession: JE0242
R:Alim, M.A.; Yanaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis. Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMV>

Query Match 19.7%; Score 695.5; DB 2; Length 215;
Best Local Similarity 63.1%; Pred. No. 2.2e-29;
Matches 135; Conservative 33; Mismatches 44; Indels 3; Gaps 3;

QY 460 IVMTQTPTSLLVAGDRVTITCKASQSVND-VAWYQOKPGQSPKLLIYSTSRYAGVDP 518
Db 2 IVLTQSPGTLSPGERATISCRASQSVSNVLAHWYQOKPGQAPSLLIYDASSRATGIPD 61
QY 519 RFGSGVGTDFTLTISVQAEAAVFCCQDYNPP-TFGGGTKLEIKRAADAAPTVISIPP 577
Db 62 RFGSGSGTDFTILTISGLEPEDFAVYCOO-YDRPPWTFGQGTKVEIKRTVAAPSVEIPP 120
QY 578 PSSEQLTSGASVVCFNNFYPMKIDGSRQGVNLNSWTDQDSKDSYSTMSSTL 637
Db 121 PSDEQLKSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTLSSTL 180
QY 638 TLTKDYERHNSYTCETHATKTSTSPIVKSFNRE 671
Db 181 TLSKADYEKHVYACEVTHQGLSPVTKSFNRGE 214

RESULT 35
B31790
Ig heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C/Accession: B31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:title: Preliminary crystallographic data, primary sequence, and binding data for an an
A:Reference number: A92686; MUID:89034213; PMID:3182835

A:Accession: B31790
A:Molecule type: mRNA
A:Residues: 1-254 <SCH>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>

Query Match 19.4%; Score 683.5; DB 2; Length 254;
Best Local Similarity 63.18%; Pred. No. 1.1e-28;
Matches 146; Conservative 22; Mismatches 48; Indels 13; Gaps 8;

Qy 1 EVQLQQSGDPLVKKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRIENPENGVTLY 60
Db 1 EVQLVESGDDLKPKGSLKLSCAASGFSFSSVCMGSMWRQTPDKLEWVATISNGGGITYY 60

Qy 61 NQKFKDKATLIVDKSSSTAYMELRSLTSEDSVAYYCARSTMITNYVMDYWGQGTSTVTS 120
Db 61 PDSVKGREFTISRDAKNTLYLQMSSLKSEDSAMYTCARRERYDENGFAFWGQGTLLTVSA 120

Qy 121 AKTTPEPSVYPLAP--GSAAQNTSMVTLCLCKLVKGYPEPVTV--TW---NSGSISSG-VHT 172
Db 121 AKTTAPSVYPLAPVPCVCGXDDTGGSSVTLCLCKLVKGYPEPVTLTWXXXNSGSISSGXVHT 180

Qy 173 PPAVLQS--DIYTLSSSVTVPS--TWP-SETVT-CNVAHPASSTKVDDK 216
Db 181 PPAVLQSXXDLTYLSSSVTVTSSTWXPXSQISITCNVAHPASSTKVDDK 229

RESULT 36

Ig kappa chain N1G93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; Tazaki, T.; et al. A new subgroup of k type light chains (VKV) identified in cases of AL amyloidosis. J Biol Chem 271:1241-1246 (1996)
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amyloidosis. J Biol Chem 271:1241-1246 (1996)
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:16-90/Domain: immunoglobulin homology <IMM>

Query Match 19.3%; Score 679.5; DB 2; Length 215;
Best Local Similarity 61.0%; Pred. No. 1.4e-28;
Matches 130; Conservative 33; Mismatches 49; Indels 1; Gaps 1;

Qy 460 IVMTQTPTSLVSGADRVITICKASQSVNSDVAVTQQKPGQPKLLISVTSRYAGVDP 519
Db 2 IVMTQSPATLSVSPGERATLSCRASQSVATNVVYMKLGQAPRLIYDASTRATGP 61

Qy 520 FSGSGYGTDFLTITSSVQAEDAAVFECCDYNRPPTFGGKTLEIKRAD-AAPTVSIFFP 578
Db 62 FSGSGSTFTLTISLQSEDAFYIYCHNNAWPPTFGGKIVETKRRTVAAAPSVIFPP 121

Qy 579 SSEQLTSGASVWCFNLNFPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSLT 638
Db 122 SDEQLKGTASVWCLLNFPYFREAQVQKVDNALQSGNSQESVTEQDSKDSVYLSLT 181

Qy 639 LTKDEYERHNSYTCETHKTSTSPVKSFRNE 671
Db 182 LSKADYBKHYACEVTHQGLSSPVTKSFRNGE 214

RESULT 37

Ig kappa chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S33161
R:Foley, R.C.; Beh, K.J.; et al. The structure of the sheep IgG heavy chain variable region. J Biol Chem 268:1241-1246 (1993)
A:Description: The structure of the sheep IgG heavy chain variable region. J Biol Chem 268:1241-1246 (1993)
A:Reference number: S33161
A:Accession: S33161
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
P:16-90/Domain: immunoglobulin homology <IMM>

A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: S33161
A;Accession: S33161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <POL>
A;Cross-references: EMBL:X54110; NID:G237103; PIDN:CAA38046.1; PID:gl364221
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>

Query Match 19.2%; Score 675; DB 2; Length 230;
Best Local Similarity 59.4%; Pred. No. 2.7e-28;
Matches 126; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVDPDR 519
DB 18 IQVTSFSSLSASLTERVSTICTSQSVSNLYLNWYQKQSPKLLIYATRLHTDVPDR 77

QY 520 FSGSGYGTDTLTISVQAEADAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTIVIFPPS 579
DB 78 FSGSGGTDTLTISLEANDATYICLVSTPLAFGGGTNVEIKRSDAQSPVLFKPS 137

QY 580 SEQLTGGASVWFLNFPYKDNVWKIDGSRQNGVNSWTDQDSKDYMSSTLTTL 639
DB 138 EEQLRTGTVSWCLVNDVFPKDNVVKVGVDTQNSFNQSFQNSFTDQDSKDYSLSTLT 197

QY 640 TKDEYEHNSYTCETHATKSTSTPIKVSFNRNE 671
DB 198 SSSEYQSHNAYACEVSHKSLPTALVKSPKNE 229

RESULT 38
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;338/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 673.5; DB 2; Length 470;
Best Local Similarity 28.1%; Pred. No. 7.9e-28;
Matches 187; Conservative 78; Mismatches 161; Indels 239; Gaps 18;

QY 1 EVQLQQSGPDIVKPGASVKISKASGYSTGYMHVWYQKQSPKLLIGRINPNNGVTLY 60
DB 20 QVQRESGPSLVKPSQILSTCTVSGFSLSYALTWRQAPGKALEHWGGIT-SGGTTY 78
QY 61 NQKFDKATLTVDKSTSTAYMELSLTSEDSAVYICARST---MITNYMDVWGQGTSTV 117

DB 79 NPALKSRSLITKNSKQSVLSVSVTPEDATYYCARSTYGEVGDGAIDAWGQGLVLT 138
QY 118 VSSAKTTPSPVYPLAPGSAQTNSMTLGLCLVKGYFPEPVTTWNSGSLSSSGVHTPEAVL 177
DB 139 VSSASTTAPKVPYFLSSCCGDKSSSTVTGLCVSYNPEPVTTWNSGALKSGVHTPEAVL 198
QY 178 QSD-LYTLSSSVTPSPSTPESETVNCNVAHPASSTKYDKKIVPRDGGPSEKSEINEKD 236
DB 199 QSSGLYSLSSMVTVPST-SGQFTCNVAHPASSTKYDKKIVPRDGGPSEKSEINEKD 248
QY 237 LRKXSELOGTALGNLKOIYYNSKAITSEKSAQDLTNTLLFKGFTTGHWPWNLVLDL 296
DB 249 CCPPPELPGG---PSVFIFPPKP-----KDTLT---ISGTFEVTCTVVVDV 287
QY 297 GSTAATSEYEGSSVDLYGAYYGYQCAGGTENKATACMYGVTLHDNNRLTEKKVPIINLWI 356
DB 288 G-----HD-----DPEVKFSWFV 300

QY 357 DGKO---TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFH 412
DB 301 DDVEVNTATTKPREQNFSTYRV-VSALRIQHDWTGK-----EFKCKVH----- 345

QY 413 SSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLYTT-SIVMTQTPTSLNS 472
DB 346 -NEG-----LPAPIVR-----TISRT----- 360

QY 473 AGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLT 532
DB 361 -----KGPAREPQ----- 368

QY 533 ISSVQAEADAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTIVIFPPSSEOLTSGGASVVC 592
DB 369 -----VYVLAPQELSKSYSLTC 388

QY 593 FLNNFYPKDINVKWKIDGSRQNGVNSWTDQDSKDYMSSTLTTLTKDEYEHNSYTC 652
DB 389 MVTGFPDYIAVQNRNGQPESEDKYGTTPQLDADSSYFLYSLKLRVDRNSWQEGDTYTC 448

QY 653 BATHK 657
DB 449 VVWHE 453

RESULT 39
S29593
Ig kappa chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S29593
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29593
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-197 <SEY>
A;Cross-references: EMBL:X57856; NID:G52588; PIDN:CAA40991.1; PID:G52589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 18.8%; Score 663.5; DB 2; Length 197;
Best Local Similarity 72.9%; Pred. No. 8.7e-28;
Matches 132; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVAGDRVTITCKASQSV---SND---VAWYQKQKQSPKLLISYTSRYA 514
DB 17 IVMTQAAPSIPTFGESASISCRSKSLHNSGTYLYWFLQRFQSPQLLIYKSNLAS 76

QY 515 GVPDRFSGSGYGTDTLTISVQAEADAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTIV 574
DB 77 GVPDRFSGSGGTSTLTISRVEAEDVGFYFCMQHLEYPTFGGTTKLEIKRADAAPTIV 136

QY 575 IPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSDKSTYSMS 634
Db 137 IPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSDKSTYSMS 196

QY 635 S 635
Db 197 S 197

RESULT 40
S69131
Ig heavy chain (DOR) - human (fragment)
N:Alternate names: anti-riboflavin IgG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppani, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; PMID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOR) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.8%; Score 661.5; DB 2; Length 241;
Best Local Similarity 59.4%; Pred. No. 1.4e-27;
Matches 130; Conservative 35; Mismatches 51; Indels 3; Gaps 3;

QY 1 EYQLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPKGLGWIGRINENNGVTLY 60
Db 1 QVQLVQSGVERKVPGRASVRIKCKASGYAFENYIHWVRQAPGLGLEWMGIFNPVAG-AVS 59

QY 61 NQKFKDKATLVKDSSTTAYMELSLTSEDSAVYCAR-STMTNYVMYDYGQGTSTVTS 119
Db 60 SEKFRDLVMSDTSANTVSMQLRLRSDDTGRYFCARVSYDFSGYGMVWGQGTIVTS 119

QY 120 SAKTTPPSVPLAPGSAQTSMWTLGCLVKGYPPEVPTVWNSGSLSGVHTFAVLQS 179
Db 120 SASTKGPSVPLAPGSRSTSTALGCLVLDYDPEVPTVWNSGALTSVGVHTFAVLQS 179

QY 180 D-LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKI 217
Db 180 SGLYSLSSVTVPPSSNFGTYTCNVDEKPSNTKVDTV 218

RESULT 41
A23746
Ig kappa chain V-III (KAP cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Gniso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAP, a monoclonal immunoglobulin
A:Reference number: A23746; PMID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 18.7%; Score 659.5; DB 2; Length 215;
Best Local Similarity 62.0%; Pred. No. 1.6e-27;
Matches 132; Conservative 31; Mismatches 49; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITCKASQSV-SNDVAWYQKPGQSPKLLISYTSRYAGVPD 518

Db 2 IVTQSPATLSLSPGERATLISGGASQSVSNYLAWYQKFGQAPRLLIYDASSRATGIPD 61
QY 519 RFGSGSGTDTLTITISSVQAEDAAYFCQODYNSPPTFGGCTKLEIKRAAAPTSTFPP 578
Db 62 RFGSGSGTDTLTITISLPEDEFVYGYQYGSPLTFGGCTKVEIKRTVAAPSVFPP 121

QY 579 SSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSDKSTYSMSSTLT 638
Db 122 SDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLT 181

QY 639 LTKDEYERHNSYTCEATHTKTSTPIVKSENRNE 671
Db 182 LSKADYEKKHYAGETHQGLSSPVTKSFNRGE 214

RESULT 42
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 18.7%; Score 658; DB 2; Length 216;
Best Local Similarity 60.8%; Pred. No. 1.9e-27;
Matches 131; Conservative 30; Mismatches 49; Indels 6; Gaps 3;

QY 460 IVMTQTPTSLVSGADRVITCKASQSV-SNDVAWYQKPGQSPKLLISYTSRYAG 515
Db 2 IVLTQSPDFLAFLSLGERATINCKSSQVLYNSKNFLAWYQKFGQ-PKLLI-WANVRESG 59

QY 516 VPRFRSGSGVGTDTLTITISSVQAEDAAYFCQODYNSPPTFGGCTKLEIKRAAAPTSTI 575
Db 60 VPRFRSGSGVGTDTLTITISNLQALVAVYCCQYYSTPYSGQGRLEIKRTVAAPSVFI 119

QY 576 FPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSDKSTYSMS 635
Db 120 FPPSDEQLKSGTASVVGLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLS 179

QY 636 TLTLTKDEYERHNSYTCEATHTKTSTPIVKSENRNE 671
Db 180 TLTLTKADYEKKHYACEVTHQGLSSPVTKSFNRGE 215

RESULT 43
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459
A:Accession: S31459
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <PAT>
A:Cross-references: EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 17.6%; Score 619.5; DB 2; Length 472;
Best Local Similarity 25.7%; Pred. No. 4.9e-25;

Matches	172;	Conservative	83;	Mismatches	170;	Indels	*245;	Gaps	15;
QY	1	EVQLQSGPD	LKPKGASV	KISKASGY	STGYTMHW	KSPGKLE	IGWIRIN	PNNGVILY	60
DB	18	QVRLQSGF	SLATLLQ	TLSVCTC	TISGFLS	NNYGVDM	VRQAPG	KALEFWL	GGSGYD
QY	61	NQKFKDK	KATLTV	DKSFTT	AYMELR	LSLTSD	SAVYTC	ABSTMLTN	VM----
DB	77	NPVLKSR	LGITKDT	SKSVSL	TLSTVT	TEDTAV	YCARVD	YDSSHAP	AVASVDF
QY	116	VTYSSAK	TPPSVY	PLAPGSA	AAQTMV	TLGLCV	KGYFPE	PTVTWNS	GSLSGV
DB	137	ISVLSAT	TPPKYV	PLTSCG	DTSSSIV	TLGCLV	SSYMP	PEPTVTW	NSGALTS
QY	176	VLOSD-	LYTLSS	VTPSS	TWSTP	ETVTC	VAHPAS	TKVDK	IVPRDS
DB	197	ILOSSG	LYLSSV	TVTPAS	TSGAQT	ICNVAH	PASSTK	VDKRV	EP--SCP
QY	235	KDLRK	KSELQ	TALGNL	KQIYYN	SKAIT	SSKSAD	QFLTN	TLKPKG
DB	245	DPCKH	CRCP	PPPEL	PGGPSV	FI	PPKP	-----	KDILT
QY	295	DLGSA	TAA	TSYEG	SSVDLY	GAYYGY	QCAG	TPNKTAC	MYGGVTL
DB	288	DVGG	-----	-----	-----	-----	-----	-----	-----
QY	355	WIDGK	QTTP	IDKVT	SKKEV	-----	-----	-----	-----
DB	301	FVD	-----	-----	-----	-----	-----	-----	-----
QY	408	LIVFH	SEGS	TVSYD	LFDQA	QGYPT	LLRIYR	DNTTIS	TSLSIS
DB	350	AL	-----	-----	-----	-----	-----	-----	-----
QY	468	SLLSV	AGDR	VTIT	CKASQ	SVNDV	AWYQ	KGPSP	KLLISY
DB	364	-----	-----	-----	-----	-----	-----	-----	-----
QY	528	DFTLT	ISSVQ	AEDA	AAVYF	COQDYN	SPPTF	GGTLEI	KRADAA
DB	369	-----	-----	-----	-----	-----	-----	-----	-----
QY	588	ASVVC	FNNY	PKDIN	VKKID	SERQ	NGVLN	SWTD	QSKD
DB	386	LSVT	CLVT	GFPDY	IAVEW	KQNGP	ESDKY	GTTSQ	LADG
QY	648	NSYT	CEATH	K	657	-----	-----	-----	-----
DB	446	DTYAC	VNHE	455	-----	-----	-----	-----	-----
RESULT	44								
A49444	Ig gamma-1 heavy chain (New) - human (fragment)								
C:Species	Homo sapiens (man)								
C:Date	03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999								
C:Accession	A49444								
R:Saul, F.A.; Poljak, R.J.									
Proteins	14, 363-371, 1992								
A:Title	Crystal structure of human immunoglobulin fragment								
A:Reference	number: A49444; PMID:93066153; PMID:1438175								
A:Accession	A49444								
A>Status	preliminary								
A:Molecule	type: protein								
A:Residues	1-220 <SAU>								
A>Note	sequence modified after extraction from NCBI backbone								
A:Note	this sequence report includes corrections based on crystal structure refinement								
C:Superfamily	immunoglobulin C region; immunoglobulin homology								
C:Keywords	immunoglobulin								
F:137-202	Domain: immunoglobulin homology <IM>								
Query Match	17.3%; Score 611; DB 2; Length 220;								
Best Local Similarity	54.3%; Pred. No. 5.2e-25;								

Matches	120;	Conservative	36;	Mismatches	61;	Indels	4;	Gaps	3;
---------	------	--------------	-----	------------	-----	--------	----	------	----

QY	1	EYLOQSGPDLVKPGASVKISKASGYFTGYVYHWMVKQSPKGLEWIGRINPNNGVTLY	60
Db	1	QVQLFQSGPGLVPRPQTLSLCTVSGTSTFDYDYYWTVRQPPGRGLEWIGYVF-YTGITLL	59
QY	61	NQKFKDKATLTVDKSGSTAYMELRLSTEDSAVYVCARSTMITNYVMWYWGQGSVTVSS	120
Db	60	DPSLRGRVTMLVNTSKQFSLRLSSVTAAADVYCARNLIAAG--IDWQGGSLVTVSS	117
QY	121	AKTTPEPVYPLAPGSAATNSMVTLGCLVKGYFPEPPTVTWNSGSLSSGVHTFPAVLQSD	180
Db	118	ASTKGPSVFPLAPSKSKISGGTAALGCLVKDYFPEPVTIVSNNSGALTSGVHTFPAVLQSS	177
QY	181	-LYTLSSSVTVPSSTWPGSETVTCNVAHPASSTKVDKKIIVPR	220
Db	178	GLYSLSSVTVPSSSILGTQTYCNVNHKPSNTKVDKVEPK	218

RESULT	45
A33953	enterotoxin D precursor - Staphylococcus aureus
C:	Species: Staphylococcus aureus
C:	Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
C:	Accession: A33953
R:	Bayles, K.W.; Iandolo, J.J.
J.	Bacteriol. 171, 4799-4806, 1989
A:	Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
A:	Reference number: A33953; MUID:89359112; PMID:2549000
A:	Accession: A33953
A:	Status: preliminary
A:	Molecule type: DNA
A:	Residues: 1-258 <BAY>
A:	Cross-references: GB:M28521; NID:91492109; PIDN:AA806195.1; PID:g758691
C:	Superfamily: enterotoxin B

Query Match	17.3%;	Score	611;	DB	2;	Length	258;		
Best Local Similarity	51.1%;	Pred. No.	6.4e-25;						
Matches	118;	Conservative	35;	Mismatches	78;	Indels	0;	Gaps	0;

QY	226	SEKSEINEKDLKKSELOGTALGNLKQIYYVNSKAITSEKSADQFLNTLLPKGFTG	285
Db	26	NEMIDSVKELKKSELSSTALNNKHSYADKNPIIGENKSTGQDFLENTLLYKKFTD	85
QY	286	HPWYNDLLVDLSTAATSEVGSSVDLYGAVYGYQCAGTPNKTCMTGGVTLHDNNELT	345
Db	86	LINFEDLLINFNSKEWAQHFKSNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLK	145
QY	346	EKKVPINLMIDGQTTVIDIKVTSKKEVTVOELDQARHYLNGFGLYNSDSGGKQV	405
Db	146	ERKKIPINLWINGQVEVSLDKVQTDKNVTVOELDAQARRYLOKDLKLYNNDTLGGKIQ	205
QY	406	RGILVPHSSSGSVSYDLDPACQVPTLLRIYRDNTTISSTSLISLYL	456
Db	206	RGKIEFDSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTISTEHLHDIYLY	256

RESULT	46
SI4683	Ig mu chain precursor, membrane-bound (clone 201) - human
C:	Species: Homo sapiens (man)
C:	Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:	Accession: SI4683; S08047
R:	Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
J.	Nucleic Acids Res. 18, 4278, 1990
A:	Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:	Reference number: SI4683; MUID:90332450; PMID:2115996
A:	Accession: SI4683
A:	Molecule type: mRNA
A:	Residues: 1-627 <FRI>
A:	Cross-references: EMBL:X17115; NID:933450; PIDN:CAA34971.1; PID:g33451
C:	Superfamily: immunoglobulin C region; immunoglobulin homology
C:	Keywords: immunoglobulin; membrane protein

QY 637 LTLTKDEYERHNSYTCEATHKTSPIVKSFNRE 671
 Db 195 LSLTKAQYNSHVSIVTCEVH-NSGSAIVQSFNRGD 228

RESULT 49
 S29594
 Ig gamma chain (MM65) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S29594
 R:Seymour, R.
 submitted to the EMBL Data Library, February 1991

A:Reference number: S29593
 A:Accession: S29594
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-178 <SEY>
 A:Cross-references: EMBL:X57857; NID:G52590; PIDN:CAA40992.1; PID:G52591
 C:Keywords: immunoglobulin

Query Match 16.0%; Score 562; DB 2; Length 178;
 Best Local Similarity 73.5%; Pred. No. 1.4e-22;
 Matches 108; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVQLQSGDPLVPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
 Db 14 EVQLQSGDPLVPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 73

QY 61 NQKFKDKATLTVDKSSITAYMELRLSTSDSAVYCARSTMIINVMYDYGQGTSTVSS 120
 Db 74 DPXFGKATLTVDKSSITAYMELRLSTSDSAVYCARSTMIINVMYDYGQGTSTVSS 131

QY 121 AKTTPPSVYPLAPGSAQTNSMTLGC 147
 Db 132 AKTTPPSVYPLAPGSAQTNSMTLGC 158

RESULT 50
 I54782
 gene Pvt-1a/Ig-Ck protein - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Sep-2000
 C:Accession: I54782
 R:Huppi, K.; Siwarski, D.
 Int. J. Cancer 59, 848-851, 1994

A:Title: Chimeric transcripts with an open reading frame are generated as a result of tr
 A:Reference number: I54782; MUID:95080867; PMID:7989128
 A:Accession: I54782
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-126 <RSS>
 A:Cross-references: GB:S76258; NID:G913277; PIDN:AAB32752.1; PID:G913278
 C:Genetics:
 A:Gene: Pvt-1a/Ig-Ck
 C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 15.9%; Score 561; DB 2; Length 126;
 Best Local Similarity 93.0%; Pred. No. 1e-22;
 Matches 107; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 557 GGGTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSRQNG 616
 Db 11 GAAAKVKSINADAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPRDINVKWKIDGSRQNG 70

QY 617 VLNSWTDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNRE 671
 Db 71 VLNSWTDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNRE 125

RESULT 51
 PL0011
 Ig heavy chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: PL0011
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: PL0011; MUID:88142863; PMID:3125424
 A:Accession: PL0011
 A:Molecule type: mRNA
 A:Residues: 1-151 <CHE>
 A:Experimental source: cell line 4C11
 A:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMV>
 F:50-54/Region: complementarity-determining 1
 F:69-85/Region: complementarity-determining 2
 F:118-125/Region: complementarity-determining 3
 F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 15.9%; Score 560.5; DB 2; Length 151;
 Best Local Similarity 80.3%; Pred. No. 1.3e-22;
 Matches 110; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

QY 1 EVQLQSGDPLVPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
 Db 20 EVQLQSGDPLVPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 79

QY 61 NQKFKDKATLTVDKSSITAYMELRLSTSDSAVYCARSTMIINVMYDYGQGTSTV 117
 Db 80 NEKFKDKATLTVDKSSITAYMELRLSTSDSAVYCARSTMIINVMYDYGQGTSTV 133

QY 118 VSSAKTTPPSVYPLAPG 134
 Db 134 VSSAKTTPPSVYPLAPG 150

RESULT 52
 G1M5
 Ig gamma-1 chain C region, secreted form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence_revision 24-Sep-1981 #text_change 16-Jul-1999
 C:Accession: A02159; A26234; A26236
 R:Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.; I
 Cell 18, 559-568, 1979

A:Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain g
 A:Reference number: A02159; MUID:80045036; PMID:115593
 A:Accession: A02159
 A:Molecule type: DNA
 A:Residues: 1-324 <HON>
 A:Cross-references: GB:J00453
 A:Notes: the sequence was determined from the germline gene
 A:Note: Lys-324 is removed posttranslationally
 R:Obata, M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kataoka, T.; Shimizu, A.; Mano, Y.; Sei
 Gene 9, 87-97, 1980

A:Title: Immunoglobulin gamma-1 heavy chain gene: structural gene sequences cloned in a
 A:Reference number: A26234; MUID:80202559; PMID:6769752
 A:Accession: MOPC 31C
 A:Cross-references: A26234
 A:Molecule type: mRNA
 A:Residues: 76-324 <ORA>
 A:Cross-references: GB:V00775; NID:G51652; PIDN:CAA24153.1; PID:G51653
 R:Rogers, J.; Clarke, P.; Salser, W.
 Nucleic Acids Res. 6, 3305-3321, 1979

A:Title: Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain.
 A:Reference number: A26236; MUID:80012837; PMID:113776
 A:Accession: MOPC 21
 A:Molecule type: mRNA
 A:Residues: 170-275, 'D', 277, 'D', 279-322 <ROG>
 A:Cross-references: GB:V00795; NID:G51830; PIDN:CAA24176.1; PID:G780265

R:Adetugbo, K.
J. Biol. Chem. 253, 6068-6075, 1978
A:Title: Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma 9
A:Reference number: A26237; MUID:78242288; PMID:98524
A:Contents: annotation; MOPC 21
A:Note: this is the final paper in a series reporting the protein sequence, the disulfide
A:Note: there are a number of differences from the sequence shown
C:Genetics:
A:Introns: 1/1; 98/1; 111/1; 218/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; Glycoprotein; heterotetramer; immunoglob
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-110/Region: hinge
F:131-200/Domain: immunoglobulin homology <IM2>
F:237-304/Domain: immunoglobulin homology <IM3>
F:27-82,138,198,244-302/Disulfide bonds: #status experimental
F:102/Disulfide bonds: interchain (to light chain) #status experimental
F:104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:174/Binding site: carbohydrate (Asn) (covalent) #status experimental

```

Query Match      15.8%; Score 557; DB 1; Length 324;
Best Local Similarity 28.3%; Pred. No. 5.3e-22;
Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTTSSVYPLAPGSAAGTNSMTLGLVKGYPPEVTWNSGSLSSGVHTFPAVLQSD 180
DB 1 AKTTTSSVYPLAPGSAAGTNSMTLGLVKGYPPEVTWNSGSLSSGVHTFPAVLQSD 60
QY 181 LYTLLSSVTPBSPSTWPCVTCNVAHPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK 240
DB 61 LYTLLSSVTPBSPSTWPCVTCNVAHPASSTKVDKIVPRDCG----- 103
QY 241 SELQGTALGNLQKIYYNNSKAITSSSEKSAQDLTNTLLFKGFTGHPWYNLLVDLGSTA 300
DB 104 CKPCICTVPEVSSVFIPEPK-----PKDVLITL----- 132
QY 301 ATSEYEGSVLDLYGAYGYQCAGGTPNTKACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360
DB 133 -----TP-KVTCVVDIS-----KDDPEVQFSWFVD--- 157
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
DB 158 -DVEVHTAQTPREQFNSTFRVSSELPIMHODWLNGKEFKCRVNSAAPAPIEK----- 211
QY 412 HSSEGSTVSYDLFDAQGGYPTDLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLIV 471
DB 212 -----TISK----- 216
QY 472 SAGDRVTITCKASQSVSNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGDTFTL 531
DB 217 ----- 216
QY 532 TISSVQAEADAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGASVV 591
DB 217 -----KGRKAPQVYTIIPPKQMAKDKVSLT 243
QY 592 CFLNNFYKDNVKKIDGSERON-----GVLNSWTDDSDKSTYSMSSTLTITKDYER 646
DB 244 CMITDFPEDITVENQWNGQPAENYKNTQPMNT-----NGSYFVYSKLVQKSNWEA 296
QY 647 HNSYTCEATHK 657
DB 297 GNTFTCSVLHE 307

```

RESULT 53
GIMSM
Ig gamma-1 chain C region, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: B02159; A02160; B02158

R:Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.; K
Cell 18, 559-568, 1979
A:Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma chain g
A:Reference number: A02159; MUID:80045036; PMID:115593
A:Accession: B02159
A:Molecule type: DNA
A:Residues: 1-393 <HON>
A:Cross-references: GB:J00453
A:Note: the sequence was determined from the germline gene
R:Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
A:Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmem
A:Reference number: A02160; MUID:82197626; PMID:6804950
A:Accession: A02160
A:Molecule type: mRNA
A:Residues: 323-393 <TYL>
R:Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
Cell 26, 19-27, 1981
A:Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma c
A:Reference number: A02158; MUID:82115295; PMID:6799207
A:Accession: B02158
A:Molecule type: DNA
A:Residues: 323-366 <ROG>
A:Note: this sequence is the translation of the first exon of the M segment
C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
n code membrane-bound chains in that it contains an alternative 3' end, encoded in separ
C:Genetics:
A:Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; Glycoprotein; heterotetramer; immunoglob
F:131-200/Domain: immunoglobulin homology <IM>
F:340-357/Domain: transmembrane #status predicted <TYM>
F:358-393/Domain: intracellular #status predicted <INT>
F:174,278/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match      15.8%; Score 557; DB 1; Length 393;
Best Local Similarity 28.3%; Pred. No. 6.8e-22;
Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTTSSVYPLAPGSAAGTNSMTLGLVKGYPPEVTWNSGSLSSGVHTFPAVLQSD 180
DB 1 AKTTTSSVYPLAPGSAAGTNSMTLGLVKGYPPEVTWNSGSLSSGVHTFPAVLQSD 60
QY 181 LYTLLSSVTPBSPSTWPCVTCNVAHPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK 240
DB 61 LYTLLSSVTPBSPSTWPCVTCNVAHPASSTKVDKIVPRDCG----- 103
QY 241 SELQGTALGNLQKIYYNNSKAITSSSEKSAQDLTNTLLFKGFTGHPWYNLLVDLGSTA 300
DB 104 CKPCICTVPEVSSVFIPEPK-----PKDVLITL----- 132
QY 301 ATSEYEGSVLDLYGAYGYQCAGGTPNTKACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360
DB 133 -----TP-KVTCVVDIS-----KDDPEVQFSWFVD--- 157
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
DB 158 -DVEVHTAQTPREQFNSTFRVSSELPIMHODWLNGKEFKCRVNSAAPAPIEK----- 211
QY 412 HSSEGSTVSYDLFDAQGGYPTDLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLIV 471
DB 212 -----TISK----- 216
QY 472 SAGDRVTITCKASQSVSNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGDTFTL 531
DB 217 ----- 216
QY 532 TISSVQAEADAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGASVV 591
DB 217 -----KGRKAPQVYTIIPPKQMAKDKVSLT 243

```

QY 592 CFLNPFYKPDINVKWKIDGSRQN-----GVLSNWDQSDKSDTYSMSSTLTTLTKDEYER 646
 Db 244 CWITDFPEDITVEMQWQNPENKNTQPMNT-----NGSYFVYKLVNPKNSWNEA 296
 QY 647 HNSYTCETHK 657
 Db 297 GNTFTCSVLHE 307

RESULT 54
 KIMS
 Ig kappa chain C region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Dec-1980 #sequence_revision 17-Dec-1982 #text_change 16-Aug-1996
 C:Accession: B90262; A90778; B93736; A92322; A93748; A02119
 R:Swasti, J.; Milstein, C.
 Biochem. J. 128, 427-444, 1972
 A:Title: The complete amino acid sequence of a mouse kappa light chain.
 A:Reference number: A90262; MUID:73053310; PMID:4638343
 A:Contents: myeloma protein MOPC 21
 A:Accession: B90262
 A:Molecule type: protein
 A:Residues: 1-52, 'BSBTZWB', 60-106 <SVA>
 R:Swasti, J.; Milstein, C.
 Biochem. J. 126, 837-850, 1972
 A:Title: The disulphide bridges of a mouse immunoglobulin G1 protein.
 A:Reference number: A90259; MUID:73008899; PMID:5073237
 A:Contents: annotation; MOPC 21, disulfide bonds
 A:Note: Cys-106 is involved in a light-heavy chain bond
 R:Hamlyn, P.H.; Brownlee, G.G.; Cheng, C.C.; Gait, M.J.; Milstein, C.
 Cell 15, 1067-1075, 1978
 A:Title: Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA
 A:Reference number: A90778; MUID:75084137; PMID:103625
 A:Accession: A90778
 A:Molecule type: mRNA
 A:Residues: 1-106 <HAM>
 R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.
 Nucleic Acids Res. 9, 4485-4494, 1981
 A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxy method
 A:Reference number: A93736; MUID:82059477; PMID:6170937
 A:Contents: MOPC 21
 A:Accession: A92322
 A:Molecule type: DNA
 A:Residues: 1-106 <HA2>
 R:Max, E.E.; Maizel Jr., J.V.; Leder, P.
 J. Biol. Chem. 256, 5116-5120, 1981
 A:Title: The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa gene
 A:Reference number: A92322; MUID:81191915; PMID:6262318
 A:Accession: A92322
 A:Molecule type: DNA
 A:Residues: 1-106 <MAX>
 R:Altanburg, W.; Neumaier, P.S.; Steinmetz, M.; Zachau, H.G.
 Nucleic Acids Res. 9, 971-981, 1981
 A:Title: DNA sequence of the constant gene region of the mouse immunoglobulin kappa chain
 A:Reference number: A93748; MUID:81198949; PMID:6785724
 A:Accession: A93748
 A:Molecule type: DNA
 A:Residues: 1-106 <ALT>
 A:Note: The sequence was determined from the germline gene
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) and two heavy (lambda) chains held together by disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimer
 F:26-86/Disulfide bonds: #status experimental

Query Match 15.8%; Score 556; DB 1; Length 106;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-22;
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 ADAAPTYSIFPPSSQELTSGASVVCFLNNFYPKIDNVKWKIDGSRQNGVLSNWDQSDS 626
 Db 1 ADAAPTYSIFPPSSQELTSGASVVCFLNNFYPKIDNVKWKIDGSRQNGVLSNWDQSDS 60

QY 627 KDSYMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSERNNE 671
 Db 61 KDSYMSSTLTTLTKDEYERHNSYTCETHKTSPIVKSERNNE 105

RESULT 55
 A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
 C:Accession: A56446
 R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
 J. Biol. Chem. 270, 7829-7835, 1995
 A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the native protein.
 A:Reference number: A56446; MUID:95229583; PMID:7713873
 A:Accession: A56446
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-268 <TAN>
 A:Cross-references: GB:U20617
 C:Keywords: heterotrimer; immunoglobulin

Query Match 15.8%; Score 556; DB 2; Length 268;
 Best Local Similarity 26.7%; Pred. NO. 4.7e-22;
 Matches 152; Conservative 36; Mismatches 55; Indels 326; Gaps 9;

QY 1 EVQLQQSGPDLVKGASVKISCKASGYSTFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 Db 3 QVQLQESGAEIVKPGASVKLSCTTSQFNIDYTHWVKQRPQGLEWIGRIANGITKY 62

QY 61 NQKPKRATLTVDKSTTAYMEIRLSLTSDESAVYCARSTMTINMYDYGQSTSTVSS 120
 Db 63 DPKEQGRATTAADTSNTAYLSLTSDESAVYCA-SYLLTRY-ENYWGQSTTVTS- 119

QY 121 AKTTPSVYPLAPSAQAQTNSMTVLTGLCVKGYPEPTVTWNSGSLSSGVHTFPAVLQSD 180
 Db 120 ----- 119

QY 181 LYTLLSSVTVPSTWPTETVCNVAHPASTKVDKKIVPRDSGGSPSEKSEINEKDLRKK 240
 Db 120 -----SGG----- 122

QY 241 SELQALGNLKKIYYNKAITSSEKSAQFLNTLLPKGFTGHPWYNDLLVDLGSTA 300
 Db 123 ----- 122

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMGVGLHDNNRLTEKRVPINLWIDGKQ 360
 Db 123 -----GG----- 127

QY 361 TTPIDKVKTSKEVTVOELDQARHLYHKGFLYNSDSFGKVGQGLIVFHSSEGSTVS 420
 Db 128 -----GDSGG----- 135

QY 421 VDLFDAQGYPTLLRIYRDNTTISSTLSISLYLTTISIVMTQTPSTLLVSAGDRTIT 480
 Db 136 -----DIETQSPAIMSASLGEKVTMS 157

QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDPDFSGSGYGTDFLTITSSVQAE 540
 Db 158 CRASSV-NFIWYQKSDASPKLWVYTSHPGVPARFSGSGSGNSYSLTISSEMED 216

QY 541 AAVYFCQDYNPPTFGGTTKLEIKEDA 569
 Db 217 AATYCCQPTSPPTFGSGTKLEIKRSAA 245

RESULT 56
 PS0017
 Ig gamma-1 chain C region - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999

C;Accession: PS0017; C25941
R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MUID:89232738; PMID:3149946
A;Accession: PS0017
A;Molecule type: DNA
A;Residues: 1-326 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: C25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 220-326 <BR3>
C;Genetics:
A;Introns: 98/1; 113/1; 220/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>

Query Match	15.6%	Score 550;	DB 2;	Length 326;
Best Local Similarity	27.7%;	Pred. No. 1.2e-21;		
Matches 150;	Conservative	64;	Mismatches 90;	Indels 238; Gaps 14;
QY	121	AKTTPPVVYPLAPGSAACQTSMTV	LGCLVKGYPPEPVTWNSGSLSGVHTP	PAVLQSD 180
DB	1	AETAPSVYPLAFCGTALKSNMTV	LGCLVKGYPPEPVTWNSGALSGVHTP	PAVLQSG 60
QY	181	LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDK	KIIVPRDSGSGSEKSEBEINEK	DLRKK 240
DB	61	LYTLSSSVTPSPSTWPSQVTCNVAHPASSTKVDK	KIIVPRNCGGDCPC	----- 109
QY	241	SELQGTALGNLKOIYYVNSKAITSSSEKSAQDLTNTLL	FKGFFTGHPWYNDLLVDL	LGSTA 300
DB	110	-----ICITSEVSS-----	VFIFPKPDVL	----- 130
QY	301	ATSEYEGSSVDLYGAYGYOCAGTGNKTKACMYGGVTL	HDNNRLTEBKYPINLWDG--	358
DB	131	-----TITL-----	TP-KVTCVVVDIS-----	QDDPEVHFSEFVDVE 162
QY	359	---KQTPVPIDKVKTSKEVTVQELDIQARHYLHGKFLY	NSDSFGGKVQRGVLIVHSS	E 415
DB	163	VHTAQTRPPEQFNSTFR--SVSELPIHQLDNLGR--	-----	196
QY	416	GSTVSYDLPDAQOQYPTLLRIYRDNTTISSTLSLSLYL	TYTTSIVMTQFTSLLVSAGD	475
DB	197	-----	-----	196
QY	476	RVITTCASQSVSNDVAVYQKPGQPKLLISYTSSRYAGV	PDFRFGSGYGTDFTLTISS	535
DB	197	--TFRCVK--	-----	TSAAPPSPIENTISK 217
QY	536	VOAEDAARYFCQDYNSPPTFGGQTKLEIKRAADAAPT	VSIFPPSSRLQSLSGGASVVCFLN	595
DB	218	PE-----	GRQV-----	PHVYTMSTFKEMTQNEVSIICMVK 249
QY	596	NFYPKDINVKWKIDGERQNGVUNSWTDOGSKDSYMS	SMSTLTPLTKDEXEVRHNSYTCEAT	655
DB	250	GFYPPIIYVEWQMGQFOEN-YKNTPTTMDT-DGSYFL	YSKLNKVKKEKMQQGNFTTCSVL	307
QY	656	HK 657		
DB	308	HE 309		

```

RESULT 57
IG gamma-2a chain C region - rat
PS0019
CISpecies: Rattus norvegicus (Norway rat)
CDate: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
CAccession: PS0019; D25941

```

R:Brueggemann, M.
Gene 74, 473-482, 1988
A>Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A:Reference number: P50017; MUID:89232738; PMID:3149946
A:Accession: P50019
A:Molecule type: DNA
A:Molecule residues: 1-322 <BRU>
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A>Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397; PMID:3016742
A:Accession: D25941
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 216-322 <BR2>
C:Genetics:
A:Introns: 98/1; 109/1; 216/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-84/Domain: immunoglobulin homology <IMM>

```

Query Match      15.3%; Score 539; DB 2; Length 322;
Best Local Similarity 28.2%; Pred. No. 4.5e-21;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15

QY      121 AKTTPEPVVPLAPSAAGTNSMWTGCLVKGYGPPEPVTWNSGSLSSGVHIFPAVLQSD 180
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1 AETTPSVVPLAPGTALKSNMWTGCLVKGYGPPEPVTWNSGALLSGVHIFPAVLQSG 60

QY      181 LYTLASSVTVPSSWTWPSETVTCNVAHFASSTKVDKIIVPRDSGGPSEKSEEINEKDRLKK 240
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      61 LYTLTSSVTVPSSWTWSQAUTCNVAHFASSTKVDKIIVPREC----- 102

QY      241 SELOQTALGNLKYIYYNSKAITSSEKSADQFLTNTLLFKGFPTHFWNDLIIVDLGSTA 300
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      103 -----NPGCGTGSEVSS-----VFIPPKTKDVL----- 126

QY      301 ATSEYEGSSVDLYGAYGYQCAGGTGNKTAACMGYVTLHDNNELTEEKVPINLMAIDG--- 358
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      127 -----TITL-----TP-KVTCVVVDISQND-----PEVRSWTFDDVE 158

QY      359 ---KQTVPIDKVTKTSKEVTVQELDLQARHYLHGKFGLYNDSFGKGQRGLIVFHSS 415
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      159 VHTAQTHAPEXQNSLTLR--SVSELPIVHRDWLNKGK-----TFCKKN----- 199

QY      416 GSTVSYDLFDQAQGYPDTLLRIYRDNTTISSLSLSLYTTSIVMTQPTSLIVSAGD 475
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      200 -----SGAFAPAI----- 207

QY      476 RVITICKASQSVNDVAWYOQKQGQPXKLILSYTSSRYAGVDPFRFSGSGYGDFTLTISS 535
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      208 -----EKSIS-----KPEGTPR----- 219

QY      536 VOAEADAAYVFCQDYNSPPTFGGQTKLEIKRADAAPTVSIFFPSGEOLTSGASVVVCFLN 595
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      220 -----GFQVYTMAPPEEMTQSQVSIICMVK 245

QY      596 NFYPKDIVNKWKIDGSBRONGVLNSWTDQDSKDSITYSMSSTLTLLFKDEYERNHSVTCAT 655
       |||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      246 GFYPDPIYTEWMNGQQQDEN-YKNTPTTMDT-DGSFYLYSKLVNKKETWQOQNTFTCSVL 303

QY      656 HK 657
       |
Db      304 HE 305

```

RESULT 58
S29690
IG heavy chain VDJ region - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C:Accession: S29690
R:Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.

C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:20-150/Product: Ig heavy chain V region #status predicted <MAT>
 F:20-117/Domain: variable region <VRG>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 15.0%; Score 527; DB 2; Length 150;
 Best Local Similarity 79.7%; Pred. No. 7.2e-21;
 Matches 106; Conservative 4; Mismatches 21; Indels 2; Gaps 1;
 QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 EVLQOQFGAELVKPGTSVKISKASGYIFTDYNMVKQSHGKSLWIGDIDPFDSSY 79
 QY 61 NQKFKDKATLTVDKSSITAYMELRLSITSDSAVYVCARSTMITNTVMYWGQGTSTVTVSS 120
 DB 80 NQKFKGKATLTVDKSSNTAYMELRLSITSDTAVYVCARGGF--PYGMDYWGQGTSTVTVSS 137
 QY 121 AKTTPPSVYPLAP 133
 DB 138 AKTTPPSVYPLAP 150

RESULT 62
 A46507
 Ig alpha chain - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
 C:Accession: A46507
 R:Mansikka, A.
 J. Immunol. 149, 855-861, 1992
 A:Title: Chicken IGA H chains. Implications concerning the evolution of H chain genes.
 A:Reference number: A46507; MUID:92340889; PMID:1634774
 A:Accession: A46507
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-585 <MAN>
 A:Cross-references: GB:S40610; NID:g251907; PID:g251908
 A>Note: sequence inconsistent with the nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBI:109906, NCBI:109907)
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 516.5; DB 2; Length 585;
 Best Local Similarity 24.4%; Pred. No. 1.4e-19;
 Matches 174; Conservative 99; Mismatches 228; Indels 211; Gaps 25;
 QY 2 VQLQOQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLYN 61
 DB 21 VTLDESGGLQTPGGALSLVKASGFTFSSYSMGMRQAPGKLEWVAGIDDDGSGTGYG 80
 QY 62 QKFKDKATLTVDKSSITAYMELRLSITSDSAVYVCARSTMITNVV--MDYWGQGTSTVTV 118
 DB 81 PAVQGRATISRDNGSGTVRLQNLNLRADTATYCAKASCGGACASIDAWHGTEVIV 140
 QY 119 SSAKTTPPSVYPLAPGSAQNTSMVTLGCLVKGYFPFPTVTVMNSGSL--SSGYHTFPFV 176
 DB 141 SSASASRPTLYQLPLPDCDPNVTGCLVTSFLPFPVTVTTCGAADATATVSLPVA 200
 QY 177 LQSDLYTLSSVTVPSSTWPSSTVTCNVAHFASSTKDKIVPRDSGGPSEKSEINEKD 236
 DB 201 TTGGTYSLTALTVPRELQGNFVFCRAQHAATGADV-KETIGDGVCP-----CLVEGL 278
 QY 237 LRKXSELOGTALGNLQIYYNSKAITSSSEKADQFTNTLLFGFTGHPFWNDLLVDL 296
 DB 249 -----IFTSKVTLSSDPTQEDFERRVLV-----CLVEGL 278
 QY 297 GSTAATSEYEGSSVDLYGAYGYOCAGGTENKTA-----CMYGGVTLHDNRLTEKK 349
 DB 279 PSAGAAQWLQDNEM-----TPAPESDESGCDSTESGYTQMSRVNVTKRS- 325
 QY 350 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHLHGKFLGYNLSDSGFGGKVGRLI 409

Db 326 -----WEGGAQ-----FGCRVTHGAL 341
 QY 410 VHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNTTISSTLSISLYLYTTGIVMTQPTSL 469
 Db 342 --KEPTATVSTDC-DATPQ-----LQVSL-----LPPLLEEL 371
 QY 470 LVSGAGDRVTITCKASQSVND---VAVYQKQPOQSKPLIISYTSRYAGVDPDRFSGSYG 526
 Db 372 LVS--HNATVTCVVSNAADAGVSVWSRSSG--GLDVSQTEDRQA-----414
 QY 527 TDTLTLSISVCAEDAAVYFCQDQYNSPPTFGGKTLE-----IKRADA---APTVS 574
 Db 415 -DRYTVRSF-----LRVCAEENNGGETFGCSVRREGVVVAEESIRKETDTFLHAPSVY 467
 QY 575 IFFPSSEQLT-SGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQD-----625
 Db 468 VFPPEAELSLOETATLTCTWASSFLP-----SSILLTWTQQNPISPNQY 512
 QY 626 -----SKDST-YMSSTLTILTKDEYERHNSYCEATHK-TSTSPIVKSNRN 670
 Db 513 LIFPEKOGDFYSLYSKLVSVEDWQRGDVGVCVGHGDIPLNFIHKSIDKN 564

RESULT 63
 A49982
 Ig heavy chain V region (BA7.1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: A49982
 R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
 J. Biol. Chem. 269, 2805-2813, 1994
 A:Title: Topology of an amiloride-binding protein.
 A:Reference number: A49982; MUID:94132051; PMID:8300613
 A:Accession: A49982
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-120 <LIN>
 A:Cross-references: GB:I24802; NID:g452096; PIDN:AAA98740.1; PID:g452097
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 14.6%; Score 514; DB 2; Length 120;
 Best Local Similarity 81.7%; Pred. No. 2.6e-20;
 Matches 98; Conservative 6; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVLQOQSGPELVKPGASVKISKASGYSTGYIHWKQSHVKSLEWIGHISPYNGATTY 60
 QY 61 NQKFKDKATLTVDKSSITAYMELRLSITSDSAVYVCARSTMITNTVMYWGQGTSTVTVSS 120
 DB 61 NQKFKDTASLTVDKSSITAYMELRLSITSDSAVYVCARPNYCHYTMDYWGQGTSTVTVSS 120

RESULT 64
 A49633
 Ig lambda-like chain, V-C region - nurse shark
 C:Species: Ginglymostoma cirratum (nurse shark)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: A49633
 R:Greenberg, A.S.; Steiner, L.; Kasahara, M.; Flajnik, M.F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10603-10607, 1993
 A:Title: Isolation of a shark immunoglobulin light chain cDNA clone encoding a protein re
 A:Reference number: A49633; MUID:94068449; PMID:8248152
 A:Accession: A49633
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-238 <GRE>
 A:Experimental source: spleen
 A>Note: sequence extracted from NCBI backbone (NCBI:141012, NCBI:141013)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 14.6%; Score 513.5; DB 2; Length 238;
Best Local Similarity 48.6%; Pred. No. 6.4e-20;
Matches 105; Conservative 38; Mismatches 68; Indels 5; Gaps 3;

QY 460 IVMTQPTSLYSAGDRVITCKASQSYSDVAVYQKQSPKLLISVTSRYAGVDPDR 519
DB 22 INTQSPPLVSLVGLGTATITCTASQSYSDVAVYQKQSPKLLISVTSRYAGVDPDR 81

QY 520 FSGSGGTFTLTISVQAEAAVFCQDYNPSP---TFGGGTKEIKRAADAAPTVSIF 576
DB 82 FSGSGGTFTLTISVQAEAAVFCQDYNPSP---TFGGGTKEIKRAADAAPTVSIF 576

QY 577 PPSSEQL-TSGASVCFNFPYKIDINVKWIDSEKQNGVLSWTQDSDKSYNSVS 635
DB 142 PPSQDQVQTKGTATLVCLANHFYDPELVQWKKQGAVIDSGVQTS-NYLRSASDSTYSVSS 200

QY 636 TLTLTKDEYERHNSYCEATHKTSTSPVKSFNRE 671
DB 201 LTLTSGSDWESNARFSCALHTVLSPLSKSISRSE 236

RESULT 65
Ig heavy chain precursor V region (F6-3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0012
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0012
A:Molecule type: mRNA
A:Residues: 1-166 <CHE>
A:Experimental source: cell line F6-3
C:Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylch
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-151/Product: Ig heavy chain V region #status predicted <MAT>
F:47-130/Domain: immunoglobulin homology <IMM>
F:63-67/Region: complementarity-determining 1
F:82-96/Region: complementarity-determining 2
F:131-140/Region: complementarity-determining 3
F:152-166/Domain: C region (fragment) #status predicted <COR>

Query Match 14.5%; Score 510.5; DB 2; Length 166;
Best Local Similarity 73.9%; Pred. No. 5.9e-20;
Matches 99; Conservative 9; Mismatches 25; Indels 1; Gaps 1;

QY 1 EVOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 33 QVQLQSGPELVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 92

QY 61 NQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMTITNYMDYWGQTSVTSS 120
DB 93 KENFKGRATLTVDKSSSTAYMELRLSITSDSAVYICAREGGFGN-SLDYWGQTSVNVSS 151

QY 121 AKTTPPSVYPLAPG 134
DB 152 AKTTPPSVYPLAPG 165

RESULT 66
A27609
Ig heavy chain precursor V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988

A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A:Reference number: A27609; MUID:88154467; PMID:3126234
A:Accession: A27609
A:Molecule type: DNA
A:Residues: 1-139 <KLE>
A:Cross-references: EMBL:M19401; NID:G195441; PIDN:AAA38303.1; PID:G553392
C:Genetics:
A:Introns: 16/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 506; DB 2; Length 139;
Best Local Similarity 80.8%; Pred. No. 8e-20;
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVOLQSGPELVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 79

QY 61 NQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMTITNYMDYWGQTSVTSS 120
DB 80 NQKFKGRATLTVDKSSSTAYMELRLSITSDSAVYICARYSYAYMDYWGQTSVTSS 139

RESULT 67
137267
Ig heavy chain V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: 137267
R:Ruffi-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: 137267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 503; DB 2; Length 128;
Best Local Similarity 79.7%; Pred. No. 1e-19;
Matches 98; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 2 VOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLYN 61
DB 6 VOLQSGPELVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLYN 65

QY 62 QKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMTIT---NYMDYWGQTSVT 117
DB 66 QKFKGRATLTVDKSSSTAYMELRLSITSDSAVYICARGLTTVVAKSYFYDYWGQGTTLT 125

QY 118 VSS 120
DB 126 VSS 128

RESULT 68
PS0057
Ig heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: PS0057
R:Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy
A:Reference number: PS0057; MUID:89197817; PMID:2467902
A:Accession: PS0057

A:Molecule type: DNA
A:Residues: 1-135 <VAO>
A:Cross-references: GB:D00307; NID:9220448; PIDN:BA00213.1; PID:9220449
A>Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C:Comment: the gene encoding this protein was isolated from a hybridoma that produces an Ig heavy chain precursor V region; immunoglobulin homology
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-13/Domain: signal sequence #status predicted <SIG>
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 502; DB 2; Length 135;
Best Local Similarity 82.5%; Pred. No. 1.2e-19;
Matches 99; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

Qy 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLV 60
Db 20 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLV 79
Qy 61 NQKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSIVTVSS 120
Db 80 NQKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSIVTVSS 135

RESULT 69
A34891
Ig heavy chain precursor V region - ladyfish
C:Species: Elops saurus (ladyfish)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000
C:Accession: A34891
R:Amemiya, C.T.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990
A:Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and analysis
A:Reference number: A34891; MUID:90138916; PMID:2105490
A:Accession: A34891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <AME>
A:Cross-references: GB:M26182; NID:9213134; PIDN:AAA49338.1; PID:9213135
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495.5; DB 2; Length 568;
Best Local Similarity 22.8%; Pred. No. 1.6e-18;
Matches 159; Conservative 109; Mismatches 225; Indels 203; Gaps 24;

Qy 4 LQSQGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLVYK 63
Db 22 LQSQGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLVYK 81
Qy 64 FKDKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSIVTVSSAKT 123
Db 82 VKGRFTISRDNRSKQQLVLMNSLRADTAIVYCAR--VYGYAFDYWGRGTMVTVTGEQ 139
Qy 124 TPSPVYPLAPGSAQTSMVTLGCLVGVYFPEPTVTVWNSGLS--SGVHTFPVAVLQSDLY 182
Db 140 ASPVFPVLV--SCATSGYVTVGIGKGLYPLDSTFTFNSKSDTLDTLYLQPSVLSGCKY 197
Qy 183 TLSSSVTPSPSTWPTVTCNVHPASSTKVYDKXIVPRDGGPSEKSEINEKDLRKSE 242
Db 198 D-----RVSH-----ARTEGDFKSKAE 215
Qy 243 LQ-GTALGNLKIYYNSKATTSSE--KSADQFLNTLLPKGFTGHPWINDLLVLDLST 299
Db 216 FKCTTELGKK-----TPVVIKPEPPKPPKPPVLSIMT-----PSQFEITLN----- 258
Qy 300 AATSEYEGSSVDLYGAYGYOCAGGTENKTACMYGGVTLHDNNRLTECKKVPINLWI-DG 358
Db 259 -KTATFACLAIDFPKGHSEK-----WLRDG 283
Qy 359 KQTVPIDKVTISKETVTVGLD-QARHYLHGKGLVNSDFGKVGQRLIVFHSSEGST 418
Db 359 KQTVPIDKVTISKETVTVGLD-QARHYLHGKGLVNSDFGKVGQRLIVFHSSEGST 418

Db 284 KEVTDGIATLTCEQKK-----GDKSFTASSFLQASESQW 317
Qy 419 VSYD-----LFDAGQVDPDLRIYRDNMTTISSTLSISLYLVTTSIVMTQTPTSLVSA 473
Db 318 KRLDGTFTCFIQEGEITE-----QTVKYSSAECSPEAQIDAKISPTPEELFLQ- 367
Qy 474 GDRVLTICKASQSVS--NDVAV--YQORPGQ-----SPKLISYTSRYAGVPDRFSG 522
Db 368 -QRTLTICKITGDVGRNVTVWEGSEVRVGQDFEQRMISKLLIDYE----- 413
Qy 523 SGYGTDFTLTISVQAEDAAVYFCQDYNPPT-----FGGKTLEIKRADAAPT 573
Db 414 -----EMKNRTYCTCKVEHSDLPSPPLATSYRREGCKWQ-----SPTV 451
Qy 574 SIPEPSEQLTSGASVVCFLNNFYPKDINVKKIDGSEKQNGVLSWTDQDSKDTYSM 633
Db 452 FILAP-AEQNLSTVLICVAKDFYEPQLVLSLWDDQPVETDV--PTTEVVKTEGTSYV 508
Qy 634 SSTLTITKQBYEHRNSVTCETHKTSTSPVKSFN 669
Db 509 FSQLTIPASDWDGSGVYSCAVHETVWESVVKTI 544

RESULT 70
C37267
Ig heavy chain V region (Py69) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: C37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Giemney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495; DB 2; Length 128;
Best Local Similarity 77.2%; Pred. No. 2.7e-19;
Matches 95; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

Qy 2 VOLQSQGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLV 61
Db 6 VOLQSQGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLV 65
Qy 62 QKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCAR-----STMITNYMDYWGQTSVT 117
Db 65 QKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARPGYGNVYTVYFYDYGQGTTLT 125
Qy 118 VSS 120
Db 126 VSS 128

RESULT 71
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of a
A:Reference number: PS0023; MUID:89232725; PMID:3149944
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas

A:Accession: A32658
A:Molecule type: DNA
A:Residues: 1-330 <YAM>
A:Cross-references: GB:J00470
A:Note: the sequence was determined from the germline gene
R:Ollio, R.; Auffray, C.; Morchamps, C.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests t
A:Reference number: A32658; MUID:81223894; PMID:6787604
A:Accession: A32658
A:Molecule type: DNA
A:Residues: 1-330 <OLL>
A:Note: the sequence was determined from the germline gene
R:Lyse, J. Biochem. 43, 423-435, 1974
R:Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Biochem. 43, 423-435, 1974
A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-a
A:Reference number: A32659; MUID:74175517; PMID:4831970
A:Contents: annotation; myeloma protein MOPC 173
A:Note: this is one paper in a series reporting the sequence; for additional references, s
A:Note: this sequence differs from that shown at a number of positions
R:de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A:Title: Determination of the primary structure of a mouse gammaC2a immunoglobulin. Iden
A:Reference number: A32660; MUID:73056887; PMID:4565406
A:Contents: annotation; MOPC 173, disulfide bonds
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-113/Region: hinge
F:137-206/Domain: immunoglobulin homology <IM2>

R:Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin gene
A:Reference number: I57809; MUID:90097953; PMID:2513486
C:Accession: I57809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 373-399 <RES>
A:Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C:Comment: The sequence of residues 1-328 was assumed to be identical with the corresponding
C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous with
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:137-206/Domain: immunoglobulin homology <IMM>
F:346-363/Domain: transmembrane #status predicted <TM>
F:364-399/Domain: intracellular #status predicted <INT>
F:180/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 14.0%; Score 491.5; DB 1; Length 399;
Best Local Similarity 26.4%; Pred. No. 1.7e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;

QY 121 AKTTPSVYPLAPGSAATNSMTLGLVKGVEPEPVTVWNSGLSGVHTFPAVLQSD 180
Db 1 AKTAPSVYPLAPVCGDTTGSVTLGCLVKGVEPEPVTVWNSGLSGVHTFPAVLQSD 60

QY 181 LYTSSSVTPSPSTWSPSTCNVAHPASSTKVDKIVPRDSGGPSEKSEBINEKDLRKK 240
Db 61 LYTSSSVTPSTWSPSTCNVAHPASSTKVDKIEPR--GPTIKPCP----- 108

QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDFLNTLLFKGFFTHGHPYNDLLVDLGSTA 300
Db 109 ----- 108

QY 301 ATSEYEGSVDLGAYGYCAGGTENKTAQMGVGVTLHNNRLTEKKVPINLWIDGKQ 360
Db 109 -----PCKCPAPN-----LLGGPSVF----- 124

QY 361 TTVPIDKVKTSKKEVTVOELDQARHYLHGKGLYNSDSFGKQVQRLIVFHSSEGSTVS 420
Db 125 -----IPPKIKDVLMI---SLSPIT 143

QY 421 YDLFDAQOQYPTLLRIYRNDTITSSLSLSLYLTTSIVMTQTPFSLLSAGDRVIT 480
Db 144 CVVDVSEDDP-----VQISWFVNVEVHTAQOT----- 174

QY 481 CKASQSVSNDVAVYQKQPGQSPKLLISYTSRYAGVDFRFGSGYGTDFTLTSSVOAED 540
Db 175 -----HREDYNSTLRVV--- 186

QY 541 AAVYFCQDYNSPTFGGTTKLEIKRAD-----AAPTVISFPSPSSQLT 584
Db 187 SALPIQHODWVSGKEF-----CKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 242

QY 585 SGASVVCFLNFPKQINVAWKIDGGERQN-----GVLSNWTQDQSKDSTYSMSLTLL 639
Db 243 KKQVTLICWVDWPDIDYVETWNGKTELNKNTEPVLDS-----DGSYFMYSLRV 295

QY 640 TKDSYERHNSVTCATHK-TSTSPIVKSFNR 669
Db 296 EKNWVERNSYSCSVHEGLHNHHTTKSFSR 326

RESULT 74

S20639

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C:Accession: S20639
R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacti
A:Reference number: S20639
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-125 <LOS>
A:Cross-references: EMBL:X65004; NID:g52598; PIDN:CAA46137.1; PID:g52599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 13.9%; Score 489.5; DB 2; Length 125;
Best Local Similarity 76.0%; Pred. No. 5e-19;
Matches 95; Conservative 8; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60

QY 61 NQFKDKATLTVDKSTTAYMELSLTSDSAVYCARSTMITNYV-----MDYWGQG 113
Db 61 NEKFKGKATLTDSKSSSTAYMELSLTSDSAVYCARXRVNYYVLRSSLYAMDYWGQ 120

QY 114 TSVTV 118
Db 121 TSVTV 125

RESULT 75

S41394

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C:Accession: S41394

R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.

submitted to the EMBL Data Library, January 1994

A:Description: Structural characterization of an (NZB X NZW)F1 mouse-derived Igm anti-DNP

A:Reference number: S41393

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <MAR>

A:Cross-references: EMBL:229586; NID:g452354; PIDN:CAA82703.1; PID:g1334080

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 13.9%; Score 488; DB 2; Length 120;
Best Local Similarity 76.7%; Pred. No. 5.7e-19;
Matches 92; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVLOQSGAELVKPGASVKLSCKASGYTFTSYMHVWKQPGQGLEWIGEIDPSDSYTY 60

QY 61 NQFKDKATLTVDKSTTAYMELSLTSDSAVYCARSTMITNYVMDYWGQTSVTYSS 120
Db 61 NQFKGKATLTVDKSSSTAYMQLTSDSAVYCARRYGSRVSMYWGQTSVTYSS 120

Search completed: August 12, 2004, 13:33:05

Job time : 27.2583 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: August 12, 2004, 13:22:49 ; Search time 14.7627 Seconds
(without alignments)
2370.233 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSPDVLKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	31.4	257	1	ETXE STAAU
2	948	26.9	257	1	ETXA STAAU
3	611	17.3	258	1	ETXD STAAU
4	557	15.8	324	1	GC1_MOUSE
5	557	15.8	393	1	GC1M_MOUSE
6	556	15.8	106	1	KAC_MOUSE
7	550	15.6	326	1	GC1 RAT
8	539	15.3	322	1	GCA RAT
9	491.5	14.0	330	1	GCA_MOUSE
10	491.5	14.0	399	1	GCM_MOUSE
11	481.5	13.7	117	1	HV12_MOUSE
12	481	13.7	139	1	HV07_MOUSE
13	480.5	13.6	117	1	HV13_MOUSE
14	480	13.6	118	1	HV51_MOUSE
15	479	13.6	336	1	GCB_MOUSE
16	479	13.6	405	1	GCE_MOUSE
17	472	13.4	106	1	KACA RAT
18	467	13.3	335	1	GCB_MOUSE
19	458.5	13.0	120	1	HV03_MOUSE
20	457	13.0	106	1	KACB RAT
21	454	12.9	137	1	HV11_MOUSE
22	450.5	12.8	140	1	HV02_MOUSE
23	446	12.7	333	1	GCB RAT
24	437.5	12.4	138	1	HV48_MOUSE
25	437.5	12.4	329	1	GCC RAT
26	433	12.3	120	1	HV50_MOUSE
27	425	12.1	117	1	HV09_MOUSE
28	423	12.0	149	1	HV54_MOUSE
29	422	12.0	117	1	KV5A_MOUSE
30	420.5	11.9	136	1	HV15_MOUSE
31	417	11.8	117	1	HV04_MOUSE
32	415	11.8	117	1	HV10_MOUSE
33	414	11.8	117	1	HV49_MOUSE

34	413	11.7	117	1	HV06_MOUSE
35	413	11.7	329	1	GC2_CAVPO
36	406.5	11.5	133	1	KV4B_HUMAN
37	406	11.5	134	1	KV4C_HUMAN
38	404	11.5	117	1	HV05_MOUSE
39	401	11.4	329	1	GC3_MOUSE
40	401	11.4	398	1	GC3M_MOUSE
41	397	11.3	330	1	GC1_HUMAN
42	396.5	11.3	121	1	HV01_MOUSE
43	396.5	11.3	327	1	GC4_HUMAN
44	395	11.2	114	1	KV4A_HUMAN
45	395	11.2	136	1	KV5B_MOUSE
46	392	11.1	117	1	HV52_MOUSE
47	385	10.9	147	1	HV1C_HUMAN
48	378	10.7	326	1	GC2_HUMAN
49	375	10.6	108	1	KV1M_HUMAN
50	372.5	10.6	129	1	KV3H_HUMAN
51	370	10.5	117	1	HV1G_HUMAN
52	369	10.5	108	1	KV1H_HUMAN
53	368.5	10.5	109	1	KV3D_HUMAN
54	368	10.4	129	1	KV1K_HUMAN
55	364.5	10.3	109	1	KV3F_HUMAN
56	364.5	10.3	129	1	KV3L_HUMAN
57	362	10.3	117	1	HV1B_HUMAN
58	361.5	10.3	109	1	KV3B_HUMAN
59	361.5	10.3	113	1	KV2G_MOUSE
60	361	10.2	109	1	KV4D_HUMAN
61	360	10.2	108	1	KV5M_MOUSE
62	360	10.2	128	1	KV3K_HUMAN
63	358	10.2	108	1	KV5K_MOUSE
64	358	10.2	121	1	KV4O_HUMAN
65	357.5	10.2	129	1	KV3M_HUMAN
66	357	10.1	108	1	KV1S_HUMAN
67	356	10.1	108	1	KV5P_MOUSE
68	356	10.1	323	1	GC_RABIT
69	355	10.1	108	1	KV1P_HUMAN
70	355	10.1	108	1	KV5L_MOUSE
71	354	10.1	108	1	KV1Y_HUMAN
72	354	10.1	108	1	KV5N_MOUSE
73	353	10.0	108	1	KV1N_HUMAN
74	353	10.0	108	1	KV5O_MOUSE
75	352	10.0	108	1	KV5U_MOUSE
76	351	10.0	114	1	KV1E_HUMAN
77	351	10.0	114	1	KV1A_MOUSE
78	348	9.9	108	1	KV1G_HUMAN
79	347	9.9	108	1	KV1R_HUMAN
80	345.5	9.8	107	1	KV1D_HUMAN
81	345	9.8	108	1	KV1V_HUMAN
82	345	9.8	131	1	KV3I_MOUSE
83	344	9.8	108	1	KV1C_HUMAN
84	344	9.8	111	1	KV3L_MOUSE
85	344	9.8	129	1	KV1X_HUMAN
86	343	9.7	111	1	KV3J_MOUSE
87	343	9.7	111	1	KV3M_MOUSE
88	343	9.7	111	1	KV3C_MOUSE
89	342.5	9.7	109	1	KV3E_HUMAN
90	342	9.7	111	1	KV3N_MOUSE
91	342	9.7	111	1	KV3T_MOUSE
92	341.5	9.7	117	1	HV42_MOUSE
93	341	9.7	106	1	KAC_HUMAN
94	341	9.7	108	1	KV1K_HUMAN
95	340.5	9.7	109	1	KV1T_HUMAN
96	340	9.7	111	1	KV3Q_MOUSE
97	339	9.6	108	1	KV1O_HUMAN
98	339	9.6	111	1	KV3R_MOUSE
99	338.5	9.6	108	1	KV3A_HUMAN
100	337	9.6	108	1	KV1A_HUMAN

ALIGNMENTS

RESULT 1

ETXE STAAU STANDARD; PRT; 257 AA.
 ID ETXE STAAU STANDARD; PRT; 257 AA.
 AC P1293;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type E precursor (SEE).
 ENTE.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN=MJB285;
 RX MEDLINE=88257005; PubMed=3384800;
 RA Couch J.L., Soltis M.T., Betley M.J.;
 RT "Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene".
 RL J. Bacteriol. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=36022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal enterotoxins".
 RL Nat. Struct. Biol. 2:680-686(1995).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MEC class II (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: M21319; A28179;
 CC PDB: 1SEE; 15-OCT-95.
 CC InterPro: IPR008992; Bact_endotox.
 CC InterPro: IPR006177; Bctr1_tox.
 CC InterPro: IPR006123; Staph/Strep_toxin.
 CC InterPro: IPR006126; Staph/Strep_tox.
 CC InterPro: IPR006173; Staph_tox_OB-
 CC Pfam: PF02876; Staph_Strep_tox_C7_1.
 CC Pfam: PF01123; Staph_Strep_toxin; 1.
 CC PRINTS: PR00279; BACTRUTOXIN.
 CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 CC Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 CC 3D-structure.
 FT SIGNAL 1 27 ENTEROTOXIN TYPE E.
 FT CHAIN 28 257 ZINC (BY SIMILARITY).
 FT METAL 211 211 ZINC (BY SIMILARITY).
 FT METAL 249 249 ZINC (BY SIMILARITY).
 FT METAL 251 251 ZINC (BY SIMILARITY).
 FT HELIX 33 35
 FT HELIX 39 41
 FT STRAND 42 42
 FT TURN 46 47
 FT HELIX 48 51
 FT HELIX 52 54
 FT STRAND 59 64
 FT TURN 66 67
 FT STRAND 69 69

FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 84
 FT STRAND 90 94
 FT TURN 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 115 116
 FT TURN 118 119
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 142
 FT STRAND 152 152
 FT STRAND 154 155
 FT TURN 156 157
 FT STRAND 163 163
 FT STRAND 171 171
 FT STRAND 173 175
 FT HELIX 176 190
 FT TURN 191 191
 FT STRAND 203 211
 FT STRAND 219 221
 FT STRAND 227 227
 FT HELIX 234 239
 FT STRAND 242 244
 FT TURN 245 247
 FT STRAND 249 257
 SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;
 Query Match 31.4%; Score 1107; DB 1; Length 257;
 Best Local Similarity 89.7%; Pred. No. 1.1e-61;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 226 SEKSEENEXDLRKSELOGTALGNLKOIYYNSKAITSEKSGADQTLTLLFKGFFTG 285
 DB 25 SEKSEENEXDLRKSELOGTALGNLKOIYYNEKAITENKESDDQPLETLFKGFFTG 84
 QY 286 HPWYNLLVLGSLTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGLHNNRLT 345
 DB 85 HPWYNLLVLGSLKDAITNKYKGVLDLYGAYGYQCAGGTPNKTACMGVGLHNNRLT 144
 QY 346 BEKVPINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHYLHGKGLYNSDFGKVK 405
 DB 145 BEKVPINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHYLHGKGLYNSDFGKVK 204
 QY 406 RGLVFRHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISTSLISLYLYTT 458
 DB 205 RGLVFRHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTINSENHLIDLYLYTT 257
 RESULT 2
 ETXA STAAW STANDARD; PRT; 257 AA.
 ID ETXA STAAW STANDARD; PRT; 257 AA.
 AC P13163.
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN ENTA OR MW1889.
 OS Staphylococcus aureus (strain MW2), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-acquired MRSA.";

RL Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FR1337;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RJ J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RY Huang T.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RJ J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schach E.M., Zaitseva I., Zaitsev V.N., Dohlisten M., Kalland T.,
RT Schlievert P.M., Chlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin
type A.";
RJ EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schach E., Dohlisten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
Zn2+ at 2.7-A resolution. Implications for major histocompatibility
complex class II binding.";
RJ J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins.";
RJ Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97343473; PubMed=9191070;
RA Schach E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
enterotoxins A and C2 reveals remarkable similarity and
dissimilarity.";
RJ J. Mol. Biol. 269:270-280(1997).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
for the toxin interaction with MHC class II.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP004828; BAB95754.1; -;
DR EMBL; M18970; AAA26681.1; -;
DR PIR; A28664; A28664.
DR PDB; 1BSF; 11-JUL-96.
DR PDB; 1SXT; 19-NOV-97.
DR PDB; 1DYO; 21-FEB-02.
DR PDB; 1I4G; 21-MAR-01.

DR PDB; 1I4H; 21-MAR-01.
DR PDB; 1L05; 18-DEC-02.
DR PDB; 1SEA; 15-OCT-95.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure; Complete proteome.
FT SIGNAL 1 24 ENTEROTOXIN TYPE A.
FT CHAIN 25 257
FT DISULFID 120 130
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 3).
FT HELIX 28 31
FT TURN 32 33
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
FT TURN 56 56
FT STRAND 59 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 108 116
FT TURN 118 119
FT TURN 125 126
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 149
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160
FT HELIX 164 166
FT STRAND 167 171
FT STRAND 173 175
FT HELIX 176 191
FT TURN 193 194
FT HELIX 197 199
FT TURN 200 200
FT STRAND 205 212
FT STRAND 218 221
FT TURN 222 223
FT HELIX 230 233
FT HELIX 234 237
FT TURN 238 239
FT STRAND 242 244
FT STRAND 248 255
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCAIF14677 CRC64;
Query Match 26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7.3e-52;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEBINEKDLRKKSSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLPKGFPTG 285
DB 25 SEKSEBINEKDLRKKSSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLPKGFPTG 84
QY 286 HPWYNDLLVDLGSTAAITSEYEGSSVDLYCAYGYOCAGTTPKTKACMYGCVTLHNNRLT 345

Db 85 HSWNDLLVDFOSKIDVYKKGKVDLYGAYGYCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGGKVQ 405
 Db 145 EEKVPINLWDGKQNTVPLETKVKNKNTVOELDLQARHYLHGKFGYNSDSFGGKVQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRNTTSSLSISLYTT 458
 Db 205 RGLIVFHTSTPSVNYDLFGAQQYNTLLRIYRDNKTNSNMHDIYLYTS 257

RESULT 3

ETXD STAAU STANDARD; PRT; 258 AA.
 ID ETXD STAAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type D precursor (SED).
 OS Staphylococcus aureus.
 GN Bacteria; Firmicutes; Bacilliales; Staphylococcus.
 OC NCBI_TaxID=1280;
 OX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359112; PubMed=2549000;
 RA Bayles K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D";
 RL J. Bacteriol. 171:4799-4806(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN=ATCC 23235;
 RX MEDLINE=97157473; PubMed=9003758;
 RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W.,
 RA Dohlsten M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization";
 RL EMBO J. 15:6832-6840(1996).
 CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -1- SUBUNIT: Homodimer; zinc-dependent.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 ENBL; M28521; AAB06195.1; -
 DR PIR; A33953; A33953.
 DR HSP; P13163; 18XT.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_Strep_tox_C1.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRIOTXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Zinc.
 FT SIGNAL 1 25
 FT CHAIN 26 258 ENTEROTOXIN TYPE D.
 FT METAL 212 212 ZINC.

FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
 SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A2BD42597FD CRC64;
 Query Match 17.3%; Score 611; DB 1; Length 258;
 Best Local Similarity 51.1%; Pred. No. 5.2e-31;
 Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;
 QY 226 SEKSEENKDLKRLKSELOQTALGNLKLQIYYNSKAITSEKSDAQFLNTLLFKGFFTG 285
 Db 26 NENIDSVKEKELHKKSLSTALNNKHSYADKNPIIGENKSTGDOFLENTLLYKXFFTD 85
 QY 286 HPWYNLLVLDLSTATSEYEGSSVDLYGAYGYCAGGTPNKTACMYGGVTLHDNNRLT 345
 Db 86 LINFEDLLINFNSKEMAKHFKSKNDVYPIRYGNCYGGSEIDRTACTYGGVTPEHGK 145
 QY 346 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGGKVQ 405
 Db 146 ERKKIPINLWINGVQKEVSLDKVQTKNTVQELDAQARYLQDKLYNNDLGGKIQ 205
 QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRNTTSSLSISLYLY 456
 Db 206 RGKIEFDSGSKVSYDLFQVKGDFEKLRIYSDNKNLTSTLHLDIVLY 256

RESULT 4

GCI MOUSE
 ID GCI MOUSE STANDARD; PRT; 324 AA.
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 19 gamma-1 chain C region secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=8020559; PubMed=5769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid";
 RL Gene 9:187-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salser W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gamma1 chain";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";

```

RL Biochem. J. 126:837-850(1972).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01868-1; Sequence=Displayed;
CC Note-May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=External;
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00793; CA24172.1; -
DR EMBL; V00793; CA24173.1; -
DR EMBL; V00793; CA24174.1; -
DR EMBL; V00793; CA24175.1; -
DR EMBL; V00795; CA24176.1; -
DR PIR; A02159; GIMS.
DR GlycoSuiteDB; P01868; -.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00407; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT /FTID=CAR_000055.
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1P2C93 CRC64;

Query Match 15.8%; Score 557; DB 1; Length 324;
Best Local Similarity 28.3%; Pred. No. 1.6e-27;
Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

121 AKTTPPSVYPLAPGSAQTNSVTLGCLVKGYPPEVTVTWNSGLSSGVHTFPVAVLQSD 180
1 AKTTPPSVYPLAPGSAQTNSVTLGCLVKGYPPEVTVTWNSGLSSGVHTFPVAVLQSD 60
181 LYTLSSSVTVPSSTVPSSTVTCNVAHPASSTKVDKVIIVRDGSGPSEKSEINKEKDLRKK 240
61 LYTLSSSVTVPSSTVPSSTVTCNVAHPASSTKVDKVIIVRDGSGPSEKSEINKEKDLRKK 103
241 SELQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTGHPWYNLLVLDLQSTA 300
104 CKPCLCTVPESSVSVIFPPK-----PKDVLITL----- 132
301 ATSEYEGSVLDYGAYGYQCAGTTPNKTACMYGGVTLHNNRLTEKKKVPINLWDGKQ 360
133 -----TP-KVTCWWDIS-----KDDPEVQFSNFDV--- 157

```

```

QY 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIVF 411
DQ 158 -DVEVHTAQTPREEQNFSFRSVSELPIMHQDLNGKFKCRVNSAAPPAPTEK----- 211
QY 412 HSSEGSIVSYDLFDPAQOQYEDTLIRIYRDNTTSSISLSISLYTTSIVMTQTPSLIV 471
DQ 212 -----TISKT----- 216
QY 472 SAGDRVITITCKASQSVSNDAVYQKPGQPKLLISVTSRYAGVDPDRFSGSGVGTDFTL 531
DQ 217 ----- 216
QY 532 TISSVQAEADAIVFCQDYNPSPTFFGGTKLEIKRADAPTIVSIFPPSSQLTSGGASVV 591
DQ 217 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 243
QY 592 CFLNNFYPKDINVKWIKDGSERON-----GVLSNWTQDSKDSYSTSMSSLTLTIKDEYER 646
DQ 244 CMITDFPEDITVEWQNGQPAENYKNTQPMNT-----NGSYFYVKLVNOKNWEA 296
QY 647 HNSYTCETHK 657
DQ 297 GNTFTCSVLHE 307

RESULT 5
GCIM MOUSE STANDARD; PRT; 393 AA.
ID GCIM MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.P., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01869-1; Sequence=Displayed;

```



```

RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RL kappa chain.";
RN Nucleic Acids Res. 9:971-981(1981).
RP SEQUENCE FROM N.A.
RX MEDLINE=83329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RL phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
CC !- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; V00807; CAA24189.1; -.
DR PIR; B90262; K1MS.
DR PDB; 1AIF; 01-FEB-97.
DR PDB; 1FSK; 02-OCT-00.
DR PDB; 1KE5; 08-APR-98.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 1KCU; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96495; Igc-C.
DR InterPro; IPR007110; Igc-like.
DR InterPro; IPR003597; Igc1.
DR InterPro; IPR003006; Igc_MHC.
DR Pfam; PF00047; Igc 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; Igc LIKE; 1.
DR PROSITE; PS00290; Igc_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11778 MW; 4351PF5EP49AE9S CRC64;

Query Match 15.8%; Score 556; DB 1; Length 106;
Best Local Similarity 100.0%; Pred.No. 3.9e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 ADAAPTQVSIFFPSSEQLTSGGASVVCFLNNFYPKDIYKWKIDGSRONGVLSWTDQDS 626
Db 1 ADAAPTQVSIFFPSSEQLTSGGASVVCFLNNFYPKDIYKWKIDGSRONGVLSWTDQDS 60

QY 627 KDSTYSMSSTLTLDKDEYERHNSYTCETHAKTKTSTSPVKSFNNE 671
Db 61 KDSTYSMSSTLTLDKDEYERHNSYTCETHAKTKTSTSPVKSFNNE 105

RESULT 7
GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Igc-like.
DR InterPro; IPR003597; Igc1.
DR InterPro; IPR003006; Igc_MHC.
DR Pfam; PF00047; Igc 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; Igc LIKE; 3.
DR PROSITE; PS00290; Igc_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EP49B9DA CRC64;

Query Match 15.6%; Score 550; DB 1; Length 326;
Best Local Similarity 27.7%; Pred.No. 4.3e-27;
Matches 150; Conservative 64; Mismatches 90; Indels 238; Gaps 14;

QY 121 AKTTPSVYPLAPGSAQAQTNMVTGLCLVKGYFPEPVTVVNSGSLSSGHHFPAVLQSD 180
Db 1 AETTPSVYPLAPGSAQAQTNMVTGLCLVKGYFPEPVTVVNSGSLSSGHHFPAVLQSG 60

QY 181 LYTLSSVTVPSSTWSEVTCNVNAPASSTKVDKXIVPRDSGGPSEKEEINEKDLRKK 240
Db 61 LYTLSSVTVPSSTWSEVTCNVNAPASSTKVDKXIVPRDSGGPSEKEEINEKDLRKK 109

QY 241 SELQGTALGNLKIYYNNSKAITSSSEKSDAQFLTNLLFKGFTGHPWYNDDLVLGSGTA 300
Db 110 -----ICTGSEVSS-----VFIPPKFDVL----- 130

QY 301 ATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGVTLHDNNRLTEKKVPLNLDG-- 358
Db 131 -----TITL-----TP-KVTCVVDIS-----QDDPEVHFSWFVDVE 162

QY 359 ---KQTTVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVPHSSE 415
Db 163 VHTAQTRPPEQFNSTFR--SVSELPILHQDWLNGR----- 196

QY 416 GSTVSYDLFDAQGGQPDTLRLRYRONTTISSTLSISLYLYTTSIVMTQTSLVLSAGD 475
Db 197 ----- 196

QY 476 RVITTCASQSVSNVDVWYQQKPGQSPKLLISYTSRYAGVDPDRSGSGYGDFTLTIS 535
Db 197 --TFRCV-----TSAAPPSPIEKTSK 217

QY 536 VOAEADAAYFCOODYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLN 595
Db 218 PE-----GRQV-----PHVYVMTSPFTEEMTQNEVSTICWVK 249

QY 596 NFYPKDIYKWKIDGSRONGVLSWTDQDSKDSTYSMSSTLTLDKDEYERHNSYTCETH 655
Db 250 GFYPDDIYVEWOMQGOEN-YKNTPTMTD-DGSYFLYSLKLVKKEKQOQNTETCSVL 307

QY 656 HK 657
Db 308 HE 309

```

```

RESULT 8
GCA_RAT      STANDARD;      PRT;      322 AA.
ID  P20760;
AC  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig gamma-2A chain C region.
OS  Rattus norvegicus (Rat)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
SEQUENCE FROM N.A.
RX  MEDLINE=69232738; PubMed=3149946;
RA  Brueggemann M.;
RT  "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL  Gene 74:473-482(1988).
CC  -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license-agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  ENBL: M13804; AAA41376.1; ALT_INIT.
DR  PIR; PS0019; PS0019.
DR  HSP; P01842; 7FAB.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_WHC.
DR  Pfam; PF00047; Ig_2.
DR  SMART; SM00407; IGc1; 2.
DR  PROSITE; PS00835; IG_LIKE; 3.
DR  PROSITE; PS00290; IG_WHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT  NON_TER 1 1
FT  DOMAIN 6 98 IG-LIKE 1.
FT  DOMAIN 115 212 IG-LIKE 2.
FT  DOMAIN 221 317 IG-LIKE 3.
FT  DISULFID 27 82
FT  DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 136 196
FT  DISULFID 242 300
FT  CARBOHYD 172 172 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ  SEQUENCE 322 AA; 35186 MW; E8EAL36A9DE01EDB CRC64;

Query Match 15.3%; Score 539; DB 1; Length 322;
Best Local Similarity 28.2%; Pred. No. 2e-26;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15;

QY 121 AKTTPSVYPLAGSAAQTNSWTLGCLVKGYPEPVVTWNSGSLSSGVHTFPVAVLQSD 180
D 1 AETTPSVYPLAGTALKNSWTLGCLVKGYPEPVVTWNSGSLSSGVHTFPVAVLQSG 60
QY 181 LYLTSSTVTPSPSTWTCNVAHPASSTKVDKIKVPRDSGGPSEKSEINEKDLRKK 240
D 61 LYLTSSTVTPSPSTWSSQAVTCNVAHPASSTKVDKIKVPRC----- 102
QY 241 SELQGTALGNLKIYYNSKAISSSEKSAQDFLTNLLFKGPTGHPWYNDLLVDLGSTA 300
D 103 -----NPGCGTGEVSS-----VFIFPKTKDVL----- 126
QY 301 ATSEYEGSSVDLYGAVYGYCAGTGTPKNTACTMGGVTLHDNNRLTEKKVPINLWIDG-- 358
D 127 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSEWIDVVE 158

```

```

QY 359 ---KQTTPIDKVKTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQVQRLIVFHSSE 415
D 159 VHTAQTHAPEKQSNSTLR--SVSELPVIVHRDWLNGK-----TFKCKVN----- 199
QY 416 GSTVSVDLFDQAQGYPDTLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSAGD 475
D 200 -----SGAFFAPI----- 207
QY 476 RVTTICKASQSVNDVAMVYQQKFGQPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSS 535
D 208 -----EKXIS-----KPEGTPR----- 219
QY 536 VQAEAAVYFCQDYNPPFFGGTGLKLEIKRAAAPTVSIFPPSSBQLTSGGASVVCFLN 595
D 220 -----GPOVYTMAPPKEEMTQSVSITCMVK 245
QY 596 NFPKIDINVKKIDGSRQNGVLNSWTDQDSKDYSSMSSTLTLTDEYRHNSYTCBAT 655
D 246 GFYPDPDIYTEMKXNGQPOEN-YKNTPTPMDT-DGSYFLYSKLVAKKETWQOGNTFTCSVL 303
QY 656 HK 657
D 304 HE 305

RESULT 9
GCAA_MOUSE      STANDARD;      PRT;      330 AA.
ID  P01863;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig gamma-2A chain C region, A allele.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
SEQUENCE FROM N.A.
RX  MEDLINE=81076554; PubMed=6777755;
RA  Sikorav J.-L., Auffray C., Rougeon F.;
RT  "Structure of the constant and 3' untranslated regions of the murine
RT  Balb/c gamma 2a heavy chain messenger RNA.";
RL  Nucleic Acids Res. 8:3143-3155(1980).
RN  [2]
SEQUENCE FROM N.A.
RX  MEDLINE=81198976; PubMed=6262729;
RA  Yamawaki-Katsoka Y., Miyata T., Honjo T.;
RT  "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT  and evolution of heavy chain genes: further evidence for intervening
RT  sequence-mediated domain transfer.";
RL  Nucleic Acids Res. 9:1365-1381(1981).
RN  [3]
SEQUENCE FROM N.A.
RX  MEDLINE=81228694; PubMed=6787604;
RA  Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT  "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT  suggests that exons can be exchanged between genes in a multigenic
RT  family.";
RL  Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN  [4]
MYELOMA PROTEIN MOPC 173.
RX  MEDLINE=74175517; PubMed=4831970;
RA  Bourgois A., Fougereau M., Rocca-Serra J.;
RT  "Determination of the primary structure of a mouse IgG2a
RT  immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT  for the evolution of immunoglobulin structure and function.";
RL  Eur. J. Biochem. 43:423-435(1974).
RN  [5]
DISULFIDE BONDS.
RX  MEDLINE=73056887; PubMed=4565406;
RA  de Preval C., Fougereau M.;
RT  "Determination of the primary structure of a mouse gamma G2a

```

```

RT immunoglobulin. Identification of the disulfide bridges.;
RL Eur. J. Biochem. 30:452-462(1972).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2MSA.
DR PDB; 1E4W; 12-JUL-01.
DR PDB; 1E4X; 12-JUL-01.
DR PDB; 1XNU; 06-MAY-99.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 14.0%; Score 491.5; DB 1; Length 330;
Best Local Similarity 26.4%; Pred. No. 1.8e-23;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;

QY 121 AKTTPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPVTVTVNSGSLSGVHTFPAVLQSD 180
Db 1 AKTAPSVYPLAPGCDPTGSGVTLGCLVKGYFPEPVTLTVNSGSLSGVHTFPAVLQSD 60

QY 181 LYTLSSSVTVSPSTVTCNVAHPASSTKVCKIVPRDSGGPSKSEINEKDLRKK 240
Db 61 LYTLSSSVTVSTWPSQSIICNVAHPASSTKVCKIEPR---GPTKPCP----- 108

QY 241 SELQGTALGNLKKQIYYNNSKAITSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 109 ----- 108

QY 301 ATSEYEGSSVDLYGAYGYCAGGTENKTACMYGGVTLHDNNRLTEBKVPINLWIDQK 360
Db 109 ----- 108

QY 361 TVPIDKVTSSKEVTVOELDLQARHVLHGRFGLYNSDSFGKVGQGLVHFHSGEGSTVS 420
Db 125 -----IPPKIKVLMI---SLSPVT 143

QY 421 YDLFDAQQQYPTLLRIYRDNNTTSSLSLSLYTTSIVMTQPTSLVSGADRVTIT 480
Db 144 CVWVDVSEDDP-----VQISWFVNNVEVHTACTQT----- 174

QY 481 CKASQSVNDVAVYQKQPGQPKLLISYTSRYAGVPDRFGSGYGTDFTLTSSVQAE 540
Db 175 -----HREDYNSTLRV----- 186

QY 541 AAVTFCQDYNSTPTFGGTKLEIKRAD-----AAPTVFIPFPSSQLT 584
Db 541 AAVTFCQDYNSTPTFGGTKLEIKRAD-----AAPTVFIPFPSSQLT 584

```

```

Db 187 SALPIQHODWMSCKEP----KCKVNNKDLPAPIERTISKPKGVRAPQVTVLPPPEEMT 242
QY 585 SGGASVVCFLNFPYKIDINVKWKIDSERQN-----GVLSNWTQDSKOSTYSMSSTLTL 639
Db 243 KQCVTLTCMTDMPEDIVYVETNNGKTELNYKNTPEVLDS-----DGSYFMSKLRV 295
QY 640 TKDYEHRHNSYTCETHK-TSTSPIVKSNR 669
Db 296 EKNWVERNSYSCSVVHEGLHNHHTTKSPSR 326

RESULT 10
GCAM_MOUSE
ID GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG gamma-2A chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222130; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=External;
CC Note=Probably the major isoform;
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
EMBL; J00471; AAB59661.1; ALT_INIT.
DR PIR; A02154; G2MSA.
DR PDB; 1KB5; 08-APR-98.
DR PDB; 1YEE; 15-OCT-97.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing; 3D-structure; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 121 220 IG-LIKE 2.
FT DOMAIN 229 325 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT POTENTIAL.

```

FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 399 AA; 44020 MW; 4C381388FAED3FF0 CRC64;
 Query Match 14.0%; Score 491.5; DB 1; Length 399;
 Best Local Similarity 26.4%; Pred. No. 2.4e-23;
 Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
 QY 121 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGYPFPVTVWNSGLSSGVHFFPAVLQSD 180
 DB 1 AKTTPSVYPLAPGSDTTGSSVTLGCLVKGYPFPVTVWNSGLSSGVHFFPAVLQSD 60
 QY 181 LYLTLSSSVTPSWTSEVTCNVAHPASSTVKKIVPRDGGSPSEKSEBINEKDLKK 240
 DB 61 LYLTLSSSVTPSWTSPQSTCNVAHPASSTVKKIEPR---GTIKPCP----- 108
 QY 241 SELQGTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTGHPWYNDLLVLGSTA 300
 DB 109 ----- 108
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGVTLHDNNLTTEEKKVPINLWDGKQ 360
 DB 109 -----PKCPAPN-----LLGSPSVF----- 124
 QY 361 TTVPIDKVKTSKEVTQVELDLQARHLYHGKFLGYNLSDSFGKVGKORGLIVFHSSEGSTVS 420
 DB 125 -----IFPKIKDVLMI---SLSPIVT 143
 QY 421 YLFLDAQGYDPLRLIYRDNNTISLSISLYLTVTSIVMTQPTSLLSVAGDRVIT 480
 DB 144 CVVDVSDDDPD-----VQISWVFNNEVHTAQQT----- 174
 QY 481 CKASQSVNDVANYQKPGSPKLLISYTSRYSAGYDPRFSGSGYGTDFLTLSISSVQAE 540
 DB 175 -----HREDNSILRVV----- 186
 QY 541 AAVYFQDDYNSPPTFGGKTKLBKAD-----AAPTYSIFPPSSEQT 584
 DB 187 SALPIQHDDWMSKEF-----CKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 242
 QY 585 SGASVVCFLNNYPKIDINKWIDQSERQN-----GVLSNWDQDSDSTYSMSLT 639
 DB 243 KKQVTLTCMTDMPEDPIYVWVNNKGTNLNXTNTEPVLDS-----DGSYFMSKURV 295
 QY 640 TKDEYERHNSYTCETHK-TSTSPVVKFSNR 669
 DB 296 EKNWVERNSYSCSVVHGLNHHHTTKSPSR 326
 RESULT 11
 ID HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region WOPC 104E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424 (1982).
 CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02039; MEMS4E.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT DOMAIN 1 116 IG-LIKE
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447B41 CRC64;
 Query Match 13.7%; Score 481.5; DB 1; Length 117;
 Best Local Similarity 78.3%; Pred. No. 1.8e-23;
 Matches 94; Conservative 8; Mismatches 15; Indels 3; Gaps 1;
 QY 1 EVQLQQSGDPLVPGASVKISKASGYSTFYGMHWKSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVQLQQSGDPLVPGASVKMSKASGYTFTDYMKWKQSHGSKLEWIGDINPNNGTYS 60
 QY 61 NQKFKKATLTVDKSSSTAYMELSLTSEDSAVYCYCARSTMTNMYDMYMGQSTVTSS 120
 DB 61 NQKFKKATLTVDKSSSTAYMQLSLTSEDSAVYCYCARD---YDMYFDVWGAGTITVTSS 117
 RESULT 12
 ID HV07_MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M.; Faskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D.;
 RT "Heavy chain variable region contribution to the NpB family of antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637 (1981).
 CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPE ANTIBODIES).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; J00529; AAA38170.1; -.
 DR PIR; A90809; MEMS18.
 DR PDB; 1A6U; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 149 FRAMEWORK-1.

```
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match
Best Local Similarity 13.7%; Score 481; DB 1; Length 139;
Matches 89; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEIVKPGASVKLSCKASGYFTFTSWHWVVKQSPGKLEWIGRIDPNSGGTKY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMTITNYMDYWGQGSTVTVSS 120
Db 80 NEKFKGKATLTVDKPSSTAYMQLSLTSDSAVYVCARYDYGSSYFDYWGQGITLTVSS 139
```

```
RESULT 13
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevering B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS; THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC PIR; A26242; MEMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447B41 CRC64;
```

```
Query Match
Best Local Similarity 13.6%; Score 480.5; DB 1; Length 117;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGPELVKPGASVKNSCKASGYFTFTDYMVKVQSHGKLEWIGDINPNNGTSTY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMTITNYMDYWGQGSTVTVSS 120
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSAVYVCARDY---WYFDWVGAGITVTVSS 117
```

```
RESULT 14
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84192519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEB4C762A018 CRC64;

Query Match
Best Local Similarity 13.6%; Score 480; DB 1; Length 118;
Matches 95; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGPELVKPGASVKISCKASGYFTFTDYMVKVQSHGKLEWIGDINPNNGTSTY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMTITNYMDYWGQGSTVTVSS 120
Db 61 NQKFKGKATLTVDKSSSATYMLRLSTSDSAVYVCARGYDPPF--DVMGTGTTVTVSS 118

RESULT 15
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE IG gamma-2B chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE A).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner P.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
gamma 2b heavy chain messenger RNA.";
RL Science 206:1229-1303(1979).
```

[3]
SEQUENCE FROM N.A.
MEDLINE=80081502; PubMed=117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine gamma
2b immunoglobulin heavy chain."
Science 206:1303-1306 (1979).
[4]
SEQUENCE FROM N.A. (ALLELE B).
MEDLINE=82173203; PubMed=6803173;
Oillo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma
2a and gamma 2b chain genes."
Nature 296:761-763 (1982).
[5]
CARBOHYDRATE-LINKAGE SITE THR-105.
MEDLINE=94216359; PubMed=7512967;
Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,
Irimura T., Takahashi N., Kato K., Arata Y.;
"O-glycosylation in hinge region of mouse immunoglobulin G2b."
J. Biol. Chem. 269:12345-12350 (1994).
RL J. Biol. Chem. 269:12345-12350 (1994).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01866-1; Sequence=Displayed;
CC Note=May be the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01867-1; Sequence=External;
CC -1- O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH IS
MODIFIED WITH 2 STALIC ACID RESIDUES.
CC -1- PM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
CC -1- MISCELLANEOUS: The a allele sequence is shown.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; S25057; G2MS11.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98
FT DOMAIN 127 226
FT DOMAIN 235 331
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 115 115
FT DISULFID 118 118
FT DISULFID 150 210
FT DISULFID 256 314
FT CARBOHYD 105 105
FT MOD_RES 336 336
FT VARIANT 163 163
FT VARIANT 194 194
FT VARIANT 300 300
FT VARIANT 301 301
FT VARIANT 301 301
FT CONFLICT 25 25
FT CONFLICT 36 36
FT CONFLICT 239 239
FT CONFLICT 336 336
SQ SEQUENCE 336 AA; 7D875662607C3568 CRC64;
Query Match 13.6%; Score 479; DB 1; Length 336;
Best Local Similarity 27.6%; Pred.No.1.1e-22;
Matches 151; Conservative 47; Mismatches 110; Indels 240; Gaps 14;
QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEVTVTWNSGSLSSGVHTTFFAVLQSD 180

Db 1 AKTTPPSVYPLAPGCGTTCGSSVTLCGLVKGYPPEVTVTWNSGSLSSGVHTTFFAVLQSG 60
QY 181 LYTLSSSVTPSPSTWPSQVTCNVAPASSTKVDKIVPRDGGPSEKSENE-----KD 236
Db 61 LYTMSSSVTPSPSTWPSQVTCNVAPASSTKVDKIVPRDGGPSEKSENE-----ISTINPCPKCE 114
QY 237 LRK--KSELQGTALGNLKOIYYNNSKAITSSSEKSAQFLNTLLPKGFTTGHFWYNDLLV 294
Db 115 CHKCPAPNLEG---GPSVFIPPNIKDV-----LMI 142
QY 295 DLGSTAATSEYEGSSVDLYGAYIGYQCAGGTPNKATCMYGGVTLHDNRLTEKKVPINL 354
Db 143 SL-----TP-----146
QY 355 WIDGKQTTVIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVGQGLIVFHSS 414
Db 147 ----KVTCVVVD-----VSEDDPDVQISWVNN-----VEVHTA 176
QY 415 EGSVSVYDLFDACQOYPTLLRIYRDNNTTSSLSISLYLYTTSIVMTQTPTSLVVSAG 474
Db 177 QTCHREDY-----NSTIRVVS-----193
QY 475 DRVTITCKASQSVNSVDVAVYQXPGQSKLLISYTSRYAGVDPDFSGSGYGTDFLTIS 534
Db 194 -----TLPIQ 198
QY 535 SVQAEADAAYFCQDYNSPPTFGGTMLEIKRAADAAPTVSIFPPSSQOLTSGGASVVCFL 594
Db 199 HQDWMSKEFKCKVNNKDLSPERTISKLGIVRAPQVILPPPAQLSEKDVSLTCLV 258
QY 595 NNFPKIDINVKMKIDGSRQN-----GVLSWTDQDSKSTYSMSSTLTUTKDEYERHNS 649
Db 259 VGFNPGDISVEMTNGTNGTEENYKDTAPVLD-----DGSYFIYSKLNKMTSKWEKIDS 311
QY 650 YTCEATHK 657
Db 312 FSCNVRHE 319
RESULT 16
GCEM_MOUSE STANDARD; PRT; 405 AA.
ID GCEM_MOUSE
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2b chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 335-405 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Katsuo Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627 (1982).
RN [2]
RP SEQUENCE OF 335-378 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
RT immunoglobulin gamma chains."
RL Cell 26:19-27 (1981).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01867-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01866-1; Sequence=External;

Notes-May be the major isoform;
 CC -!- PTM: DISULFIDE BONDS BY HOMOLGY WITH OTHER IG GAMMA CHAINS.
 CC -!- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be
 CC identical with the corresponding region of the secreted form.
 CC -!- MISCELLANEOUS: The A allele sequence is shown.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; J00462; AAB59659.1; ALT_INIT.
 CC
 CC PIR; C02154; G2MSBM.
 CC PDB; 1CIC; 11-YAR-03.
 CC MGD; MG1:96445; Igh-3.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_c1.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00407; IgC1; 2.
 CC PROSITE; PS00835; Ig-Like; 3.
 CC PROSITE; PS00290; Ig_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
 CC Alternative splicing; 3D-structure; Repeat.
 CC NON TER 1
 CC DOMAIN 6 98 IG-LIKE 1.
 CC DOMAIN 127 226 IG-LIKE 2.
 CC DOMAIN 235 331 IG-LIKE 3.
 CC INTERCHAIN (WITH A LIGHT CHAIN).
 CC INTERCHAIN (WITH A HEAVY CHAIN).
 CC INTERCHAIN (WITH A HEAVY CHAIN).
 CC INTERCHAIN (WITH A HEAVY CHAIN).
 CC INTERCHAIN (WITH A HEAVY CHAIN).
 CC INTERCHAIN (WITH A HEAVY CHAIN).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 370 405
 CC DOMAIN 370 405
 CC SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;
 CC
 CC Query Match 13.6%; Score 479; DB 1; Length 405;
 CC Best Local Similarity 27.6%; Pred. No. 1.4e-22;
 CC Matches 151; Conservative 47; Mismatches 110; Indels 240; Gaps 14;
 CC
 CC 121 AKTTPSVYPLAPGSAAGTNSMTVLGCLVKGVEPEPTVTWNSGLSGVHTFPAVLQSD 180
 CC 1 AKTTPSVYPLAPGCGDTTSSVTLGCLVKGYPFESVTWNSGLSSSVHTFPALLQSG 60
 CC 181 LYTSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRSDSGGFSKSEINE- ---KD 236
 CC 61 LYTWSSTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRSDSGGFSKSEINE- ---SGP- ---ISTINCPCKE 114
 CC 237 LRK- ---KSELOFALGNLQIYYNSKAITSEKSAQDFLNTLLFKGFFHGHVNDLLV 294
 CC 115 CHKPAPEL- ---GPSVFIFPPNKKV- ---VSEDDPDVQISWFFNN- ---VEVHTA 176
 CC 295 DLGSAATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEKKVPINL 354
 CC 143 SL- ---TP- --- 146
 CC 355 WIDGKQTTPIDKVKTSKVEVTVDLQAHYHKGFLYNSDSFGKVGQGLIVPHSS 414
 CC 147 ---KVTCCVVD- ---VSEDDPDVQISWFFNN- ---VEVHTA 176
 CC 415 EGSTVSVDLFDAQGYPTLRLIRVDRNTTSSLSISLVLYTTSIVMTQTPTSLVLSAG 474
 CC 177 QTQTHREDY- ---NSTRVVS- --- 193
 CC 475 DRVTITKASOSVNDVAVQKPGQSKLLISYTSRYAGVPRDFSGGYGTDFTLITIS 534

Db 194 -----TLPIQ 198
 QY 535 SVQAEAAVYFCQDYNSPTFGGTTKLEIKRADAAPTIVIFPPSSQLTSGGASVVCFL 594
 Db 199 HQDWMSGKFKCKVNNKDLSPITRTISKIKGLVRAPQVILPPAPQLSRKQVSLTCLV 258
 QY 595 NNFPKPDINVKWKIDGSERON-----GVLSNWDQSDKSTYSMSSTLTITKDEYERHNS 649
 Db 259 VGFNPGDISVEWTSNGHTTEENYKDTAPVLDS-----DGSYFIYKLNKMTSKWKETDS 311
 QY 650 YTCEATHK 657
 Db 312 FSCNVRHE 319
 RESULT 17
 KACA RAT
 ID KACA RAT STANDARD; PRT; 106 AA.
 AC P01836;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RX MEDLINE=82082587; PubMed=6273908;
 RA Sheppard H.W., Gutman G.A.;
 RT "Allelic forms of rat kappa chain genes: evidence for strong
 RT selection at the level of nucleotide sequence."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02118; KIRTA.
 DR HSSP; P01842; 2MCG.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS00835; Ig-Like; 1.
 DR PROSITE; PS00290; Ig_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1
 FT DOMAIN 5 102 IG-LIKE.
 FT DISULFID 26 86
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;
 Query Match 13.4%; Score 472; DB 1; Length 106;
 Best Local Similarity 83.8%; Pred. No. 6.1e-23;
 Matches 88; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 567 ADAAPTIVIFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWDQDS 626
 Db 1 ADAAPTIVIFPPSMEQLTSGGATVCFVNNFYPRDISVKKWKIDGSEQRDGVLDSDVDQDS 60
 QY 627 KOSTYSMSSTLTITKDEYERHNSYCEATHKSTSTPIVKSFNRE 671
 Db 61 KOSTYSMSSTLTITKDEYERHNSYCEATHKSTSTPIVKSFNRE 105
 RESULT 18
 GCAB MOUSE
 ID GCAB MOUSE STANDARD; PRT; 335 AA.
 AC P01864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
[2]
SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Stroberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of IgA and IgB allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -1- MISCELLANEOUS: The sequence differs from that of the a allele,
CC from BALB/c mice, at 15% of the positions.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00479; -; NOT ANNOTATED_CDS.
CC PIR; A02153; G2MSAB.
CC DR PDB; 1BOG; 23-VAR-99.
CC DR PDB; 1HH6; 26-JAN-01.
CC DR PDB; 1HH5; 24-JUL-03.
CC DR PDB; 1HH6; 08-FEB-01.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003597; Ig_c1.
CC DR InterPro; IPR003006; Ig_MHC.
CC DR Pfam; PF00047; Ig; 2.
CC DR SMART; SM00407; IGc1; 2.
CC DR PROSITE; PS50835; IG_LIKE; 3.
CC DR PROSITE; PS00290; IG_MHC; 1.
CC KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
CC 3D-structure; Repeat.
CC FT NON TER 1 1
CC FT DOMAIN 6 98 IG-LIKE 1.
CC FT DOMAIN 126 225 IG-LIKE 2.
CC FT DOMAIN 234 330 IG-LIKE 3.
CC SEQUENCE 335 AA; 36596 MW; FA332792CBB13C6 CRC64;
Query Match 13.3%; Score 467; DB 1; Length 335;
Best Local Similarity 25.5%; Pred. No. 6.1e-22;
Matches 149; Conservative 40; Mismatches 110; Indels 286; Gaps 13;
QY 121 AKTTPSPVPLAPGSAQTNSMTLGLVKGYPPEVTVTNWGSLSGGVHTTFAVLQSD 180
DB 1 AKTTPSPVPLAPGSAQTNSMTLGLVKGYPPEVTVTNWGSLSGGVHTTFAVLQSG 60
QY 181 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKYDKKIVPRDGGPSKSEINEKDLKK 240
DB 61 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKYDKKIEPR----- 100

QY 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFTGHPWYNLLDLGSTA 300
DB 101 ----- 100
QY 301 ATSEYEGSSVDLYGAYVYQAGGTGPNKTACMYGGVTLHDNNRLTEBKVPINLWDGKQ 360
DB 101 -----VPIT-----QN 106
QY 361 TTVPIDKVTSKKEVTVQELDLQARHVLHCKFGLYNSDSFGKVGQGLIVFHSSESTVS 420
DB 107 PCPPHQRVPCCAA-----PDLGGP----- 126
QY 421 YDLFDAQGGVPTLLRIYRDNNTTSSTLSISLYLTTSIVMTQTPTSLVSAGDRVTIT 480
DB 127 -SVIFPPKIKDVL-----ISLSPWTCVV----- 152
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRVAGVDPDRFSGSGYGTDFLTITISSVQAE 540
DB 153 -----DVSSED-----DPDVQISW-----FYNNVEVHT 174
QY 541 AAVYFCQDYNSTPTFGGKLEIKRAD-----A 569
DB 175 AQTQTHREDYNS--TLRVSAFLPIQHODWMSGKFKVNNRALPSPIEKTISKRGPVR 232
QY 570 APTVSIFPPSSEQLTSGGASVGVCFLLNNFYPKDINVKWIDGSRQNGVLSWTDQSKDS 629
DB 233 APQVYVLPFAEEMTKKEPSLTOMITGLPAEIAVDWTSNGRTEQN-YKNTATVLDS-DG 290
QY 630 TYSVSSLTTLTKDEYERHNSYTCETHKT-----STSPVKSFNR 669
DB 291 SYFMYSKLRVQKSTWERSLFACVSVHVLNHLTLTKTISRSLGK 335
RESULT 19
HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032 (1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Ig; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654F CRC64;
Query Match 13.0%; Score 458.5; DB 1; Length 120;
Best Local Similarity 72.5%; Pred. No. 5e-22; Indels 1; Gaps 1;
Matches 87; Conservative 15; Mismatches 17;


```

QY 2 VLOQSGPDLVKPGASVKISKASGYFTGYMHVWVKSPGKLEWIGRIINPNNGVTLYN 61
Db 1 VLOQSGAELVAGSVKMSCKASGYFTSYGINVWVKRPGQGLEWIGVINGPGNYTKYN 60
QY 62 QKFKDKATLTVDKSSSTAYMEIRSLTSDSAVYYCARSTMI-TNYVMYWGQTSVTYSS 120
Db 61 EAFKKGKTLTVDKSSSTAYMQRLSITSDSAVYFCARSVYGGSYFYFDWQGGTILTVSS 120

RESULT 20
KACB RAT
ID KACB RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBT_TaxID=10116;
RN SEQUENCE FROM N.A.
RC STRAIN=Louvain;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gurman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes.";
RL J. Immunol. 115:59-62(1975).
CC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93901; KIRTB.
DR HSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IG_C1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT DOMAIN 1 1 IG-LIKE.
FT NON_TER 1 1
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 D -> N (IN REF. 2).
FT CONFLICT 2 2 N -> K (IN REF. 2).
FT CONFLICT 30 30 MISSING (IN REF. 2).
FT CONFLICT 48 48 E -> Q (IN REF. 2).
FT CONFLICT 79 79 E -> Q (IN REF. 2).
FT CONFLICT 87 87 V -> W (IN REF. 2).
FT CONFLICT 98 98 S -> N (IN REF. 2).
FT CONFLICT 100 100
SQ SEQUENCE 106 AA; 11601 MW; 4CFA7CA820DICA36 CRC64;

Query Match 13.0%; Score 457; DB 1; Length 106;
Best Local Similarity 80.0%; Pred. No. 5.2e-22;
Matches 84; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 567 ADAAPTIVIFPPSSQLTSGGASVVCFLNNFVKDINVKIKDGERQGVLSMTQDS 626
Db 1 ADAAPTIVIFPPSTFQLATGASVVCFLNNFVKDINVKIKDGERDGVLSMTQDS 60

QY 627 KDSTYSMSSTLTLDKDEYERNNSYTCETHKTSPIVKSFRNE 671
Db 61 KDSTYSMSSTLTLDKADYESHNLVTCVHVHTSSSPVVKSPFRNE 105

```

```

RESULT 21
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_TaxID=10090;
RN SEQUENCE FROM N.A.
RC MEDLINE=81234548; PubMed=6788376;
RX Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -|- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 12.9%; Score 454; DB 1; Length 137;
Best Local Similarity 70.0%; Pred. No. 1.1e-21;
Matches 84; Conservative 15; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISKASGYFTGYMHVWVKSPGKLEWIGRIINPNNGVTLY 60
Db 20 QVQLQQPGAEFVKPGASVKLSCKASGYFTSYLHMHWVWVQKPGLEWIGRIDFNSGGTTY 79
QY 61 NQKFKDKATLTVDKSSSTAYMEIRSLTSDSAVYYCARSTMI-TNYVMYWGQTSVTYSS 120
Db 80 NEHFRSKATLTIDKPSSTAYMQLSSITSDSAVYYCARVRL--GRYFDYWGQGTILTVSS 137

RESULT 22
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

```

```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RX Sims J., Rabbitts T.H., Estess P., Slaughtner C., Tucker P.W.,
RA Capra J.D.;
RA "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J00493; AAA38128.1; -.
CC PIR: A94264; HVMSG7.
CC HSSP: P01810; 2FBJ.
CC InterPro: IPR007110; Ig-like.
CC InterPro: IPR003596; Ig_V.
CC Pfam: PF00047; Ig; 1.
CC SMART: SM00406; IGV; 1.
CC PROSITE: PS50835; IG_LIKE; 1.
CC Immunoglobulin V region; Hybridoma; Signal.
CC SIGNAL 1
CC CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
CC DOMAIN 20 139 IG-LIKE.
CC NON TER 140 140
CC SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DASCE8 CRC64;
CC
CC Query Match 12.8%; Score 450.5; DB 1; Length 140;
CC Best Local Similarity 71.9%; Pred. No. 1.9e-21;
CC Matches 87; Conservative 14; Mismatches 19; Indels 1; Gaps 1;
CC
QY 1 EVQLQSGPDLVPGASVKISCKASGYSTFTYMHVWYKSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLQSGAEELVRAGSVKMSCKASGYTFTSYGINWYKQRPQGQLEWIGYINPGYINY 79
QY 61 NQKFQKATLTVDKSSSTAYWEIRLSLTSDSNAVYCARSTM1-TNYVMDYWGQGTSTVTS 119
Db 80 NEXPKGKTLTVDKSSSTAYNQLRSLTSDSNAVYCARSHYGGSYDFDITWGQGTPLTVS 139
QY 120 S 120
Db 140 S 140
CC
CC RESULT 23
CC GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89232738; PubMed=3145946;
RX Brueggemann M.;

```

```

HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HWMST7.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 12.4%; Score 437.5; DB 1; Length 138;
Best Local Similarity 68.3%; Pred. No. 1.2e-20;
Matches 82; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVLOQSGDPLVKGASVKISKASGYFTGYMHVWVQSGKGLWIGRINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVLOQPGAEVLKPGASVQLSCASGHTFTNYIHWVQRFGQGLEWIGINPNDRSNY 79
QY 61 NQKPKDKATLTVDKSTTAYMELRLTSGDSAVVYCARSTMTNVMYDYGQGSTVTS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFKKATLTVDKSSSTAYVQLSLSLTPEEFAVYCARSDGYDFV-YWGQGLTVTFS 138

RESULT 25
GCC RAT
ID GCC RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Gallfre P., Waldmann H., Calabi F.;
RT "Sequencing of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X07189; CAA30169.1; -.
DR FIK; S00847; S00847.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 12.4%; Score 437.5; DB 1; Length 329;
Best Local Similarity 26.1%; Pred. No. 4e-20;
Matches 140; Conservative 47; Mismatches 125; Indels 225; Gaps 16;

QY 121 AKTTPSVYPLAFGSAQAQNSMWTGLCLVKGYPPBPVTVTNWNSGSSGVHTTFAVLQSD 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ARTAFSVYPLVFGSGTSGSLVTLGLVKGYPPBPVTVTNWNSGSSGVHTTFAVLQSG 60

QY 181 LYLSSSVTVPSSTWPSSTVTCNVVHPASSTKVDKKIVPRDSDGGPSEKEINEKDLRKK 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 LYLSSSVTVPSSTWPSSTVTCNVVHPATKSNLKRIEPR-----RPPRPP 107

QY 241 SELQGTALGNLKIYYNKAITSSEKADQFLNTLFLKGFTHGFWNLDLVLGSTA 300
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
108 TDI-----CSCDDNLGRPSVF--IFPPKP--KDILM----- 134

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNRLTEKKVPINLWIDGKQ 350
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
135 -----ITL-----TP-KVTCVVVDVS-----EPEPDVQFS-WF- 160

QY 361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKVGQGLIVFHSSEGSTVS 420
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 -----VDNVRVFTAQTQPHQEEQLNGTFRVVSVTLHIHQDWMWSGK----- 199

QY 421 YDLFDAQQGYPDTLLRIYRDNTTISSTLSISLYLVTTSIVMTQTPTSLVSAGDRVIT 480
Db -----EPK 202

QY 481 CKASQSVNDVAMVQOKPGCKSLISYTSRVAGVDPDRFSGSGYGTDTFTLTISVQAED 540
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 CKVN-----NKDLPSP--IEKTIKPRG----- 223

QY 541 AAVYFCQDYNPPTFGGKTKLEIKRDAAPTIVSIFPPSEQLTSGASVGVCLANNFYPK 600
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
224 -----KARTPQVYTIPTPPPEQMSKNKVSILTCWTSFYPA 257

QY 601 DINWKWKIDSEKQVNLNSWTDQDSKDYMSSTLTILTKDEYERHNSYTCETHK 657
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 SISVERNG-ELEQDYKNTLPVLDSDSYFLYSLKSLVDTSDSMWRGDIYTCVVHE 312

```

```

RESULT 26
HV50 MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06379;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyrauther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBL J. 3:517-523(1984).
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; P00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453P426709834 CRC64;

Query Match 12.3%; Score 433; DB 1; Length 120;
Best Local Similarity 67.5%; Pred. No. 1.9e-20;
Matches 81; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 1 OVQLQSGPDLVPGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYCARSTMITNYMDYWGQGTSTVTVSS 120
DB 61 NEKFKSKATLTVDKSSATYMQLSSTPSDSAVYCARWDYEDRYFDVWGVTGTTVTVSS 120

RESULT 27
HV09 MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6789376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC PIR; D90809; HWS61.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.

```

```

DR InterPro; IPR003596; Ig_v.
DR Pfam; P00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 12.1%; Score 425; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 5.7e-20;
Matches 78; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 20 QVQLQSGPDLVPGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRIIDPSGTTY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYCAR 98
DB 80 NEKFKSKATLTVDTSSTAYMQLHSLTSDSAVYCAR 117

RESULT 28
KV5A_MOUSE
ID KV5A_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 35, Last annotation update)
DE Ig kappa chain v-v region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347(1978).
CC -!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

```

or send an email to license@isb-sib.ch).
CC EMBL; J00561; AAA38776.1; -.
DR PIR; A90823; KVM511.
DR HSSP; P80382; LWL.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 129 FRAMEWORK-3.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 FRAMEWORK-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match
Best Local Similarity 12.0%; Score 423; DB 1; Length 149;
Matches 82; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 450 IWTOTPTSLVSDAGRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPDR 519
D 43 IVMTQSHKFMKTSVGDRIYVITCKASQSVSTVAVYQKPGQSPKLLISYTSRYAGVPDR 102

QY 520 FSGSGYGTFTLTISVQAEAAVYFCQDYNPSPTFGGKLEIKR 566
D 103 FTGSGSGYGTFTLTISVQAEAAVYFCQDYNPSPTFGGKLEIKR 149

RESULT 29
HV14 MOUSE
ID HV14_MOUSE STANDARD; PRT; 117 AA.
AC P01758;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 108A precursor.
GN IGH-VJ558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81245215; PubMed=6789211;
RA Givol D., Zakut R., Efron K., Rechavi G., Ram D., Cohen J.B.;
RT "Diversity of germ-line immunoglobulin VH genes.";
RL Nature 292:426-430(1981).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00488; AAA38519.1; -.
DR PIR; A02041; HVMS8A.
DR HSSP; P01810; 2FBJ.
DR MGP; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.

```

```

DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match
Best Local Similarity 12.0%; Score 422; DB 1; Length 117;
Matches 83; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVLQSGPDLVKGASVKISCKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 60
D 20 EVLQSGPDLVKGASVKISCKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 79

QY 61 NQKFKSKATLTVDKSSTTAYMELRLSTSDSAVYYCAR 98
D 80 NQKFKSKATLTVDNSSSTAYMELSLTSDSAVYYCAR 117

RESULT 30
HV15 MOUSE
ID HV15_MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00494; AAA38130.1; -.
DR PIR; A02042; HVMSB1.
DR HSSP; P01772; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
FT DOMAIN 20 135 IG-LIKE.
FT NON TER 136 136
SQ SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35B CRC64;

Query Match
Best Local Similarity 11.9%; Score 420.5; DB 1; Length 136;
Matches 84; Conservative 11; Mismatches 22; Indels 3; Gaps 2;

```


RT "Developmentally controlled and tissue-specific expression of
 RT unarranged VH gene segments.";
 RL Cell 40:271-281(1985).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC The European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M13788; AAA38506.1; --
 DR PIR; A02035; MHMSB4.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 B4.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117
 FT SEQUENCE 117 AA; 12834 MW; B8862PAC67ABD345 CRC64;
 Query Match 11.8%; Score 414; DB 1; Length 117;
 Best Local Similarity 78.4%; Pred No. 2.7e-19;
 Matches 76; Conservative 10; Mismatches 11; Indels 0; Gaps 0;
 QY 2 VQLQSGDPLVKPGASVKISCKASGYSTGYMHWKQSPGKGLWIGRINPNNGVTLYN 61
 Db 21 VQLQPGAEVLKPGASVKLSKASGYTFTSYMHWKQRPGRGLEWIGNIDPNSGGKYN 80
 QY 62 QKFKDXTLTVDKSTTAYMELRLTSDSAVYYCAR 98
 Db 81 EKFKSKATLTVDKPSSTAYMQLSSLTSDSAVYYCTR 117
 RESULT 34
 ID HV06 MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region 102 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6;
 RC MEDLINE=81234548; PubMed=6789376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
 CC PIR; A02032; HVMS02.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117
 FT SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;
 Query Match 11.7%; Score 413; DB 1; Length 117;
 Best Local Similarity 80.2%; Pred No. 3.1e-19;
 Matches 77; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
 QY 2 VQLQSGDPLVKPGASVKISCKASGYSTGYMHWKQSPGKGLWIGRINPNNGVTLYN 61
 Db 21 VQLQPGAEVLKPGASVKSVKASGYTFTSYMHWKQRPGRGLEWIGRIHPSDSDTYN 80
 QY 62 QKFKDXTLTVDKSTTAYMELRLTSDSAVYYCA 97
 Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSDSAVYYCA 116
 RESULT 35
 ID GC2 CAVPO STANDARD; PRT; 329 AA.
 AC P01862;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2 chain C region.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1] SEQUENCE OF 1-3.
 RP Trischmann T.M.;
 RA Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RX MEDLINE=71058471; PubMed=5538606;
 RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cysteine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).

```

RN DISULFIDE BONDS.
RP MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC !- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; GZGP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003106; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS50835; IG-LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
FT SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 11.7%; Score 413; DB 1; Length 329;
Best Local Similarity 23.6%; Pred. No. 1.3e-18;
Matches 136; Conservative 61; Mismatches 104; Indels 276; Gaps 17;

QY 120 SAKTTPSVPLAPGSAOATNSMTLGLVKGYPFPPVTWNSGLSSGVHTFFAVLQS 179
DB 1 SAKTTPSVPLAPGSAOATNSMTLGLVKGYPFPPVTWNSGLSSGVHTFFAVLQS 60
QY 180 DLYTLSSVTPSGTWPESTVTCNVAPASSTKVDKKI-----VPRDS 222
DB 61 GLYSLTSMWTPS-----SOKATCNVAHPASSTKVDXTEPIRTPZBPCTCKPAPPENL 116
QY 223 GGPSEKSEBINEKRLKSELQGTALGNLQVYVNSKAITSSSEKSAQDFTLTLFKGF 282
DB 117 GGPS-----VFIPPKP-----128
QY 283 FTGHPWYNDLLVLGTAATSEYEGSSVDLYGAYGYCAGGTPNKTKAGYGVTLHDNN 342
DB 129 -----KDTLMISL-----TPRVT-CVVVDVS-----148
QY 343 RLTEKKVPINLWDGK-----QTTVPIDKVKTSKEVTVOELDLQARHVLHGKFLYNS 397
DB 149 --QDEPEVQTFWVDNKPVNAETKPRVEQYNTFFVESV--LPIQHWLKGK-----198
QY 398 DSFGGKQVGRGLVIFHSSEGSTVSYDLFDAQGYVPTDLLRIYRDNNTTISLSLSLYLT 457
DB 199 -----198
QY 458 TSIVMTQTPSLVLSAGDRVTITCKASQSVNSDVANVYQKPGSPKLLISYSSRYAGVP 517
DB 199 -----EFCKV-----YKALPAP---TEKTSKTKGAP 224
QY 518 DRFSGSGYGTDFLTISSVQAEDAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFP 577
DB 225 -----RMPDVTYLP 233
QY 578 PSSEQLTSGASVVCFLNFPYKDIINVKW---KIDGSEKRGVNLNWTODSKDSTYSMS 634
DB 234 PSRDELSKSVTVCLTINFPADIDHVEWASNRVPVSEK--YKNTPPIEDA-DGSYFLY 290
QY 635 STLTLTKDEYERHNSYTCETHKSTSTSPIV-KSFNRN 670
DB 291 SKLTVDKSAMDQGGIVYTCVNVHNAHNVTKAISRS 327

```

```

RESULT 36
KV4B HUMAN
ID KV4B HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00022; CAA77317.1; -
CC PIR; A01904; K4HJL.
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 83 114 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 115 122 BY SIMILARITY.
FT DISULFID 43 114
FT NON TER 133 133
FT SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 11.5%; Score 406.5; DB 1; Length 133;
Best Local Similarity 63.9%; Pred. No. 9.5e-19;
Matches 85; Conservative 16; Mismatches 21; Indels 11; Gaps 3;

QY 444 ISSSTLSLSLYLT-----SIWMTQTPSLVLSAGDRVTITCKASQSV-----SNDVAV 493
DB 2 VLQQTQVPSLILWISLGAYGDIWMTQSPDSLAVSGERATINCKSSQSVLSNNKNVLA 61
QY 494 YQKQPGSPKLLISYSSRYAGVPDRFSGSGYGTDFLTISSVQAEDAAVYFCQDYNSP 553
DB 62 YQKQPGSPKLLIYASTRESGVDRFSGSGYGTDFLTISLQAEADVAVVYCOQ-YDTI 120
QY 554 PTFGGTKLEIKR 566
DB 121 PTFGGTKVEIKR 133

RESULT 37

```



```

KV4C_HUMAN
ID   KV4C_HUMAN          STANDARD;          PRT;   134 AA.
AC   P06314;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-IV region B17 precursor.
OS   Homo sapiens (Human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041854; PubMed=2997713;
RA   Marsh P., Mills F., Gould H.;
RT   "Detection of a unique human V kappa IV germline gene by a cloned
RL   cDNA probe.";
RL   Nucleic Acids Res. 13:6531-6544(1985).
RN   [2]
RP   REVISION TO 76.
RA   Marsh P.;
RL   Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X02990; CAA26733.1; -.
DR   HSP; P03362; 1WT.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      20
FT   CHAIN           21     134   IG KAPPA CHAIN V-IV REGION B17.
FT   DOMAIN          21     43   FRAMEWORK-1.
FT   DOMAIN          44     60   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN          61     75   FRAMEWORK-2.
FT   DOMAIN          76     82   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN          83     114  FRAMEWORK-3.
FT   DOMAIN          115     121  COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN          122     133  FRAMEWORK-4.
FT   DISULFID        43     114   BY SIMILARITY.
FT   NON_TER         134     134
SQ   SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match          11.5%; Score 406; DB 1; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-18;
Matches 84; Conservative 15; Mismatches 24; Indels 10; Gaps 2;

QY  444 ISSTSLISLXYLT-----SIWMTQTPTSLVSGADRVITTCASQSV-----SNDVAV 493
DQ  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ  2 VLQTVFSLLMWISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSLYSNDKNVLA 61
QY  494 YQKPGQPKLLISYTSRYAGVDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNP 553
DQ  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ  62 YQKPGQPKLLIYWASTRESGVDRFSGSGYGTDFLTITSSVQAEVAVYVCOQYNLP 121
QY  554 PTFGGGTKEIKR 566
DQ  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ  122 WTFGGGTKEIKR 134

RESULT 38

```

```

HV05_MOUSE
ID   HV05_MOUSE          STANDARD;          PRT;   117 AA.
AC   P01749;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ig heavy chain V region 3 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPB family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:825-837(1981).
CC   -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC   RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; J00536; AAA38605.1; -.
DR   PIR; A02031; HVMS3.
DR   HSP; P01810; 2FBJ.
DR   MGD; MGI:96486; Igh-VJ558.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_V.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1      19
FT   CHAIN           20     117   IG HEAVY CHAIN V REGION 3.
FT   DOMAIN          20     49   FRAMEWORK-1.
FT   DOMAIN          50     54   COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN          55     68   FRAMEWORK-2.
FT   DOMAIN          69     85   COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN          86     117  FRAMEWORK-3.
FT   DISULFID        41     115   BY SIMILARITY.
FT   NON_TER         117     117
SQ   SEQUENCE 117 AA; 13016 MW; 427C861C53975EDC CRC64;

Query Match          11.5%; Score 404; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 1.1e-18;
Matches 75; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY  1 EVQLQSGPDLVKPGASVKISCKASGYSTGYMHWKSPGKGLWIGRIINPNNGVTLY 60
DQ  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ  20 QVQLQPGALVRPGSSVKLSCKASGYTFTSYMDVWKVQKPGQGLEWIGNIYPSDSETH 79
QY  61 NQKFKDKALITVDKSTTAYMELRLSTDSAVYYCAR 98
DQ  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ  80 NQKFKDKALITVDKSTSTAYMQLSLTSDSAVYYCAR 117

RESULT 39
GC3_MOUSE
ID   GC3_MOUSE          STANDARD;          PRT;   329 AA.
AC   P22436;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)

```

DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene";
 RL EMBO J. 3:2041-2046(1984).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
 CC PIR; B02156; G3MSM.
 CC HSSP; P01857; 1FC1.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003587; Ig cl.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00407; Igc1; 2.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 KW NON_TER 1 1
 FT DOMAIN 1 97 CHI.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CHI.
 FT DOMAIN 224 327 CHI.
 FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
 Query Match 11.4%; Score 401; DB 1; Length 329;
 Best Local Similarity 24.6%; Pred. No. 7.2e-18;
 Matches 135; Conservative 51; Mismatches 111; Indels 252; Gaps 15;
 QY 123 TTPSVYPLAPGAAOTNSMTGLCLVGVFPPTVTWNSSLSGSGVHTFPAVLQSDLY 182
 DB 2 TTPSVYPLVPGSDTSGSVTLGCLVGVFPPTVTWNSSLSGSGVHTFPAVLQSDLY 61
 QY 183 TLSSSVTPSTWPTSTVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKKE 242
 DB 62 SLSSLVTPSTWPTSTVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKKE 105
 QY 243 LQGTAL--GNLKIYYNSKAITSSSEKADQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
 DB 106 PGSSCCPGNI-----LG--- 118
 QY 301 ATSEYEGSSVDLYCAYGYQCAGGTNKTACMYGVTLHNNRLTBKVPINLWIDGQ 360
 DB 119 -----GPSVFIF-----DPK-----PKDALMISLTPKV 141
 QY 361 TTPIDKVTISKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVGRLVHSSSEGSTVS 420
 DB 142 TCVVVD-----VSEDD----- 152
 QY 421 YDLFDAQQYQPDLLRIYRNTTISSTLSISLYLTTISVTMTPTPTSLLSAGDRVTIT 480
 DB 153 -----PDVHVSFWFNKEVHT----- 168
 QY 481 CKASQSVNDVAVYQKPGGPKLLISYTSRYAGVPDRFSGSGYGTDP-TLTISVQAE 539
 DB 169 -----AWTQPREAQ-----YNSTRFVVSALPIQIQ 193
 QY 540 D---AAVVFQCDYNSPPTFGGKTKLEIKRAADAPTVISPPSSEQLTSGGASVVCFLNN 596

DB 194 DWMRGKFKCKVANKALPAPIERTISKPKGKRAQTPQVYTIPTPPREQMCKKVKSLTCLVIN 253
 QY 597 FYPKIDNVKWKIDGSRQVGLNSWTDQDSK-----DSTYSMSSTTLTKDEYERHN 648
 DB 254 FFEAISVEVE-----RNGEL-----EQDYKNTPPILDSDGTLYFLYSLKLTVDTSWLOGE 303
 QY 649 SYTCEATHK 657
 DB 304 IFTCSVVHE 312
 RESULT 40
 GC3M MOUSE
 ID GC3M MOUSE STANDARD; PRT; 398 AA.
 AC P03987;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-3 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene";
 RL EMBO J. 3:2041-2046(1984).
 CC [2]
 CC SEQUENCE OF 328-398 FROM N.A.
 CC MEDLINE=84041483; PubMed=6314258;
 CC Konaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
 CC Wall R.;
 CC "The structure of the mouse immunoglobulin in gamma 3 membrane gene
 CC segment";
 CC Nucleic Acids Res. 11:6775-6785(1983).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; J00451; AAB59655.1; -
 CC EMBL; V01526; CAA24767.1; ALT_SEQ.
 CC PIR; A02156; G3MSM.
 CC HSSP; P01857; 1FC1.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003587; Ig cl.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00407; Igc1; 2.
 CC PROSITE; PS00835; IG_LIKE; 3.
 CC PROSITE; PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 KW NON_TER 1 1
 FT DOMAIN 1 97 CHI.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CHI.
 FT DOMAIN 224 327 CHI.
 FT TRANSMEM 346 362 POTENTIAL.
 FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
 FT CONFLICT 333 333 E -> G (IN REF. 2).
 FT CONFLICT 342 342 E -> Q (IN REF. 2).
 FT CONFLICT 388 388 P -> F (IN REF. 2).
 FT SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

```

Query Match      11.4%; Score 401; DB 1; Length 398;
Best Local Similarity 24.6%; Pred. No. 9.4e-18;
Matches 135; Conservative 51; Mismatches 111; Indels 252; Gaps 15;

QY 123 TTPSPVPLAPGSAAGTNSWTLGCLVKGYPPEPTVTWNSGSLSSGVTTPAVLQSDLY 182
DB 2 TTPSPVPLAPGSAAGTNSWTLGCLVKGYPPEPTVTWNSGSLSSGVTTPAVLQSDLY 61

QY 183 TLSSSVTPSPSTWPTETVCNVAHPASSTKVDKIIPRDSGSPSEKSEINEKOLRKKSE 242
DB 62 SLSSLVTPSPSTWPTETVCNVAHPASSTKVDKIIPRDSGSPSEKSEINEKOLRKKSE 105

QY 243 LOGTAL--GNLQKIYYNSKAITSEKSAQDPLTNLLFKGFTGHPWYNDLLDLSGTA 300
DB 106 PFGSSCPPGNI-----VSDD-----LG--- 118

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPIINLWIDGK 360
DB 119 -----GPSVFIF-----PPK-----PKDALMISLTPKV 141

QY 361 TVPFDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDFGKVGKRGVILVHSSSEGSTVS 420
DB 142 TCWVVD-----VSDD----- 152

QY 421 YDLFDAQGYQPTLLRIYRDNTTISSTLSISLYLVTTSIVMTQPTPTLLVSAGDRVTIT 480
DB 153 -----PDVHVSFWVDNKEVT----- 168

QY 481 CKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPFGSGYGTDF-TLTSSVQAE 539
DB 169 -----AWTQPREAQ-----YNSFRVVSALPIQHQ 193

QY 540 D---AAVFCQDYNSTPFFGGTKLEIKRADAAPTIVSIFPPSSBOLTSGASVVCPLNN 596
DB 194 DMWGRKFKCKVNNKALPAPIERTSKPKRAQTPQVITIPPPRQMSKKVSLTCLVTN 253

QY 597 FYPKDINKWKIDGSRQNGVLSNWDQDSK-----DSTYSMSLTITLTKDEYERHN 648
DB 254 FSEALSVEWE-----RNGEL-----EQDYKNTPPILSDGTGYFLYSLKLTVDTSWLQGE 303

QY 649 SYTCEATHK 657
DB 304 IFTCSVWHE 312

```

```

RESULT 41
ID_GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]

```

```

RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
RN [9]
RP MISCELLANEOUS: NIE has the GIM(17) allotypic marker, 97-K, and the
CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC GIM(3) marker and the GIM (non-1) markers.
CC [1]- MISCELLANEOUS: NIE also differs in the amidation states of
CC 35, 116, 198, 269 and 272.
CC [1]- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC [1]- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [11]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [12]

```

DR PDB; 1D6V; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1H2H; 12-JUN-02.
 DR PDB; 1I7Z; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; .
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006855; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure. 1 1
 KW NON_TER 1 98
 FT DOMAIN 1 98 CHI.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 147
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 166
 FT TURN 168 171
 FT STRAND 176 179
 FT TURN 180 181
 FT STRAND 182 190
 FT STRAND 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 260 265
 FT STRAND 270 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 305 312
 FT TURN 313 314

FT TURN 316 317
 FT STRAND 320 325
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 11.3%; Score 397; DB 1; Length 330;
 Best Local Similarity 24.9%; Pred. No. 1.3e-17;
 Matches 135; Conservative 46; Mismatches 126; Indels 236; Gaps 16;
 QY 121 AKTTPSPVPLAGSAAQTNSMVTGLCLVKGYPPEPVTVTNSSGSLSSGSGVHTTFAVLQSD 180
 DB 1 ASTKGPSVFLAFSSKSTSGTAAALGCLVLDYPPPEPVTVSNWSGALTSGVHTTFAVLQSS 60
 QY 181 -LYTLSSVTVPSSTWPTSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSESEINEKDLRK 239
 DB 61 GLYSLSSVTVPSSSLGTQYICNVNHPKPNSTKVDKKEPKSC----- 103
 QY 240 KSELQGTALGNLKOIYYNSKAITSEKSDAQELTNTLLFKGFETGHPWYNDLLVDLGST 299
 DB 104 -----DRTHCTPPCPAPELLGGPSVF--LFPKP--KDTLM----- 135
 QY 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLMIDGK 359
 DB 136 -----ISRTEPVT-CVVVDVS-----HEDPEVKENWYVDG- 164
 QY 360 QTVPIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKGVQRLIVPHSSSEGSTV 419
 DB 165 ---VEVHNKTKPREEQ-----YNSY---RVSVLTVLHQDWLNGK 200
 QY 420 SYDLFDAQGVDPDTLLRIYRDNTTISLSLSLYLTVTSIVMTQTPTSLLSAGDRVTI 479
 DB 201 EY----- 202
 QY 480 TKKASQSVNDVAVYQKQPKLISYTSRYAGVDPDRFSGSGYGTDTLTLSVQAE 539
 DB 203 KCKVS-----NKALPAP--IEKTSKAKGP----- 226
 QY 540 DAAYFCQDYNPPTGGGKLEIKADAAPTISIIPPSSEQLTSGASVQVCFANFY 599
 DB 227 -----REPQYTLPPSRDELTKNOVSLTKLVKGFY 257
 QY 600 KDINVKWKIDGSEKQ-----GVLSNWTQDQSDKSTYSMSSTLTLTDEYERNHSYTCFA 654
 DB 258 SDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQQGVFSCSV 310
 QY 655 THK 657
 DB 311 MHE 313

RESULT 42

HV01_MOUSE
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 region of immunoglobulin heavy chain MPC11.";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

```
CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GWS511.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR007110; Iq-like.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 1.
DR SMART; SM00406; Iq; 1.
DR PROSITE; PS00835; Iq-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 Iq-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 11.3%; Score 396.5; DB 1; Length 121;
Best Local Similarity 62.8%; Pred. No. 3.4e-18;
Matches 76; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

Qy 1 EVQLQQSGPDLVKPGASVKISKAGSYFTGYMHVKQSPKGLGWIGRINPNNGVTLY 60
Db 1 EAQLQSGAGELVRPTSVKISKAGSYFTYWGVAERFGHLEWIGDIYFGGFTNY 60

Qy 61 NQKFKDKATLVVDKSGSTAYMELSLTSDSAVYCARSTMI-TNYVMDYQGQTSVTVS 119
Db 61 NDNLKGRKATLTADTSGSTAYIQLSLTSDSAIYHCARGIYNSPYFDSWGQGTILTVS 120

Qy 120 S 120
Db 121 S 121

RESULT 43
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RP [2]
RX SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.W., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL Biochem. J. 117:33-47(1970).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1ADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; P:antigen binding; TAS.
```

```
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Iq-like.
DR InterPro; IPR003597; Iq_c1.
DR InterPro; IPR003006; Iq_MHC.
DR Pfam; PF00047; Iq; 3.
DR SMART; SM00407; Iq; 1.
DR PROSITE; PS00835; Iq-LIKE; 3.
DR PROSITE; PS00290; Iq_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1 1
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 11.3%; Score 396.5; DB 1; Length 327;
Best Local Similarity 23.3%; Pred. No. 1.4e-17;
Matches 131; Conservative 52; Mismatches 102; Indels 277; Gaps 16;

Qy 121 AKTTPSVVPLAPCSAAQTNSVWTLGCLVKGYPPEPVTVWNSGLSSGVHTFPVQLQSD 180
Db 1 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

Qy 181 -LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKI-----VPRDSGGPSE 227
Db 61 GLYSLSVVTVFSSSLGTTCYTCNVDPKPSNKNVDKRVESKYGPCPCPAEFLGGPS- 119

Qy 228 KSEINEKOLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLPKGFTGHP 287
Db 120 -----VLFPPKPK-----KDTLMI----- 133

Qy 288 WYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTPTKTCACMYGGVTLHDNNRLTEE 347
Db 134 -----SRTPEVT-CVVVDVS-----QED 150

Qy 348 KKVPINLWIDGKQTVPIDKVKTSKEV-----TVQELDLQARHLHGKFLYNSDSF 400
Db 151 PEVOFNWYVDG---VEVHNAXTKPREQFNSTYRVSVTLVLHQDWLNGK----- 197

Qy 401 GGVQVQGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTIISTSLISLYLTTSI 460
Db 198 -----EY----- 199

Qy 461 VMTQTPTSLVSAGDRVTITCKASQSVSNDVAVYQQKPGQSPKLLISYTSRYAGVPDRF 520
Db 200 -----CKVSNK-----GLP--- 209

Qy 521 SSGGYGTDFTLTISVQAEADAAYFCQQDYNAPPTFGGQTKLEIKRADAAPTVSIPTSPS 580
Db 210 -----SSIEK-----TISKAKGQPREPQVYTLPPSQ 235

Qy 581 EQLTSGGASVVCFLNNFYPKDINVKWKIDGSEQN-----GVLSNWTQDSKDYTSMS 635
Db 236 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVDS-----DGSFFLYS 288

Qy 636 TLTLTKDEYERHNSVTCEATHK 657
Db 289 RLTVDSKRWQEGNVFSCVMHE 310

RESULT 44
KV4A_HUMAN STANDARD; PRT; 114 AA.
ID KV4A_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region Len.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonal immunoglobulin-L-chain of
 RL subgroup IV of the kappa type (Bence-Jones protein Len).";
 RN Hoppe-Sayler's Z. Physiol. Chem. 356:507-557(1975).
 RP REVISION TO 9.
 RA Salomon A.;
 RL Submitted (AUG-1996) to Swiss-Prot.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PDB; 1ERQ; 01-FEB-01.
 DR PDB; 1ERU; 03-FEB-01.
 DR PDB; 1ERQ; 09-FEB-01.
 DR PDB; 1EK3; 06-MAR-01.
 DR PDB; 1LVE; 21-JAN-98.
 DR PDB; 3LVE; 18-MAY-99.
 DR PDB; 5LVE; 28-MAR-01.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 113 FRAMEWORK-4.
 FT DISULFID 123 94 BY SIMILARITY.
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647FD1D7F236485 CRC64;
 Query Match 11.2%; Score 395; DB 1; Length 114;
 Best Local Similarity 69.9%; Pred. No. 3.9e-18;
 Matches 79; Conservative 12; Mismatches 16; Indels 6; Gaps 1;
 QY 460 IVMTQFTSLVAGDRVTITCKASQSV-----SNDVAYQKPKQSPKLLISYTSRY 513
 Db 2 IVMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPKQPKLLIYASTRE 61
 QY 514 AGVDPDFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSSPPTFGGKLEIKR 566
 Db 62 SGVDPDFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSSPPTFGGKLEIKR 114
 RESULT 45
 KV5B MOUSE
 ID KV5B MOUSE STANDARD; PRT; 136 AA.
 AC P01634; 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-V region MOPC 21 precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=82059477; PubMed=6170937;
 RA Hamlyn P.H., Gait M.J., Milstein C.;
 RT "Complete sequence of an immunoglobulin mRNA using specific priming
 RT and the dideoxynucleotide method of RNA sequencing.";
 RL Nucleic Acids Res. 9:4485-4494(1981).
 RN [2]
 RP SEQUENCE OF 30-136.
 RX MEDLINE=73053310; PubMed=4638343;
 RA Svasti J., Milstein C.;
 RT "The complete amino acid sequence of a mouse kappa light chain.";
 RL Biochem. J. 128:427-444(1972).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; V00810; CAA24192.1; ALT_TERM.
 DR PIR; A93736; KVM521.
 DR PDB; 1IGC; 03-JUN-95.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
 FT DOMAIN 30 52 FRAMEWORK-1.
 FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 64 78 FRAMEWORK-2.
 FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 127 136 FRAMEWORK-4.
 FT NON_TER 136 136
 SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;
 Query Match 11.2%; Score 395; DB 1; Length 136;
 Best Local Similarity 60.9%; Pred. No. 5e-18;
 Matches 81; Conservative 18; Mismatches 34; Indels 0; Gaps 0;
 QY 433 TLLRIYDNTTISTSTLSISLYITTSIVMTQFTSLVAGDRVTITCKASQSVNDVA 492
 Db 4 TSMGIRKMSHTLVFISILLCYLGADGNIVMTQSPKSNMSVGERVTLTCKASENVTVYS 63
 QY 493 WYQKPKQSPKLLISYTSRYAGVDPDFSGSGYGTDFLTITSSVQAEADAAVYFCQDYN 552
 Db 64 WYQKPKQSPKLLIYGASNYTGVDPDFSGSGATDFLTITSSVQAEADLADYHCGQYSY 123
 QY 553 PPTFGGKLEIKR 565
 Db 124 PYTFGGGKLEIKR 136
 RESULT 46
 HV52 MOUSE
 ID HV52 MOUSE STANDARD; PRT; 117 AA.
 AC P06327;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region VH558 A1/A4 precursor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85099340; PubMed=2578321;

```

RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M13787; AAA38499.1; -.
CC PIR; A02029; HVMGAL.
CC HSP; P01810; 2FUJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
FT SEQUENCE 117 AA; 12971 MW; 8B0BC138956DFC9D CRC64;

Query Match 11.1%; Score 392; DB 1; Length 117;
Best Local Similarity 75.5%; Pred. No. 6.3e-18;
Matches 74; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVLQSQGPDLPVPGASVKISCKASGYSTGYMHVQSPCKGLEWIGRINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 QVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKRPGQGLEWIGWYPGDGSTKY 79
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCAR 98
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCAR 117
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 47
ID_HVLC_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

```

```

CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
FT SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 10.9%; Score 385; DB 1; Length 147;
Best Local Similarity 55.5%; Pred. No. 2.3e-17;
Matches 71; Conservative 24; Mismatches 25; Indels 8; Gaps 1;

QY 1 EVLQSQGPDLPVPGASVKISCKASGYSTGYMHVQSPCKGLEWIGRINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 20 QVQLQSGAEVRKPGASRVKSCASGYTFTDSYIHWIRQAPGKLEWIGWINSQGTNY 79
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCARs-----TWITVYMDYWGQ 112
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 APRFQGRVTMTDRDASFSTAYMDLRLSRDSDSAVFYCAKSDPPFWSDYNTDYSTLDVWGQ 139
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 113 GTSVTYSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 140 GTTIVTVSS 147
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 48
ID_GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2...
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RA "Linkage and sequence homology of two human immunoglobulin gamma
RA heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RA "Structure of human immunoglobulin gamma genes: implications for
RA evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;

```

RT "Comparison of the hinge-coding segments in human immunoglobulin gamma heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass genes.";
 RT EMBO J. 1:403-407(1982).
 RN [4]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=674012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]

RP SEQUENCE OF 1-95 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:759-767(1979).
 RN [6]

RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;

RT Submitted (MAR-1980) to the PIR data bank.
 RL [8]

RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=95255298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]

RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]

RP DISULFIDE BONDS.
 RX MEDLINE=59064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;

RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
 RN [11]

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; J00230; AAB59393.1; -

DR PIR; A93906; G2HU.

DR HSP; P01857; 1FC1.

DR Genew; HGNC:5526; IGHG2.

DR MIM; 147110; -

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003623; F:antigen binding; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig ci.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON TER 1 1
 FT DOMAIN 99 98
 FT HINGE. 110
 FT CH1. 111
 FT DOMAIN 219
 FT CH2. 220
 FT DOMAIN 326
 FT CH3. 327
 FT INTERCHAIN (WITH A LIGHT CHAIN). 14
 FT DISULFID 27
 FT DISULFID 83
 FT DISULFID 102
 FT DISULFID 103
 FT DISULFID 106
 FT DISULFID 109
 FT DISULFID 109
 FT DISULFID 140
 FT DISULFID 200
 FT DISULFID 246
 FT DISULFID 304
 FT SITE 156
 FT SITE 156
 FT MOR_RES 326
 FT MOR_RES 326
 FT VARIANT 60
 FT VARIANT 60
 FT CONFLICT 109
 FT CONFLICT 109
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ

Query Match 10.78; Score 378; DB 1; Length 326;

Best Local Similarity 22.2%; Pred. No. 1.9e-16;

Matches 123; Conservative 56; Mismatches 113; Indels 262; Gaps 14;

QY 121 AKTTPPSVYPLAPGSAQTNSMVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
 DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 60

QY 181 -LYLSSSVTVFSPSTWPESETVTCNVAHPASTKVDKIVPR-----DSGGPSEK 228
 DB 61 GLYSLSSVTVFSPSNFGTQTYTCNVDPKPNKVDKTVERRKCCVCEPCPCAPPVAGS-- 118

QY 229 SEENKDLKKSELOQTALGNLQKQIYYNSKAITSEKSAQDQFLTLTLFKGFTGHPW 288
 DB 119 -----VLFPPKP-----KDTLMI----- 132

QY 289 YNDLLVLGSTATSEVEGSDVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNLTTEK 348
 DB 133 -----SRTEPT-CVVVDVS-----HEDP 150

QY 349 KVPINLMDGQTTVPIDVKTSKKEVTQVDELQARHLHGKFLYNSDSFGKVGQRL 408
 DB 151 EVQFNWIVDG-----VEVNAKTPRE----- 172

QY 409 IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISTSLSLSLYLTYTSIVNTQPTS 468
 DB 173 -----EQFNSTFRVSVLTVVHQD----- 191

QY 469 LLVSAGDRVTITCKASQSVNDVAVYQKQKQSPKLLISYSSRYAGVPDRFSSGYGTD 528
 DB 192 -----WLNQKEYC-----KVSNGGLPAP 210

QY 529 FTLTISSVQARDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTIVSIFPPSSEQLTSGGA 588
 DB 211 IETKISKTGQ-----PREPQVYTLPPSREMTKNQV 242

QY 589 SVVCFNLNFYPKDINVKWKIDGSRQN-----GVLSNWTQDSDKSTYSMSSTLTITKDE 643
 DB 243 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR 295

QY 644 YERNSTCEATHK 657

DB 296 WQQGNVFCSSVWHE 309

QY 644 YERNSTCEATHK 657

DB 296 WQQGNVFCSSVWHE 309

QY 644 YERNSTCEATHK 657

DB 296 WQQGNVFCSSVWHE 309

QY 644 YERNSTCEATHK 657

DB 296 WQQGNVFCSSVWHE 309

QY 644 YERNSTCEATHK 657

DB 296 WQQGNVFCSSVWHE 309

RESULT 49

KWIM HUMAN

ID KWIM HUMAN STANDARD; PRT; 108 AA.

AC P01605;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Lay.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 RT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RL specificities".
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01871; KIHULY.
 DR HSSP: P01607; IREI.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;
 Query Match 10.6%; Score 375; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 6.3e-17;
 Matches 74; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
 QY 460 IVMTPTSLVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
 Db 2 IQMTSPSLSVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
 QY 520 FSGSGYGTDTLTISVQAEADAAVYFCQDYNPPPTFGGKLEIKR 566
 Db 62 FSGSGYGTDTLTISVQAEADAAVYFCQDYNPPPTFGGKLEIKR 108
 RESULT 50.
 ID KV3H HUMAN STANDARD; PRT; 129 AA.
 AC P04207;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8617570; PubMed=3083417;
 RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene".
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
 CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M12740; AAA58992.1; -.
 DR HSSP: P80362; 1WTL.
 DR GO: GO:0005576; C:extracellular; NAS.
 DR GO: GO:0003823; F:antigen binding; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BB60CC14 CRC64;
 Query Match 10.6%; Score 372.5; DB 1; Length 129;
 Best Local Similarity 65.8%; Pred. No. 1.2e-16;
 Matches 73; Conservative 17; Mismatches 20; Indels 1; Gaps 1;
 QY 457 TTSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGV 516
 Db 19 TGEIVMTQSPATLSVSPGERATLSKASQSVNNLAWYQKQPPRLIYGASTRATGI 78
 QY 517 PDRFSGSGYGTDTLTISVQAEADAAVYFCQDYNPPPTFGGKLEIKR 566
 Db 79 PARFSGSGYGTDTLTISVQAEADAAVYFCQDYNPPPTFGGKLEIKR 129
 RESULT 51
 ID HV1G HUMAN STANDARD; PRT; 117 AA.
 AC P23083;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=28411108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zeng S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus".
 RL EMBO J. 7:1047-1051(1988).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

or send an email to license@sib-sib.ch).

```
CC ENBL; X07448; -; NOT_ANNOTATED_CDS.
CC DR PIR; S00476; HVH035.
CC DR HSP; P01772; 2FB4.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Signal.
CC FT SIGNAL 1 19
CC FT CHAIN 20 117 IG HEAVY CHAIN V-1 REGION V35.
CC FT DOMAIN 20 >117 IG-LIKE.
CC FT NON TER 117 117
CC SQ SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;

Query Match 10.5%; Score 370; DB 1; Length 117;
Best Local Similarity 68.4%; Pred. No. 1.4e-16;
Matches 67; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLOQSGPLVPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRIINPNNGVTLY 60
DB 20 QVLOVSGAEVKKPGASVKVSCKASGYTFGYMHVWVWVQPGGLEWGRINPNSGGTY 79
QY 61 NQKFKDKATITVDKSTTAYMELRLSTSDSAVYYCAR 98
DB 80 AQKFGQVSTRTSTSTAYMELRLSRSDDTVYYCAR 117

RESULT 52
KV1W HUMAN
ID KV1W HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups".
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01868; KIHUHU.
CC DR HSP; P80362; 1WTL.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Bence-Jones protein.
CC FT SIGNAL 23 34 FRAMEWORK-1.
CC FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 35 49 FRAMEWORK-2.
CC FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 57 88 FRAMEWORK-3.
CC FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 98 107 FRAMEWORK-4.
CC FT DOMAIN 98 107
```

```
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 10.5%; Score 369; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1.5e-16;
Matches 70; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSGADRVTTICKASQSVNDVAWYQKQSPKLLISYTSRYAGVDP 519
DB 2 IQMTQSPSLASVGDRTVITCRASQSVNSISSLYWYQKQKAPQVLIYAASSLPSGVPSR 61

QY 520 PFGSGYGTDTLTITSSVOAEDAAVYFCQDYNPPTFGGTTKLEIKR 566
DB 62 PFGSGSGTDTLTITSSLPQEDFAVYCCQNYITPTSPGQTRVEIKR 108

RESULT 53
KV3D HUMAN
ID KV3D HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region Ti.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72188439; PubMed=5027703;
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT Ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production."
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC PIR; A01895; K3HUTI.
CC DR HSP; P80362; 1WTL.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0003823; F:antigen binding; NAS.
CC DR GO; GO:0006955; P:immune response; NAS.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS00835; IG_LIKE; 1.
CC DR Immunoglobulin V region; Bence-Jones protein.
CC FT DISULFID 23 89 BY SIMILARITY.
CC FT NON TER 109 109
CC SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;

Query Match 10.5%; Score 368.5; DB 1; Length 109;
Best Local Similarity 65.7%; Pred. No. 1.6e-16;
Matches 71; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVTTICKASQSVNDVAWYQKQSPKLLISYTSRYAGVDP 518
DB 2 IVLITQSPGTLSPGERATISCRASQSVNSFLAWYQKQKAPRLIYVASSRATGIPD 61

QY 519 PFGSGYGTDTLTITSSVOAEDAAVYFCQDYNPPTFGGTTKLEIKR 566
DB 62 PFGSGSGTDTLTITSSLPQEDFAVYCCQYGVSSPSTFGQTKVELKR 109

RESULT 54
KV1W HUMAN
ID KV1W HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
```

```

DN 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 FRAMEWORK-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 FRAMEWORK-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 10.4%; Score 368; DB 1; Length 129;
Best Local Similarity 67.9%; Pred. No. 2,2e-16;
Matches 72; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDR 519
DB 24 IQMTQSPSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDR 83
QY 520 FSGSGYGDFTLTISVQAEAAVYFCQDYNSTPTFGGKLEIK 565
DB 84 FSGSGYGDFTLTISVQAEAAVYFCQDYNSTPTFGGKLEIK 129

RESULT 55
KV3F HUMAN
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE IG kappa chain V-III region POW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```

```

RN SEQUENCE
RP MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01897; K3HUPM.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 10.3%; Score 364.5; DB 1; Length 109;
Best Local Similarity 65.7%; Pred. No. 2,9e-16;
Matches 71; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

QY 460 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDP 518
DB 2 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDP 61
QY 519 RFSGSGYGDFTLTISVQAEAAVYFCQDYNSTPTFGGKLEIKR 566
DB 62 RFSGSGYGDFTLTISVQAEAAVYFCQDYNSTPTFGGKLEIKR 109

RESULT 56
KV3L HUMAN
ID KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; P00022; K3HJHA.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.

```

```

FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 10.3%; Score 364.5; DB 1; Length 129;
Best Local Similarity 64.9%; Pred. No. 3.6e-16;
Matches 72; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

QY 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAG 515
DB 19 TGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYGASSRATG 78

QY 516 VPRFSGSGVGTDFTLTISSVQAEADAAVFCQDYNPPTFGGKYLEIKR 566
DB 79 IPDRFSGSGGTDFTLTISSRLPEDFAVYCCQYGTSPRTFGQTKVEIKR 129

RESULT 57
KV1B_HUMAN STANDARD; PRT; 117 AA.
ID KV1B_HUMAN
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=63144029; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUG.
DR HSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IG_V.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 117
FT NON TER 117 117 IG-LIKE.
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 10.3%; Score 362; DB 1; Length 117;
Best Local Similarity 66.3%; Pred. No. 4.5e-16;

```

```

Matches 65; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLQQSGDPLVRPGASVKISKASGYSTGYNHWVKSPGKLEWIGRIINPVGVTLY 60
DB 20 QVQLVQSGAEVKKPGASVKISCKASGYTFNYSYHWVRQAPGQGLEWMGIINPSSGGS 79
QY 61 NQKPKDKATITVDKSTTAYWELRSLTSEDSAVVYCAR 98
DB 80 AQKPGQRTVMTTRDTSTSTVYNELSLRSEDSTAVYCAR 117

RESULT 58
KV3B_HUMAN STANDARD; PRT; 109 AA.
ID KV3B_HUMAN
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=82046598; PubMed=6794615;
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01892; K3HUSI.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG_V; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
KW DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 10.3%; Score 361.5; DB 1; Length 109;
Best Local Similarity 64.8%; Pred. No. 4.4e-16;
Matches 70; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVLSAGDRVTITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAGVPD 518
DB 2 IVLTQSPGTLSPGERATLSCRASQSVNSYLAWYQKPGQAPRLLIYGASSRATGIPD 61

QY 519 RFSGSGVGTDFTLTISSVQAEADAAVFCQDYNPPTFGGKYLEIKR 566
DB 62 RFSGSGSGGTDFTLTISSRLPEDFAVYCCQYGTSPRTFGQSKVEIKR 109

RESULT 59
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

```

RN RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
CC PIR; A01914; KVMG26.
DR HSP; P80362; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 10.3%; Score 361.5; DB 1; Length 113;
Best Local Similarity 65.2%; Pred. No. 4.6e-16;
Matches 73; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQV--SND---VAVYQKPGQSPKLLISYTSRYA 514
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 VVMTQPTSLVLSGLGERATINCRSSQSVLYSSNNKNYLAAYQKPGQAPKLLFSWASTRE 61
QY 515 GVPDRFSGSGGTDTLTITSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKR 566
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 GVPDRFSGSGGTDTLTITSSVQAEADIGYFCSTHTVPPFGGTTKLEIKR 113

RESULT 60
KV4D HUMAN STANDARD; PRT; 109 AA.
AC P83593.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal adipose tissue;
RX MEDLINE=98249779; PubMed=9588180;
RA Olsen K.E., Sletten K., Westermarck P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
SQ SEQUENCE 24 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 10.2%; Score 360; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 5.3e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQVSNDAVYQKPGQSPKLLISYTSRYAGVDR 519
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IQWTQSTSLASLGLDRVTISCRASQDISNLYNWYQKPGDGTVKLLIYTSRLHSGVFSR 61
QY 520 FSGSGYGTDTLTITSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKR 566

```

```

FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 109
FT DISULFID 23 94
FT UNSURE 23 23
FT NON TER 94 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 10.2%; Score 361; DB 1; Length 109;
Best Local Similarity 65.7%; Pred. No. 4.7e-16;
Matches 71; Conservative 12; Mismatches 19; Indels 6; Gaps 1;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQV-----SNDVAVYQKPGQSPKLLISYTSRY 513
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IVMTQSPDSLVSGLGERATINCRSSQSVLYSSNNKNYLAAYQKPGQAPKLLFSWASTRE 61
QY 514 AGVPDRFSGSGGTDTLTITSSVQAEAAVYFCQDYNSPPTFGGTTK 561
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 SGVPDRFSGSGGTDTLTITPGIQAEDVAVYICQVYRIPYTFGGQAK 109

RESULT 61
KVSM_MOUSE STANDARD; PRT; 108 AA.
ID KVSM_MOUSE AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 10.2%; Score 360; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 5.3e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQVSNDAVYQKPGQSPKLLISYTSRYAGVDR 519
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IQWTQSTSLASLGLDRVTISCRASQDISNLYNWYQKPGDGTVKLLIYTSRLHSGVFSR 61
QY 520 FSGSGYGTDTLTITSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKR 566

```

Db 62 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 108
RESULT 62
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III".
RL Nucleic Acids Res. 13:6499-6513 (1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00021; CAA77316.1; -
DR PIR; A01899; K3HU41.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT DOMAIN 21 128 FRAMEWORK-1.
FT DOMAIN 21 43 FRAMEWORK-2.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 118 128 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957P0FE3B9012 CRC64;
Query Match 10.2%; Score 360; DB 1; Length 128;
Best Local Similarity 64.5%; Pred. No. 6.8e-16;
Matches 71; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 457 TTSVMTQPTSLVLSAGDRTVITCKASQSVNDVAWYQKQPSKLLISYTSRYAGV 516
Db 19 TGEIVLTQSGTSLSPGSEATLSCRASQSVSNLAWYQKQPSKLLIRDAASSRANGI 78
QY 517 PDRFSGGSGTDFLTITSSVQAEAAVYFCQDYNPPTFGGKLEIKR 566
Db 79 PDRFSGGSGTDFLTITSLRLEPDAFVYQCYQYTSPTSTPTFGGKLEIKR 128
RESULT 63
KV5K_MOUSE STANDARD; PRT; 108 AA.
ID KV5K_MOUSE

AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype".
EL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR PIR; A01927; KVSAR.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region.
KW FRAMEWORK-1.
FT DOMAIN 1 23 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 50 56 FRAMEWORK-3.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63BFF597 CRC64;
Query Match 10.2%; Score 358; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 7.1e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;
QY 460 IVMTQPTSLVLSAGDRTVITCKASQSVNDVAWYQKQPSKLLISYTSRYAGV 519
Db 2 IQMTQTTSSLSASLGDRVTISCRASQDISNLYNWYQKQPDGTVKLLIYTSRLHSGVPSR 61
QY 520 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 566
Db 62 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 108
RESULT 64
KV40_HUMAN STANDARD; PRT; 121 AA.
ID KV40_HUMAN
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN IGKV41-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene".
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -!- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00023; CAA77318.1; -.
DR PIR; A01902; K4HU.
DR HSP; P80362; 1WTL.
DR Genew; HGNC:5834; IGKV4-1.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 10.2%; Score 358; DB 1; Length 121;
Best Local Similarity 61.7%; Pred. No. 8.3e-16;
Matches 74; Conservative 15; Mismatches 21; Indels 10; Gaps 2;

QY 444 ISSISLS:SLVLYTT-----SIWMTQTPTSLVSGADRVITCKASQSV-----SNDVAV 493
Db 2 VLQGVF:SLLMWISGAGDIVMTQSPDSLAVS:GERATINCKSQSVLYSSNNKNYLAW 61
QY 494 YQKPGQSPKLLISYTSRYAGVDPFRSGSGYGTDFLTITSSVQAEAAVYFCQDYNP 553
Db 62 YQKPGQSPKLLIYWASTRESGVDPFRSGSGYGTDFLTITSSLOAEDVAVYCYQYVSTP 121

RESULT 65
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8171307; PubMed=3127527;
RA Kilps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
DR J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC leukemia.
CC Immunoglobulins expressed in patients with chronic lymphocytic
DR PIR; P10021; K3HUHI.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.

```

```

DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 10.2%; Score 357.5; DB 1; Length 129;
Best Local Similarity 64.0%; Pred. No. 9.8e-16;
Matches 71; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

QY 457 TTSIVMTQTPTSLVSGADRVITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAG 515
Db 19 TGEIVLTQSPGTLSPGGERATLSCASQSVSSSYSLAWYQKPGQAPRLIYGASRATG 78
QY 516 VDPFRSGSGYGTDFLTITSSVQAEAAVYFCQDYNPPTFGGKLEIKR 566
Db 79 IPRFRSGSGYGTDFLTITISRLPEXDFAVYCYQYSGSPWTFGGQTKVEIKR 129

RESULT 66
KV1S_HUMAN
ID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
RT Wes).";
DR Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; K1HUWS.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein.
FT SIGNAL 1 23
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.

```

```

FT DOMAIN      89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN      98 107 FRAMEWORK-4.
FT DISULFID    23 88 BY SIMILARITY.
FT NON TER     108 108
SQ SEQUENCE    108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match
Best Local Similarity 10.1%; Score 357; DB 1; Length 108;
Matches 70; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKQPGQSKLLISYTSRYAGVPR 519
Db 2 IQMTQSPSSVASGVRVTITCKASQSVNDVAVYQKQPGQSKLLISYTSRYAGVPR 61

QY 520 FSGSGVGTDTLTISVQAEADAAVFCQDYNPPTFGGKLEIKR 566
Db 62 FSGSGSGTDTLTIDPNEEDTATYFCQSRLLPRTFGGKLEIKR 108

RESULT 67
KVSP MOUSE
ID_KVSP_MOUSE STANDARD; PRT; 108 AA.
AC P01649;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V regions (Anti-arsonate antibodies).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=77250895; PubMed=70482;
RA Capra J.D., Tung A.S., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. V. The complete amino acid sequence of the light chain
RT variable regions of anti-p-azophenylarsonate antibodies from A/J mice
RT bearing a cross-reactive idiotype."
RL J. Immunol. 119:993-999 (1977).
CC -1- MISCELLANEOUS: THE MIXTURE SEQUENCED CONTAINED AT LEAST TWO OR
CC THREE DIFFERENT LIGHT CHAINS. PEPTIDES CONTAINING THE FOLLOWING
CC SUBSTITUTIONS WERE ALSO ISOLATED: 3-VAL, 10-ILE, AND 12-LEU;
CC 22-LBU; 36-PHE, 41-GLU, AND 43-ALA; 63-THR AND 68-ARG; 76-SER,
CC 77-SER, 78-VAL, 80-ALA, AND 85-ASP; AND 100-GLN AND 107-ARG.
CC PIR; A01928; KVM5AA.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12056 MW; AE2861E6AAC09DD2 CRC64;

Query Match
Best Local Similarity 10.1%; Score 356; DB 1; Length 108;
Matches 71; Conservative 9; Mismatches 27; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKQPGQSKLLISYTSRYAGVPR 519
Db 2 IQMTQSPSSVASLGDRVSIKASQSVNDVAVYQKQPGQSKLLISYTSRYAGVPR 61

```

```

QY 520 FSGSGVGTDTLTISVQAEADAAVFCQDYNPPTFGGKLEIKR 566
Db 62 FSGSGSGTDTLTIDPNEEDTATYFCQSRLLPRTFGGKLEIKR 108

RESULT 68
GC_RABIT
ID_GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397 (1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349 (1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes."
RN Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022 (1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G."
RN Biochem. J. 116:249-259 (1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebowitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -1- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC markers and Ref.5 the E15 marker.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M16426; AAA31289.1; -.
CC PIR; A91749; GHRB.
CC HSP; P01857; 1FC1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IGC1; 2.
CC PROSITE; PS50835; IG_LIKE; 3.

```


DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1
FT DOMAIN 6 96 IG-LIKE 1.
FT DOMAIN 114 213 IG-LIKE 2.
FT DOMAIN 222 318 IG-LIKE 3.
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> S (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69B8AA118D579A8B CRC64;

Query Match 10.1%; Score 356; DB 1; Length 323;
Best Local Similarity 24.0%; Pred. No. 4.3e-15;
Matches 134; Conservative 57; Mismatches 111; Indels 256; Gaps 19;

QY 126 PSVYPLARSAQAQNSMTVGLGVKGYPPVPTVWNSGSLSSGVTTPAVLQSD-LYTL 184
DB 6 PSVFPPLAFCCGDPSTVTGLGVKGYLPEPVTWNSGTLNGVTRTPSVRQSGLYSL 65

QY 185 SSSVTPSTPSEVTVCNVAHPASTKVDKIVPRDGGSPSEKSENEIKDLKKSELQ 244
DB 66 SSVSVSTSSQP---VTCNVAHPATNTKVDKTVAPSTCKTCTPPPEL-----LG 112

QY 245 GTALGNLQIYYNSKAITSEKSDAQLTNTLLFKGFTTGHPTWNTDLLVLDGTAATSE 304
DB 113 GPSV-----FIFPPKPTLM----- 128

QY 305 YEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGKQTV 364
DB 129 -----ISRTPVET-CVVVDVS-----QDDPEVQFTWYINNEQ--- 159

QY 365 LDKVKTSKKEVTQELDLQARHLYHGKGLYNSDFGKVGKVGRLIVFHSSSGSVSYDLF 424
DB 160 ---VTARPPUREQQF----- 172

QY 425 DAQGYPTLLRIYRDNTTISSTLSLSLYTTSIVMTQPTSLVLSAGDRV---TITC 481
DB 173 -----NSTIRWS-----TLPTHQDWLGRKFKC 197

QY 482 KASQSVNDVAVYQKQKSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTISVQAE 541
DB 198 KV-----HNKALPAP---IEKTIKARGQP----- 219

QY 542 AVYFCQDYNPPTFGGKTKLEIKRAADAAPVSIFFPSSEQLTSGGASVWCFLNAYPKD 601
DB 220 -----LE-----PKVYTMGPPEELSRSLTCTNMGFTPSD 252

QY 602 INVKKIDGSEKQN-----GVINGWTDQDSKSTYSMSSTLTITKDEYERHNSYTC--- 652
DB 253 ISVEWKNKGAEDNYKTPPAVLDS-----DGSVFLYNKLSVPTSEWQGRDVTCTSV 305

QY 653 EATHKTSPIVKSFN 670
DB 306 EALHNHYTQ---KSLSRS 320

RESULT 69
KVLP HUMAN
ID KVLP HUMAN PRT; 108 AA.
AC P01608;

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG kappa chain V-I region Roy.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE
MEDLINE=68362076; PubMed=5595110;
Hiltschmann N.;
"Chemical structure of 2 kappa-type Bence Jones proteins (Roy and Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967))."
Cum.);
[2]
REVISIONS TO 39 AND 41.
Hiltschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franek F., Sugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEB5A313DF3A CRC64;

Query Match 10.1%; Score 355; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1.1e-15;
Matches 70; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVITCKASQSVNDVAVYQKQKSPKLLISYTSRYAGVDP 519
DB 2 IQMTQSPSLASVSGDRVITTCQASQDISIFLNWYQKQKSPKLLIYDASKLEAGVPSR 61

QY 520 FSGSGYGTDTLTISVQAEAAVYFCQDYNPPTFGGKTKLEIKR 566
DB 62 FSGTSGTDTLTISLQEDATYTCQDFDLPLTFGGGTVDFR 108

RESULT 70
KV5L MOUSE
ID KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
IG kappa chain V-V region HP 93G7.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]

```

SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idioType."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 FRAMEWORK-4.
FT DOMAIN 57 88 BY SIMILARITY.
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFFF58E CRC64;

Query Match 10.1%; Score 355; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1.1e-15;
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSAGDRVTITCKASQSVNDVAWYQKQPKLLISYTSRYAGVDPDR 519
Db 2 IQMTQSPSSLSASVGDRTVTITCRASQDITNYVWFQQRPGQPKVLIYGASILETGVPDR 61

QY 520 FSGSGYGTDFLTITSSVQAEADAAYVFCQDYNSSPTFGGKLEIKR 566
Db 62 FSGSGGTDFTLITSSVLEQEDITATYFCQGNMLPTFGGKLEIKR 108

RESULT 71
KV1Y HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7939311;
RX Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RX Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RX Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RX Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the V-
RT related fragment of the human kappa Bence Jones protein wat."
RL J. Mol. Biol. 147:185-193(1981).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB: 1WTU; 01-NOV-94.
DR GO: 0005576; C:extracellular; NAS.
DR GO: 0003823; F:antigen binding; NAS.

```

```

GO: 0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 FRAMEWORK-4.
FT DOMAIN 57 88 BY SIMILARITY.
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 10.1%; Score 354; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.3e-15;
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSAGDRVTITCKASQSVNDVAWYQKQPKLLISYTSRYAGVDPDR 519
Db 2 IQMTQSPSSLSASVGDRTVTITCRASQDITNYVWFQQRPGQPKVLIYGASILETGVPDR 61

QY 520 FSGSGYGTDFLTITSSVQAEADAAYVFCQDYNSSPTFGGKLEIKR 566
Db 62 FSGSGGTDFTLITSSVLEQEDITATYFCQDYLPLTFGGTKVDIKR 108

RESULT 72
KV5N MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 124B1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RX Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idioType."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.

```

```

DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEP2A2 CRC64;

Query Match
Best Local Similarity 10.1%; Score 354; DB 1; Length 108;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGADRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 108

RESULT 73
KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains."
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01872; KIHUOV.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEP2A2 CRC64;

Query Match
Best Local Similarity 10.1%; Score 354; DB 1; Length 108;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGADRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 108

RESULT 74
KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match
Best Local Similarity 10.0%; Score 353; DB 1; Length 108;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGADRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVITTCASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPDR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGQTKLEIKR 108

RESULT 75
KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 58.4605 Seconds
(without alignments)
3626.866 Million cell updates/sec

Title: US-09-900-766-1
Perfect score: 3522
Sequence: 1 EVQLQQSGFDLVKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1010	28.7	463	11 Q99LC4	Q99LC4 mus musculus
2	948	26.9	260	16 Q91M4	Q91M4 staphylococ
3	929.5	26.4	238	11 Q8VC16	Q8VC16 mus musculus
4	924.5	26.2	473	11 Q9B8L4	Q9B8L4 mus musculus
5	918	26.1	260	16 Q99SU3	Q99SU3 staphylococ
6	917.5	26.1	473	11 Q99L25	Q99L25 mus musculus
7	910	25.8	239	11 Q8VC55	Q8VC55 mus musculus
8	909.5	25.8	238	11 Q99M37	Q99M37 mus musculus
9	908	25.8	234	11 Q91WF8	Q91WF8 mus musculus
10	902	25.6	468	11 Q99L31	Q99L31 mus musculus
11	900	25.6	233	11 Q91WS9	Q91WS9 mus musculus
12	899.5	25.5	470	11 Q7TMK1	Q7TMK1 mus musculus
13	897	25.5	236	11 Q7TMK3	Q7TMK3 mus musculus
14	896	25.4	234	11 Q8R062	Q8R062 mus musculus
15	893	25.4	278	11 Q921K1	Q921K1 mus musculus
16	890.5	25.3	235	11 Q7TMK0	Q7TMK0 mus musculus

17	889	25.2	459	11 Q8R3V9	Q8R3V9 mus musculus
18	888.5	25.2	474	11 Q8R3H6	Q8R3H6 mus musculus
19	886	25.2	236	11 Q7TS98	Q7TS98 mus musculus
20	881.5	25.0	235	11 Q91W12	Q91W12 mus musculus
21	880.5	25.0	239	11 Q8K0F8	Q8K0F8 mus musculus
22	870.5	24.7	234	11 Q8R028	Q8R028 mus musculus
23	870	24.7	214	11 Q9R1A5	Q9R1A5 mus musculus
24	862	24.5	437	11 Q9R1A4	Q9R1A4 mus musculus
25	850	24.1	234	11 Q8VCP0	Q8VCP0 mus musculus
26	803	22.8	473	11 Q91Z05	Q91Z05 mus musculus
27	768	21.8	268	2 Q85217	Q85217 staphylococ
28	750	21.3	469	4 Q7Z7P5	Q7Z7P5 homo sapien
29	691	19.6	234	4 Q7Z473	Q7Z473 homo sapien
30	689	19.5	236	4 Q7Z3V4	Q7Z3V4 homo sapien
31	686.5	19.0	482	4 Q7Z351	Q7Z351 homo sapien
32	669.5	19.0	239	4 Q8NEK0	Q8NEK0 homo sapien
33	666.5	18.9	470	4 Q7Z5W1	Q7Z5W1 homo sapien
34	662.5	18.8	473	4 Q8TC63	Q8TC63 homo sapien
35	654.5	18.6	239	4 Q8TCD0	Q8TCD0 homo sapien
36	648	18.4	614	11 Q7TMT6	Q7TMT6 mus musculus
37	641	18.2	521	4 Q8N4Y9	Q8N4Y9 homo sapien
38	619.5	17.6	488	11 Q8K0F2	Q8K0F2 mus musculus
39	618.5	17.6	482	11 Q8K172	Q8K172 mus musculus
40	618.5	17.6	613	11 Q8VCX7	Q8VCX7 mus musculus
41	606	17.2	243	11 Q7TQM2	Q7TQM2 mus musculus
42	603	17.1	614	4 Q96GA6	Q96GA6 homo sapien
43	602.5	17.1	488	11 Q91WR1	Q91WR1 mus musculus
44	583	16.6	481	11 Q91WT1	Q91WT1 mus musculus
45	573	16.3	481	11 Q8VCV5	Q8VCV5 mus musculus
46	566.5	16.1	480	11 Q8K0Z4	Q8K0Z4 mus musculus
47	565	16.0	489	11 Q8VCX4	Q8VCX4 mus musculus
48	561	15.9	597	4 Q96BS9	Q96BS9 homo sapien
49	548	15.6	237	13 Q7S236	Q7S236 xenopus lae
50	545	15.5	597	4 Q8BQ38	Q8BQ38 homo sapien
51	540	15.3	588	4 Q8WUX4	Q8WUX4 homo sapien
52	540	15.3	597	4 Q9BU10	Q9BU10 homo sapien
53	540	15.3	618	4 Q96AA6	Q96AA6 homo sapien
54	537.5	15.3	613	4 Q8WUX1	Q8WUX1 homo sapien
55	535	15.2	145	11 Q924Q9	Q924Q9 mus musculus
56	535	15.2	481	11 Q91WT3	Q91WT3 mus musculus
57	534	15.2	145	11 Q924Q6	Q924Q6 mus musculus
58	533	15.1	136	11 Q7TPE3	Q7TPE3 mus musculus
59	527.5	15.0	484	11 Q99LA6	Q99LA6 mus musculus
60	527	15.0	145	11 Q924R4	Q924R4 mus musculus
61	525.5	14.9	613	4 Q96EY0	Q96EY0 homo sapien
62	523.5	14.9	500	4 Q9BRV0	Q9BRV0 homo sapien
63	519	14.7	145	11 Q924R1	Q924R1 mus musculus
64	518.5	14.7	146	11 Q924Q3	Q924Q3 mus musculus
65	515	14.6	145	11 Q924F7	Q924F7 mus musculus
66	514	14.6	143	11 Q924R0	Q924R0 mus musculus
67	514	14.6	573	4 Q8WU38	Q8WU38 homo sapien
68	508.5	14.4	117	11 Q9QXE9	Q9QXE9 mus musculus
69	507.5	14.4	142	11 Q924Q1	Q924Q1 mus musculus
70	507	14.4	143	11 Q924P6	Q924P6 mus musculus
71	506.5	14.4	140	11 Q924R2	Q924R2 mus musculus
72	506	14.4	497	4 Q8W124	Q8W124 homo sapien
73	505.5	14.4	146	11 Q924R8	Q924R8 mus musculus
74	504.5	14.3	496	4 Q96DK0	Q96DK0 homo sapien
75	503.5	14.3	298	11 Q9QVF0	Q9QVF0 mus musculus
76	502.5	14.3	168	11 Q8VDC9	Q8VDC9 mus musculus
77	500	14.2	145	11 Q924R3	Q924R3 mus musculus
78	500	14.2	145	11 Q924Q7	Q924Q7 mus musculus
79	498.5	14.2	117	11 Q9QXf0	Q9QXf0 mus musculus
80	498.5	14.2	146	11 Q924Q8	Q924Q8 mus musculus
81	496	14.1	137	11 Q924R6	Q924R6 mus musculus
82	493	14.0	241	11 Q921A6	Q921A6 mus musculus
83	492	14.0	141	11 Q924Q4	Q924Q4 mus musculus
84	492	14.0	587	13 Q7T0F1	Q7T0F1 xenopus lae
85	491.5	14.0	140	11 Q924F8	Q924F8 mus musculus
86	488	13.9	143	11 Q924R7	Q924R7 mus musculus
87	484	13.7	493	4 Q8NCL6	Q8NCL6 mus musculus
88	483	13.7	143	11 Q91VA2	Q91VA2 mus musculus
89	483	13.7	143	11 Q924Q5	Q924Q5 mus musculus


```
Db 28 SESEINEKDLKKSELOGTALGNLKIYYNEKAKTENKSHQFLOHTLIFKGFDD 87
Qy 286 HPYNDLLVDLSTAAATSEYESSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
Db 88 HSYNDLLVDLSTAAATSEYESSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 147
Qy 346 EEKVPINLWIDGKQNTVPIDKVTKSKKVTVOELDLQARHYLHGKFGLYNSDSGGKVO 405
Db 148 EEKVPINLWIDGKQNTVPIDKVTKSKKVTVOELDLQARHYLHGKFGLYNSDSGGKVO 207
Qy 406 RGLIVHSTSEGSTSVSYDLFDAQOQYPTLLRIYRDNNTTTSSTLSLSLYLYTT 458
Db 208 RGLIVHSTSEGSTSVSYDLFDAQOQYPTLLRIYRDNNTTTSSTLSLSLYLYTT 260

RESULT 3
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -
DR PIR; A27887; A27887.
DR PIR; A32448; A32448.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
```

Query Match 26.4%; Score 929.5; DB 11; Length 238;
Best Local Similarity 81.8%; Pred. No. 8e-51;

```
Matches 180; Conservative 15; Mismatches 20; Indels 5; Gaps 2;
Qy 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQV--SND---VAMVQKQFGQPKLLISVTSS 511
Db 18 SSDVMTQTPTSLVLSAGDRVTITCKASQV--SND---VAMVQKQFGQPKLLISVTSS 77
Qy 512 RYAGVPRFSSGGVGTDTTLTITSSVQAEADAAYFCQDYNPPFTGGTGLEIKRADAAP 571
Db 78 RFGVUPRFFSSGGVGTDTTLTITSSVQAEADAAYFCQDYNPPFTGGTGLEIKRADAAP 137
Qy 572 TVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSMTDQDSKDY 631
Db 138 TVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSMTDQDSKDY 197
Qy 632 SMSSTLTLTDKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 671
Db 198 SMSSTLTLTDKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 237

RESULT 4
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DE 181006O009Rik protein.
GN IGH-1 OR 181006O009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=2105660; PubMed=1217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
DR PIR; S26746; S26746.
DR HSSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
```

Query Match 26.2%; Score 924.5; DB 11; Length 473;
Best Local Similarity 33.8%; Pred. No. 4.2e-50;
Matches 239; Conservative 53; Mismatches 123; Indels 293; Gaps 15;

```
QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYHMHVWQSPGKGLWIGRINPNNGVTLY 60
D 20 QVQLKQSGAEILVKGPGASVKISKASGYSFTDYINWVKRQPGQGLEWIGKIPGSGSTYY 79
QY 61 NOKPKDKATLVDKSSITAYNELASLTSEDSAVYICARSTMITNYVMD---YWGQGSFTV 117
D 80 NEKFKGKATLADKSSITAYNQLSLSLTSEDSAVYFCARS-----CYDYDFAYWCGGLTIV 135
QY 118 VSSAKTTPSPVYPLAPGSAATNMTGLVGVKYPPEPVTVTNWNSGLSSGVHTFPFPAVL 177
D 136 VSAKTTAPVYPLAPVCGGTGSSVTLGCLVGVKYPPEPVTVTNWNSGLSSGVHTFPFALL 195
QY 178 QSDLTLLSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
D 196 QSGLLTSSVTVTSNTWPSGTITCNVAHPASSTKVDKIEPR----- 238
QY 238 RKKSELOQTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTGTHPWNLDLLVDLG 297
D 239 ----- 238
QY 298 STAATSEYEGSVLDLYGAYGYCAGCTPNKTACMYGGVTLHDNNRLTEKKYVINLWID 357
D 239 -----VPI----- 241
QY 358 GKQTTVPIDKVKTSKKEVTQVQELDQARHLYLHKGFLYNSDSFGKVGQRLVIFHSSEGS 417
D 242 ---TQNPCEPLKECPCAA-----PDLGSP----- 264
QY 418 TVSYDLPDAQGYQDPTLIRIVRDNTT--SSTSLSLSLVLYTTSIVMTQPTSLVLSAGDRV 477
D 265 ---SVFIPEPKIKDVL-----ISLSFMVTCVV----- 290
QY 478 TITCKASQSVNDVAWYQKQKPGKPKLLISYTSRYAGVDPDRFSGSGVGTDTLTITSSVQ 537
D 291 -----DVSED-----DPDQVQISW-----FYNNVE 309
QY 538 AEDAAVYFCQDYNSSPPTFGGKTKLEIKRAD----- 568
D 310 VHTAQOTQTHREDYNS--TLRVVSALPIQHQDMSGKEFKCKVNNRALPSPIETKTSRPG 367
QY 569 --AAPTQVSIIPPSSQSLTSGGASVYVCLNNFYPKDINVKWKIDGSRQNGVLSWTDQDS 626
D 368 PVRAQQTIVLPFAEMTKKEFSITCMITGELPAEIAVDVTSNGRTSQN-YKNTATVLD 426
QY 627 KDSYMSSTLTNKRDEYRHNSTCEATHK-----TSTSPIVKSPNR 669
D 427 -DGSYFMYSKLRVQKSTWERSGLFACSVVHGLNHLTTTKTISRSLGK 473
RESULT 5
Q99SU3 PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SA1761.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino T., Karamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hirayama K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
```

```
RL Lancet 357:1225-1240 (2001).
DR EMBL; AF003135; BAB43036.1; -.
DR FIR; C89984; C89984.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR008177; Bctrl_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 26.1%; Score 918; DB 16; Length 260;
Best Local Similarity 73.0%; Pred. No. 4.8e-50;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELTQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTG 285
D 28 SEKSEINEKDLRKSELTQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTG 87
QY 286 HPWYNDLLDLGSLTAATSEYEGSVLDLYGAYGYCAGCTPNKTACMYGGVTLHDNNRLT 345
D 88 HPWYNDLLDLGSLTAATSEYEGSVLDLYGAYGYCAGCTPNKTACMYGGVTLHDNNRLT 147
QY 346 EKKYVINLWIDKQTVPIIDKVKTSKKEVTQVQELDQARHLYLHKGFLYNSDSFGKVG 405
D 148 EKKYVINLWIDKQTVPIIDKVKTSKKEVTQVQELDQARHLYLHKGFLYNSDSFGKVG 207
QY 406 RGLIVFHSSEGTSTVYDLFDAQGYQDPTLIRIVRDNTT--SSTSLSLSLVLYTTS 458
D 208 RGLIVFHSSEGTSTVYDLFDAQGYQDPTLIRIVRDNTT--SSTSLSLSLVLYTTS 260

RESULT 6
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060C009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; igf.3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE989897986DA155 CRC64;

Query Match 26.1%; Score 917.5; DB 11; Length 473;
Best Local Similarity 33.8%; Pred. No. 1.2e-49;
Matches 232; Conservative 59; Mismatches 141; Indels 255; Gaps 12;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYHMHVWQSPGKGLWIGRINPNNGVTLY 60
```


Db 20 QVQLQQSDELAVKPGASVKISCKVGYTFTDTHIHWKQRPQGLEWIGVIYPRDGS TKY 79
QY 61 NQKFKDKATLTVDKSTAYWEIERSLTSSESAVYCARSTMINN-----YMDYWGOGTSV 116
Db 80 NERFKGKATLTADKSSSTATQNSLTSSESAVCFCSRGSIYGYGLYFDYWGOGTTI 139
QY 117 TVSSAKTTPPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPPVTVTNSSGLSSGVHTFPFAV 176
Db 140 TVSSAKTTPPSVYPLAPGSDTTGSSVTLGLCLVKGYFPEPPVTVTNSSGLSSGVHTFPFAV 199
QY 177 LQSDLYLTSSSVTPSTPSEVTVTCNVAHPASTKVDKIVPRDGGGSEKSEINEKD 236
Db 200 LQSDLYLTSSSVTVTSTPQSIITCNVAHPASTKVDKIKIBR-----GPTIKPCP----- 251
QY 237 LRKKSLEQGTALGNLKIYVYNSKAITSEKSAQDELNTLLFKGFTGHPWYNLDLVDL 296
Db 252 ----- 251
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNTACMYGVTLLHNNRLTEKKVPINLMI 356
Db 252 -----PCKCPAPN-----LLGGPSPV----- 267
QY 357 DGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDGFQGVQVORGLIVFHSSEG 416
Db 268 -----IFPPKIKDVLMI-----SLUS 282
QY 417 STVSYPDLFDAQGYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQFTSLLVSAGDR 476
Db 283 PMVTCVVDVSEDDP-----VCISWFWNNVEVLTAQT----- 317
QY 477 VTITCKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISV 536
Db 318 -----HREDYNSTLRVY 329
QY 537 QA-----EDAAVYFCQDYNPPTFGGTTKLEIKRADAAPTVSIFPPPSSEQLTSGGA 588
Db 330 SALPIQHODWNSGKFKCKVNNKALAPIERTISKEKGSVRAPQVYVLPPEEMTKQV 389
QY 589 SVVCFNLNFPKDNVWKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTITKDE 643
Db 390 TLTCTMTDFPEDIYEWNTNGTSLNKNTEPVLDS-----DGSYFWYSKLRVEKN 442
QY 644 YERHNSVTEATHK-TSTSPVKSFN 669
Db 443 WVERNSYSCSVHLEGLNHHHTKSFGR 469

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 25.8%; Score 910; DB 11; Length 239;
Best Local Similarity 76.0%; Pred. No. 1.4e-49;
Matches 177; Conservative 21; Mismatches 25; Indels 10; Gaps 2;

QY 449 LSISLYLT-----TSIVMTQFTSLLVSAGDRVTITCKASQSVSND-----VAWYQKPG 498
Db 6 LLVLLLTFTSPASSDVLVLTQPLSLPWNIGQASISCKSTKSLNSDGFYLDWYLOXP 65
QY 499 QGSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISVQAEADAAYFCQDYNPPTFGG 558
Db 66 QGSPQLLYLVSNRFSGVDRFSGSGGTDTFLKISRVEADLGVYTCFQSNHLPYTFGG 125
QY 559 GTKLEIKRADAAPTVSIFPPPSSEQLTSGASVWCFLNFPKDNVWKIDGSRONGVL 618
Db 126 GTKLEIKRADAAPTVSIFPPPSSEQLTSGASVWCFLNFPKDNVWKIDGSRONGVL 185
QY 619 NSWTDDQSKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPVKSFN 671
Db 186 NSWTDDQSKDSTYSMSSTLTITKDEYERHNSYTCETHTKTSTSPVKSFNENE 238

RESULT 7
Q8VC55 PRELIMINARY; PRT; 239 AA.
ID Q8VC55
AC Q8VC55
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AH21781.1; -
DR PIR; A33933; A33933.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; Ig-like.

RESULT 8
Q99M37 PRELIMINARY; PRT; 238 AA.
ID Q99M37
AC Q99M37
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AA02035.1; -
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.

```
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26344 MW; F52B06A0B801330A CRC64;  
  
Query Match 25.8%; Score 909.5; DB 11; Length 238;  
Best Local Similarity 80.5%; Pred. No. 1.5e-49;  
Matches 177; Conservative 16; Mismatches 22; Indels 5; Gaps 2;  
  
QY 457 TTSIVMTQTPSLVSGADRVITCKASQSV--SND---VAVYQKQPGQSPKLLISVTSS 511  
DB 18 SSDVVMQTPLSLPVSLGDAQSISCRSSQSIHVSNGNTYLEWYLQKPGQSPKLLIYKVN 77  
QY 512 RVAGVDPDRFSGSGYGTDFTLTISSVQAEAAVYFCQDYNPPFTGGTGLEIKRADAAP 571  
DB 78 RFGVDPDRFSGSGYGTDFTLTKISRVEADLVGYTCFQGSHPVYTFGGTGLEIKRADAAP 137  
QY 572 TVSIFFPSSSEQLTSGASVWCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 631  
DB 138 TVSIFFPSSSEQLTSGASVWCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDY 197  
QY 632 SMSSTLTITKDEYERHNSYTCEATHKTSTSPVKSFNNE 671  
DB 198 SMSSTLTITKDEYERHNSYTCEATHKTSTSPVKSFNNE 237  
  
RESULT 9  
Q91WF8 PRELIMINARY; PRT; 234 AA.  
AC Q91WF8;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015292; AAH15292.1; -.  
DR GO; GO:0005622; C:intracellular; IEA.  
DR GO; GO:0005840; C:ribosome; IEA.  
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.  
DR GO; GO:0006412; P:protein biosynthesis; IEA.  
DR InterPro; IPR007110; IG_LIKE.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR001865; Ribosomal_S2.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; 1.  
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;  
  
Query Match 25.8%; Score 908; DB 11; Length 234;  
Best Local Similarity 82.1%; Pred. No. 1.8e-49;  
Matches 174; Conservative 12; Mismatches 26; Indels 0; Gaps 0;  
  
QY 460 IVMTQTPSLVSGADRVITCKASQSVNDVAVYQKQPGQSPKLLISYTSRAGVDPDR 519  
DB 22 IQMTQTPSLVSGADRVITCKASQSDISNLYNNVYQKQPGDGTGKLLIYTSRLLYGVPSR 81  
QY 520 PFGSGYGTDFTLTISSVQAEAAVYFCQDYNPPFTGGTGLEIKRADAAPTVSIFPPS 579  
DB 198 PFGSGYGTDFTLTISSVQAEAAVYFCQDYNPPFTGGTGLEIKRADAAPTVSIFPPS 579  
  
DB 82 PFGSGYGTDFTLTISSVQAEAAVYFCQDYNPPFTGGTGLEIKRADAAPTVSIFPPS 141  
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSSSTLTLL 639  
DB 142 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSSSTLTLL 201  
QY 640 TKDEYERHNSYTCEATHKTSTSPVKSFNNE 671  
DB 202 TKDEYERHNSYTCEATHKTSTSPVKSFNNE 233  
  
RESULT 10  
Q99LJ31 PRELIMINARY; PRT; 468 AA.  
AC Q99LJ31;  
DT 01-JUN-2001 (TREMELrel. 17, Created)  
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Similar to RIKEN CDNA 1810660009 gene.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC003878; AAH03878.1; -.  
DR PDB; 2AP2; 24-NOV-99.  
DR InterPro; IPR007110; IG_LIKE.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG_LIKE; 4.  
DR PROSITE; PS00290; IG_MHC; 1.  
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;  
  
Query Match 25.6%; Score 902; DB 11; Length 468;  
Best Local Similarity 33.1%; Pred. No. 1.1e-48;  
Matches 226; Conservative 63; Mismatches 142; Indels 252; Gaps 12;  
  
QY 1 EVQLQSGDPLVKGASVKISCKASYGFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60  
DB 20 EVQLQSGDPLVKGASVKISCKASYGFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 79  
QY 61 NQKFKDKALTVDKSSTAYMELRLSITSEDSAVYVCARSTMTITNVMYDNGOGTSVTYSS 120  
DB 80 APKFDQKATITADTSNTAYLQSLTSBTDIAIYCARNLLYGGY-YDWGQGTITVTYSS 138  
QY 121 AKTTTPSVYPLAPGSAATNSMVTGLCLVKGFPFPVTVTNWNSGLSSGVHTFPVQLQSD 180  
DB 139 AKTTAPSVYPLAPVCGDITGSSVTGLCLVKGFPFPVTLTNWNSGLSSGVHTFPVQLQSD 198  
QY 181 LYTSSSVTVPSSTWPSSETVTCNVAPASSTKVDKVIIPRDSGGSPSEKSEENEDLKKK 240  
DB 199 LYTSSSVTVPSSTWPSSETVTCNVAPASSTKVDKVIIPRDSGGSPSEKSEENEDLKKK 246  
QY 241 SELQGTALGNLQIYYNSKAITSEKSDAQDLTTLTFKGFTHPWINDLLVLDGSTA 300  
DB 247 ----- 246  
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRLTEKKVPIINLWDGKQ 360  
DB 247 -----PCKCPAFN-----LLGGSVVF----- 262  
QY 361 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFLGNSDSFGKVGKQGLIVFHSSEGSTVS 420  
DB 263 -----IPPKIKQVLM-----SLSPWVT 281  
QY 421 YDLFDAQGQYPTLLRIYRDNTTISTSLISLYLTTISIVMTQTPSLVSGADRVIT 480  
DB 282 CVVDVDSDDPD-----VQISWFWNNVEVLTAQTQT----- 312
```

```

QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRSYAGVDRFSGSGYGTDFLTLSVQA-- 538
Db 313 -----HREDYNSTLRVVSALP 328
QY 539 -----EAAVYFCQDYNSPPTFGGKLEIKRADAAPVSIFFPSSSQLTSGGASVVC 592
Db 329 IQQDQWMSGKFEKCKVKNKALPAPIERTISKPGSVRAQVYVLPPEEMTKKQVLTLC 388
QY 593 FLANNFVKDINVKWKIDGSRQN-----GVLNWTQDQSKDSTYSMSSTLTITKDYERH 647
Db 389 MVTDFMPEDIVYEWNTNGKTELNVKNTPEVLDG-----DGSYFYMSKLVEKKWVER 441
QY 648 NSYTCEATHK-TGTSPIVAKSPNR 669
Db 442 NSYSCSVVHEGLNHNHTKTSFSR 464

RESULT 11
Q91WS9
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley D.M., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sutterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 25.6%; Score 900; DB 11; Length 233;
Best Local Similarity 81.8%; Pred. No. 5.6e-49;
Matches 173; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNDVAVYQKPGQSKLLISYTSRSYAGVDR 519
Db 21 IQMTQTTSLASLGRVITISGSGGIANLYNQYQKEDGTGTVKLLIYTSLSHSGVSR 80
QY 520 FSGSGYGTFTTITISVQAEADAAYFCQDYNSPPTFGGKLEIKRADAAPTIVFPFS 579
Db 81 FSGSGSGTDYSLTISNLEPEDIATYCYQYRVLPMFTFGGKLEIKRADAAPTIVFPFS 140
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 639
Db 141 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 200
QY 640 TKDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
Db 201 TKDEYERHNSYTCETHKTSTSPIVKSFNRNE 232

RESULT 12
Q7TMK1
ID Q7TMK1 PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

```

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley D.M., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Sutterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;

Query Match 25.5%; Score 899.5; DB 11; Length 470;
Best Local Similarity 34.7%; Pred. No. 1.6e-48;
Matches 233; Conservative 57; Mismatches 129; Indels 253; Gaps 16;

QY 1 EVQLQQSGPDLVKGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLQQSGPELVKGASVKISCKASGYFTGYMHVWKQSPGKLEWIGLVNPNNGTSTY 79
QY 61 NQKFKDXTATLVKDSSTTAYMELRSLTSEDSAVYVCARSTMTINY-VMDYWGQGTSTVTS 119
Db 80 NQKFKGKATLVKDSSTTAYMELNLSLTSEDSAVYVCARYYSGSYWYFDWGAGTTVTS 139
QY 120 SAKTTPSVVPLAPGSAQAQNSMWTLCGLVKGYPPEVPTVWNSGSLSSGVHPPAVLQS 179
Db 140 SATTPASVPLVPGCGDTSGSSVTLGCLVKGYPPEVPTVWNYGALSSGVRTVSSVLQS 199
QY 180 DLYTLSSSVTPSPSTWPSSETVTCNVAPASSTVKDKKIVPRDSGPGSEKEINEKDLK 239
Db 200 GFYSLSLVTPVPSSTWPSQIVICNVAPASKTELKIEPR-----IPK 243
QY 240 KSEIQGTAL--GNLKKQIYYNKAITSSEKSAQDFLNTLLFKGFFTGHPWYNDLLVDLG 297
Db 244 PSTPPGSSCPPGNI-----VSEDD-----LG 259
QY 298 STAATSEVGSSVDLYGAYYQCAGGTPNKTACMYGVTLHDNNRLTEBKYPINLWID 357
Db 260 -----GPSVFIF-----PPK-----PKDALMISLT 279
QY 358 GKQTTVPIDVKYTSKKEVTVQELDLQARHYLHGKFLGSLNDSFGKVGQRLIVFHSSEGS 417
Db 280 PKVTCVVVD-----VSEDD----- 293
QY 418 TVSVDLFDQAQGYPDTLIRYRDNTTISSTLSLSLYTTSIVMTQTPTSLVLSAGDRV 477

```

```

Db 294 -----PDVHVSFVDNKEVHT----- 309
QY 478 TITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRFGSGYGDF-TLTISSV 536
Db 310 -----AWTQPREAQ-----YNSFVWSALPI 331
QY 537 QAED---AAVYFCQDYNSTPTFGGKLEIKRADAAPTYSIPPSSEQLTSGASVVC 593
Db 332 QHQQWTRGKFKCKVNNKALPAPERTISPKGRAQTPQVTTIPPREQMKKKVSLTCL 391
QY 594 LNNFYPKDINVKKIDGSRQNGVLNSWTQDQSK-----DSTYSMSSTLTLTDXEY 645
Db 392 VTNFSEALSVEWE-----RNGEL-----EQDYKNTPIILSDGTFLYSLKLIWTDLSL 441
QY 646 RHNSYTCETHK 657
Db 442 QGEIFTCVWHE 453

RESULT 13
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZSCH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullaney S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Carrano P., Prange C.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=CZSCH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC055906; RAH55906.1; --
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03488AA6396F CRC64;

Query Match 25.5%; Score 897; DB 11; Length 236;
Best Local Similarity 80.2%; Pred. No. 8, 8e-49;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 460 IYWTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 24 IKMTQSPSMYASLGERVTITCKASQDINKSYLWYQKRPWKSPKTLIIYATSLADGVPSR 83

```

```

QY 520 FSGSGYGTDTLTITSSVQAEADAAYVFCQDYNSTPTFGGKLEIKRADAAPTYSIPPS 579
Db 84 FSGSGGQDYSITISSLESDDTATYCYLQHGESPTFGSGTKLEIKRADAAPTYSIPPS 143
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 639
Db 144 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 203
QY 640 TKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 204 TKDEYERHNSYTCETHKTSPIVKSFNNE 235

RESULT 14
Q8R062 PRELIMINARY; PRT; 234 AA.
ID Q8R062;
AC Q8R062;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC027418; RAH27418.1; --
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00390; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match 25.4%; Score 896; DB 11; Length 234;
Best Local Similarity 81.6%; Pred. No. 1e-48;
Matches 173; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 460 IYWTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 22 IQMTQTSLSASLGRVTITCSASQGISNLYLNWYQKPDGPGDKLIYYTSSLHSGVPSR 81
QY 520 FSGSGYGTDTLTITSSVQAEADAAYVFCQDYNSTPTFGGKLEIKRADAAPTYSIPPS 579
Db 82 FSGSGGTHYSITISNLEPEDIATYCYQYSQFPPTFGSGTKLEIKRADAAPTYSIPPS 141
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 639
Db 142 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLT 201
QY 640 TKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 202 TKDEYERHNSYTCETHKTSPIVKSFNNE 233

RESULT 15
Q921K1 PRELIMINARY; PRT; 278 AA.
ID Q921K1;
AC Q921K1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC012207, AAH12207.1; -.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 2.
KW Hypothetical protein_IG_LIKE; 2.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 25.4%; Score 893; DB 11; Length 278;
Best Local Similarity 76.8%; Pred. No. 2e-48;
Matches 169; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 EVCLQSGDPLVKGASVKISCKASGYSTGYVMHWKSPGKLEWIRPNNGVTLY 60
Db 20 QVQLQDQGAEVLKPGASVKLSCKASGYFTSYVMHWKRRGQGLEWIRNPSGGTNY 79
QY 61 NQPKFKATLVKDSSTTAYMELRSITSDSAVYCARSTMITNYVMDYMGQSTVTVSS 120
Db 80 NERFKATLVKDSSTVYMQLSITSDSAVYCTRGVYDDYFDVWGAGTIVTVSS 139
QY 121 AKTTPSVPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFPVAVLQSD 180
Db 140 AKTTPSVPLAPVCGGTTGSSVTLGLVKGFPEPVTWNSGSLSSGVHTFPVAVLQSD 199
QY 181 LYTLSSTVTPSPSTPSETVTQNVHPASSTKVDKKIVER 220
Db 200 LYTLSSTVTPSTPSETVTQNVHPASSTKVDKKIEPR 239

RESULT 16
Q7TMK0
ID Q7TMK0 PRELIMINARY; PRT; 235 AA.
AC Q7TMK0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mollany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC055911; AAH55911.1; -.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25861 MW; 3EBA0312A87613F4 CRC64;

Query Match 25.3%; Score 890.5; DB 11; Length 235;
Best Local Similarity 78.0%; Pred. No. 2.2e-48;
Matches 174; Conservative 18; Mismatches 30; Indels 1; Gaps 1;

QY 449 LSISLYLTTSIVMTQTPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISY 508
Db 13 ISISVMSRGESVLTQSPAIMSASLGKVTMSCRASSRV-NYMYVYQKSGASPRLIYY 71
QY 509 TSSRYAGVDFRFGSGGYGTDFTLTISVQAEADAAYVFCQDDYNSPPTFGGTTKLEIK 568
Db 72 TSNLAPGVDFRFGSGGYGTDFTLTISVQAEADAAYVFCQDDYNSPPTFGGTTKLEIK 631
QY 569 AAPTIVSIFPPSSEQLTSGGASVWCFLNNFYPKQINNVKIDGSRQNGVLSNWTDDQSKD 628
Db 132 AAPTIVSIFPPSSEQLTSGGASVWCFLNNFYPKQINNVKIDGSRQNGVLSNWTDDQSKD 691
QY 629 STYSNSSLTTLTKDEYERHNSYTCEATHKTSSTPIVKSFNRE 671
Db 192 STYSNSSLTTLTKDEYERHNSYTCEATHKTSSTPIVKSFNRE 234

RESULT 17
Q8R3V9
ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC024405; AAH24405.1; -.
DR PIR: B45837; B45837.
DR MGD: MGI:96446; IGH-4.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 4.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein_IGH-4.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 25.2%; Score 889; DB 11; Length 469;
Best Local Similarity 32.9%; Pred. No. 7.2e-48;
Matches 221; Conservative 68; Mismatches 129; Indels 254; Gaps 16;

QY 1 EVQLQQSGDPLVKGASVKISCKASGYSTGYVMHWKSPGKLEWIRPNNGVTLY 59
Db 20 EVNLVESGGGLVPGGSLRLSCAASGFTFDYINSWVRQPPGKALEWLGIRKANGYTT 79
QY 60 -YNQKFKDKATLVKDSSTTAYMELRSITSDSAVYCARSTMITNYV----MDYWGQGT 114
Db 80 EYSASVKGRTISKDNSQSILYLMNALRAEDSATYTCARDRSSYYSYSGTSFAYWGQGT 139
QY 115 SVTVSSAKITPPSVYPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFP 174
Db 140 LVTVSAAKITPPSVYPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFP 199

```

Matches 234; Conservative 69; Mismatches 124; Indels 241; Gaps 18;

QY 175 AVLOSLLYTLSSSVTPSSVTPSETVTCNVAHPASSKVDKKIVPRDSGGPSEKSEINE 234
 Db 200 AVLOSLLYTLSSSVTPSSVTPSETVTCNVAHPASSKVDKKIVPRDCG----- 248
 QY 235 KDLKKSELOGTALGNLKQIYYNNSKAITSSSEKSAOFLNTLLFKGFFTGHPWYNDLLV 294
 Db 249 -----CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 277
 QY 295 DLGSTAATSEVSGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLETKKVPINL 354
 Db 278 -----TP-KVTCVVVDIS-----KDDPEVQFSW 299
 QY 355 WIDGKQTTVPIDKVKTSKKEV-----TVOELDLQARHYLHGK-FGL-YNSDSFGGKVQ 405
 Db 300 FVD-----DVEHTACTPREBQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAFAPIE 355
 QY 406 RGLVIFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSLSLYLYTTSIYVQT 465
 Db 356 K-----TISK----- 361
 QY 466 PTSLLSAGDRVITITCKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDRFGSGY 525
 Db 362 ----- 361
 QY 526 GTDFTLTISVQAEADAAYVFCQDYNPPTFGGKTKLEIKRADAPTSTVIFPSSSEQLTS 585
 Db 362 -----KGRKAPQVYTIPTPPKQMAK 382
 QY 586 GGASVVCFLNFPKIDNVKWKIDGSRONGVLSWTDQSDKSTYSMSSTLTLTIDEYE 645
 Db 383 DKVSLTCTMITDFPEDITVQWNGQAPEN-YKNTQPIMDT-DGSFYFVSKLVQKSNWE 440
 QY 646 RHNSYTCBATHK 657
 Db 441 AGNFTCSVLHE 452

RESULT 18
 Q8R3H6 PRELIMINARY; PRT; 474 AA.
 AC Q8R3H6;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AU044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; BC025447; AAH25447.1;
 DR MGD; MGI:2144567; AU044919.
 DR GO; GO:0005489; Electron transporter activity; IEA.
 DR GO; GO:0006118; Electron transport; IEA.
 DR InterPro; IPR000345; Cytochrome_B5.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS00835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 25.2%; Score 888.5; DB 11; Length 474;
 Best Local Similarity 35.0%; Pred. No. 7.8e-48;

QY 1 EVLOQSGPDLVFKPGASVKISCKASGYSTFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
 Db 20 QVLLQSGPELVFKPGASVKISCRASGYAFSKSMWNVKRRPGKLEWIGRIFPGDGDTHY 79
 QY 61 NQFKDKATLIVDKSSTTAYMELSLTSEDSAVYCARSTMITNVMYDYGQGSVTVSS 120
 Db 80 SKFGKAKLITADKSSVTAFLQLTSLTSEDSAVYFCARDSYGY-FDDWQGGATVTVSS 138
 QY 121 AKTTTPSYVPLAPGSAQAOTNSMVTGLGVKGYFPEPVTVTNSSGSLSSGVHTFPFVAVLQSD 180
 Db 139 AKTTTPSYVPLAPGCGDTTSGSVTLGLVKGYPFESVTVTNSSGSLSSGVHTFPFVAVLQSG 198
 QY 181 LYTSSSVTVPSSTWPSSTVTCNVAHPASSKVDKKIVPRDSGGPSEKSEINE-----KD 236
 Db 199 LYTSSSVTVPSSTWPSSTVTCNVAHPASSKVDKKIEP-----SGP-----ISTINCPCKE 252
 QY 237 LFK--KSELOGTALGNLKQIYYNNSKAITSSSEKSAOFLNTLLFKGFFTGHPWYNDLLV 294
 Db 253 CHKCAPNLEG---GPSVFI PPNIKDV-----LMI 280
 QY 295 DLGSTAATSEVSGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLETKKVPINL 354
 Db 281 SL-----TP----- 284
 QY 355 WIDGKQTTVPIDKVKTSKKEV-----TVOELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVPHSS 414
 Db 285 -----KVTCVVVD-----VSEDDPQVQISWVNN-----VEVHTA 314
 QY 415 EGSTVSYDLFDAGQGYPTDLLRIYRDNNTTISSTLSLSLYLYTTSIYVQTPTSLLSVAG 474
 Db 315 QNTTHREDY-----NGTIR-----VWSA- 332
 QY 475 DRVITCKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDRFGSGYGTDTLTIS 534
 Db 333 -----LPQHQDWSGKFEKCKVN 351
 QY 535 SVOAEADAAYVFCQDYNPPTFGGKTKLEIKRADAPTSTVIFPSSSEQLTSGGASVVCFL 594
 Db 352 N-----KDLPSPIE---RTISKIQLVEAPQVWILPPPAEQLSRKDVSLTCLV 396
 QY 595 NNFPKIDNVKWKIDGSRON-----GVLSNWTDDQSDKSTYSMSSTLTITKDEVERNS 649
 Db 397 VGFNPGDISVWTSNGHTENYKDTAPVLDS-----DGSFYIYSKLDITKTSKWEKTD 449
 QY 650 YTCETHK 657
 Db 450 FSCNVRHE 457

RESULT 19
 Q7TS98 PRELIMINARY; PRT; 236 AA.
 AC Q7TS98;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Anti-colorectal carcinoma light chain.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93383497; PubMed=8372513;
 RA Tonge D.W., Hennam J.P., Greene A.R., Lee I.D., Edge M.D.;
 RT "Cloning and characterization of 116NS19, a heavy and light chain
 RT cDNAs and expression of antibody fragments in Escherichia coli.";
 RL Year Immunol. 7:56-62(1993).
 DR EMBL; S65921; AAB28160.1; -;
 SQ SEQUENCE 236 AA; 26454 MW; 2C566EBF5EA10F4C CRC64;

```
Query Match      25.2%; Score 886; DB 11; Length 236;
Best Local Similarity 79.2%; Pred. No. 4.3e-48;
Matches 168; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDR 519
DB 24 IKMTQSPSSMYASLGERVTITCKASQDINSYLFQKQPKSPKTLIYRANRLVDGVPDR 83
QY 520 FSGSGGYTDTLTISSVQAEADAAVYFCQDYNPPTFGGGTKLEIKRAAAPTYSIFPPS 579
DB 84 FSGSGGQDYSLTISSEYEDMGIVYCLQYDEPRTFGGGTKLEIKRAAAPTYSIFPPS 143
QY 580 SEOLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTL 639
DB 144 SEOLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTL 203
QY 640 TKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 671
DB 204 TKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 235

RESULT 20
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW SEQUENCE FROM N.A.
RP TISSUE=Breast tumor;
RC Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PIR; A33933; A33933.
DR PDB; 1AX1; 30-JAN-02.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW SEQUENCE 235 AA; 5FC73BDEB5E8FEF CRC64;

Query Match      25.0%; Score 881.5; DB 11; Length 235;
Best Local Similarity 76.7%; Pred. No. 8.3e-48;
Matches 171; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSISLYTTSIVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISY 508
DB 13 ISASVITSRGQIVLTQSPAIMSASPGERTVMTCSASSVSH-MHNYQKSGTSPKRWIYD 71
QY 509 TSSRYAGVDPDRSGSGYGTDTLTISSVQAEADAAVYFCQDYNPPTFGGGTKLEIKRAD 568
DB 72 TKLTSVGVDPDRSGSGSGTSYSLTISNMEADVATYVCOQWRNPPTFGVTKLEIKRAD 131
QY 569 AAPTYSIFPPSSEQLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKD 628
DB 132 AAPTYSIFPPSSEQLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 671
DB 192 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 234

RESULT 21
Q8K0F8
ID Q8K0F8 PRELIMINARY; PRT; 239 AA.
AC Q8K0F8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW SEQUENCE 239 AA; D7BE84398AA341F0 CRC64;

Query Match      25.0%; Score 880.5; DB 11; Length 239;
Best Local Similarity 76.3%; Pred. No. 9.8e-48;
Matches 174; Conservative 17; Mismatches 32; Indels 5; Gaps 2;

QY 449 LSISLYTTSIVMTQPTSLVAGDRVTITCKASQSV--SND---VAVYQKQSPK 503
DB 11 LVLSIQEINGDVVMTQTPTLTLSTVIGQPASISCKSSQSLFTNGKMYLSLLQRPQSPK 70
QY 504 LLISVTSRYAGVDPDRSGSGYGTDTLTISSVQAEADAAVYFCQDYNPPTFGGGTKLE 563
DB 71 RLISLVSKLDGVPDRSGSGGTDTLTKISRVEADLGVYICLQSTHFPTFGGGTKLE 130
QY 564 IKRAAAPTYSIFPPSSEQLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTD 623
DB 131 IKRAAAPTYSIFPPSSEQLTSGGASVGVFLNNFYPKDINVKWKIDGSRQNGVLNSWTD 190
QY 624 QDSKDSYMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 671
DB 191 QDSKDSYMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 238

RESULT 22
Q8R028
ID Q8R028 PRELIMINARY; PRT; 234 AA.
AC Q8R028;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
```

RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC028540; AAH28540.1; -	
DR	PIR; H33932; H33932.	
DR	PIR; PH1074; PH1074.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003006; Ig MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 2.	
DR	SMART; SM00406; Igv; 1.	
DR	PROSITE; PS00835; IG_LIKE; 2.	
DR	PROSITE; PS00290; IG_MHC; 1.	
KW	Hypothetical protein.	
SQ	SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;	
Query Match 24.7%; Score 870.5; DB 11; Length 234;		
Best Local Similarity 74.3%; Pred. No. 4e-47;		
Matches 168; Conservative 16; Mismatches 37; Indels 5; Gaps 1;		
QY	451 ISLYLYTTS-----IVMTQTPTSLLVSAGDRVTITCKASQSVSNDAVYQKPGQSPKLL 505	
DB	8 LSLLLLCVDSRAETTVTQSPASLSVATGEKVTIRCITSTDIIDDMWYQKPGEPKLL 67	
QY	506 ISYTSRYAGVDPDFSGSGCHDTFTLISVQAEAAVYFCQDYNSPPTFGGTTKLEIK 565	
DB	68 ISEGNLRPGVPSPFSSGGTDFVFTIENTLSEVDVADYCLQSDNNMPLTFGAGTKLELK 127	
QY	566 RADAAPTYSIPIPPSEQLTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQ 625	
DB	128 RADAAPTYSIPIPPSEQLTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQ 187	
QY	626 SKDSTYMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRE 671	
DB	188 SKDSTYMSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRE 233	
RESULT 23		
Q9RIA5	PRELIMINARY; PRT; 214 AA.	
ID	Q9RIA5	
AC	Q9RIA5; (TREMELrel. 13, Created)	
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)	
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)	
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)	
DE	Kappa light chain of Mab7 (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Wilde K.G., Yu X., Ekrannodoullah A.K.M., Misra S.;	
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scfv).";	
RT	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; AF152371; AAD40242.1; -	
DR	PDB; 1CIC; 11-MAR-03.	
DR	PDB; 1E08; 29-NOV-00.	
DR	PDB; 1K6Q; 18-DEC-02.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003006; Ig MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Ig; 2.	
DR	SMART; SM00406; Igv; 1.	
DR	PROSITE; PS00835; IG_LIKE; 2.	
DR	PROSITE; PS00290; IG_MHC; 1.	
FT	NON_TER 1	
FT	NON_TER 214	
SQ	SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;	
Query Match 24.7%; Score 870; DB 11; Length 214;		
Best Local Similarity 77.8%; Pred. No. 3.8e-47;		
Matches 165; Conservative 19; Mismatches 26; Indels 0; Gaps 0;		
QY	460 IVMTQTPTSLLVSAGDRVTITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDR 519	
DB	2 IQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQKPGKSPKTLIYRANRLVDGVPSR 61	
QY	520 PFGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTYSIIPPS 579	
DB	62 PFGSGSQDYSLTSSLEYEDMGIIYCLQYDEFPPTFGSGTKLEIKRADAAPTYSIIPPS 121	
QY	580 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYMSSTLT 639	
DB	122 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYMSSTLT 181	
QY	640 TKDEYERHNSYTCEATHKTSTSPIVKSFNRE 671	
DB	182 TKDEYERHNSYTCEATHKTSTSPIVKSFNRE 213	
RESULT 24		
Q9RIA4	PRELIMINARY; PRT; 437 AA.	
ID	Q9RIA4	
AC	Q9RIA4; (TREMELrel. 13, Created)	
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)	
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)	
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)	
DE	Gammal heavy chain of Mab7 (Fragment).	
GN	IGH-4.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Wilde K.G., Yu X., Ekrannodoullah A.K.M., Misra S.;	
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scfv).";	
RT	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
RL	EMBL; AF152372; AAD40243.1; -	
DR	PIR; B45837; B45837.	
DR	PDB; 1COK; 11-SEP-99.	
DR	PDB; 1I9I; 25-DEC-02.	
DR	PDB; 1KCU; 11-MAY-02.	
DR	MGI; 96446; Igh-4.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003006; Ig MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; Igv; 3.	
DR	SMART; SM00406; Igv; 1.	
DR	PROSITE; PS00835; IG_LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; 1.	
FT	NON_TER 1	
FT	NON_TER 437	
SQ	SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;	
Query Match 24.5%; Score 862; DB 11; Length 437;		
Best Local Similarity 32.3%; Pred. No. 3.3e-46;		
Matches 215; Conservative 66; Mismatches 130; Indels 254; Gaps 15;		
QY	2 VQLQSGPDLVKFGASVKISCKASGVFTGYVHWVQSPGKLEWIGRINNGVTLYN 61	
DB	1 VQLQSGGGGLVPGGSLKSLCAASGFTSSYANVSWVRQTPEKLEWVASFS-SGGIIYTT 59	
QY	62 QKFKDKATLTVDKSSSTTAYMELRSLTSDSAVYYYCARSTMINYVMDWGQSTVTSVA 121	
DB	60 DSVKGRFTIYKDKRNLISLQMSLSRSEDATMYCARGDYSA-----YMGPGTLTVSAA 114	
QY	122 KITPPSVYPLAPGSAQAQNTSMVTLGCLVKGYPEPVTVTWSGSLSSGVHTPPAVLQSDL 181	
DB	115 KITPPSVYPLAPGSAQAQNTSMVTLGCLVKGYPEPVTVTWSGSLSSGVHTPPAVLQSDL 174	
QY	182 YTLSSSVTPSPSTWPTVTCNVAHPASSTKYDKKIVPRDGGPSEKSEINEKOLRKKS 241	
DB	175 YTLSSSVTPSPSTWPTVTCNVAHPASSTKYDKKIVPRDCG-----C 217	


```

QY 242 ELOCTALGNLKIYVNSKAITSEKSDAQFLNTLLFKGFFTGHPWYNDLLVDLGSTAA 301
Db 218 KPCICTVPEVSSVFIPPK-----PKDVLITL----- 245
QY 302 TSEYEGSSVDLYGAYGYQCAGTPKTACMGVILHNNRLTEKKVPINLWIDGKQT 361
Db 246 -----TP-KVTCVVVDIS-----KDDPEVQFSNFD----- 270
QY 362 TVPIDVKVTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVFH 412
Db 271 DVEVHTAQTPREQFNSTFRSEIPIHQDLWLNKEFKCRVNSAAFAPTEK----- 324
QY 413 SSEGSTVSYDLFDAQGQPTLLRIYRDNTTISLSISLXYLTTISVNTQTPTSLLVS 472
Db 325 -----TISKT----- 329
QY 473 AGDRVITCKASQSVNDVAVYQKQKPGQPKLLISYSSRYAGVPRFSGSGYGTDFTLT 532
Db 330 ----- 329
QY 533 ISSVQAEADAAYFCQDYNSPPTFGGKTKLEIKRADAPTSTVFPPSSQLTSGGASVVC 592
Db 330 -----KGRPKAQVYTIPPKQMAKDKVSLTC 357
QY 593 FLNNFYPKQINVKWIDGSRQNGVLSWTDQSDKSTYSMSSTLTTLTKDEYERHNSYTC 652
Db 358 MITDFFPFEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQSNNWEAGNTPTC 415
QY 653 EATHK 657
Db 416 SVLHE 420

RESULT 25
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;

Query Match 24.1%; Score 850; DB 11; Length 234;
Best Local Similarity 76.9%; Pred. No. 7.9e-46;
Matches 163; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 460 IYNTQPTSLVSAGRVITTCASQSVNDVAVYQKQKPGQPKLLISYSSRYAGVPR 519
Db 22 IQLTQSPASLSASVGETVITTCRASENIYSLAWYQKQKPGQPKLLISYSSRYAGVPR 81
QY 520 FSGSGYGTDFTLTISVQAEADAAYFCQDYNSPPTFGGKTKLEIKRADAPTSTVFPPSS 579

```

```

Db 82 FSGSRSGTQFSLKINSLOPEDFGSYCOHSGIPTFGSGTKLEIKRADAPTSTVFPPS 141
QY 580 SEQLTSGASVVCFLNNFYPKQINVKWIDGSRQNGVLSWTDQSDKSTYSMSSTLT 639
Db 142 SEQLTSGASVVCFLNNFYPKQINVKWIDGSRQNGVLSWTDQSDKSTYSMSSTLT 201
QY 640 TKDEYERHNSYTCATHKTSTSPVKSNRNE 671
Db 202 TKDEYERHNSYTCATHKTSTSPVKSNRNE 233

RESULT 26
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; Cytochrome_B5.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 22.8%; Score 803; DB 11; Length 473;
Best Local Similarity 32.0%; Pred. No. 1.9e-42;
Matches 214; Conservative 74; Mismatches 138; Indels 242; Gaps 18;

QY 1 EVQLQQSGPDLVKPGASVKISCKASGYFTGYMHVWYKQSPGKLEWIGRINPNNGVLY 60
Db 20 EVQLVESGGGLVPGGSRKLSCKASGFTSDYGMHWVRQAPKGLWVAVINGSTTIYY 79
QY 61 NQKPKDKATLTVDKSTTAYMELRSLTSEDSAVYICARSTMITNVMYDYGQGTSTVSS 120
Db 80 ADTVKGRFTISRDNKNTLTFLQMTSLASEDTAMVYCARELWLR--IDYWGQGTITVSS 137
QY 121 AKITPPSVYPLAPCSAAQNTSMVTLGCLVKGYPEPTVITWNSGSLSSGHTTPAVLQSD 180
Db 138 AKITPPSVYPLAPCGGDTTGSSTVTLGCLVKGYPPESVITVWNSGSLSSVHTFPALLQSG 197
QY 181 LYTLSSSVTVPSSTWPSSTVTCNVAPASSTKVDKIVPRDSGPGSEKSEINE----KD 236
Db 198 LYTMSSSVTVPSSTWPSSTVTCNVAPASSTVTDKLEP---SGP---ISTINPCPCKE 251
QY 237 LRK--KSELGOTGLNLIKQIYVNSKAITSEKSDAQFLNTLLFKGFFTGHPWYNDLLV 294
Db 252 CHKCPAPNLEG---GPSVFIFPPENIKDV-----LMI 279
QY 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGTPKTACMGVILHNNRLTEKKVPINL 354
Db 280 SL-----TP----- 283
QY 355 WIDGKQTVPIDVKVTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHS 414

```

Db 284 ----KVTGVVD-----VSEDDPDVQISWFWNN-----VEVHTA 313
Qy 415 EGSTVSDLDFAQQOYPTLLRIYRNTTSSLSLSLYTTSIVMTOTPTSLVLSAG 474
Db 314 QTOQHREDY-----NSTIR-----VWSA- 331
Qy 475 DRVTITCKASQSVNDVAVYQKPGQPKLLISVTSRYAGVDFRFGSGYGTDFLTTS 534
Db 332 -----LPIQHQDWMMSGKFKCKVN 350
Qy 535 SVQAEADAATVCCQDYNPTFFGGTGLKLEIKRADAPTIVSIFPSSEOLTSGGASVVCCL 594
Db 351 N-----KDLPSPIE-----RTTSKIKGLVRAPQVYILPPAPQALSRKDVSTCLV 595
Qy 595 NNEYPKIDNVKWKIDGGERON-----GVLSWTDQDSKSTYSMSSTLTITLTKDEYERHNS 649
Db 396 VGFNPGDISVWTSNGHTENYKDTAPVLD-----DGSYFIYSKLDIKTSKWEKTD 448
Qy 650 YTCETHK 657
Db 449 FSCNVRHE 456
RESULT 27
ID O85217 PRELIMINARY; PRT; 268 AA.
AC O85217;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Enterotoxin J.
GN SEJ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KS11410;
RX MEDLINE=99052098; PubMed=9835033;
RA Zhang S., Iandolo J.J., Stewart G.C.;
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
enterotoxin determinant (sej)".
RL FEMS Microbiol. Lett. 168:227-233 (1998).
DR EMBL; AF053140; AAC78590.1; -;
DR HSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

Query Match 21.8%; Score 768; DB 2; Length 268;
Best Local Similarity 58.3%; Pred. No. 1.4e-40;
Matches 141; Conservative 39; Mismatches 62; Indels 0; Gaps 0;
Qy 228 KSEETNEKDLRKSELOQTALGNLKIYYNSKAITSEKSAQDFTLNTLLFKGFFTGHP 287
Db 27 KNETIKENLHKSELSSTLNLNRHLYFFNEKIGSEKIMTEDQDLDYTLFLKSFIFS 86
Qy 288 WTNDLLDGLSTAAATSEVEGSSVDLYGAYYQACAGTPTNKATCMYGGVTLHDNRLEE 347

Db 87 QYNDLLVQDFSKETVKNPKQKQVDLYSGYFQCGGKPKNTACMYGVTLHNNQLYDT 146
Qy 348 KKVPIINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVORG 407
Db 147 KKIPIINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVORG 206
Qy 408 LIVHPSSEGSTVSDLDFAQQOYPTLLRIYRNTTSSLSLSLYTTSIVMTOTPT 467
Db 207 LIVHPSSEGSTVSDLDFAQQOYPTLLRIYRNTTSSLSLSLYTTSIVMTOTPT 266
Qy 468 SL 469
Db 267 VL 268
RESULT 28
ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchéz A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC051328; AAH51328.1; -;
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 21.3%; Score 750; DB 4; Length 469;
Best Local Similarity 30.3%; Pred. No. 4e-39;
Matches 201; Conservative 70; Mismatches 156; Indels 236; Gaps 16;

Qy 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHWKSPGKGLGWIRINPNNGVTLY 60
Db 20 QVHLVSGAEVKPGASVKLSCKTSYGNFSSYDLIWRQAPQGLGWIRINPNNGVTLY 79
Qy 61 NQFKDKAILTVDKSSSTAYMELRLSITSDSAVYCYCARSTMTINYMDYMGOGTSVTYSS 120
Db 80 ARKFGQRTVMTTDSATTSYMEFRSLRSDDTALFYCATKSRGQVDFDSWGOGTLVTYSS 139

RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005332; AAH05332.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25702 MW; 7BPFE4ED23084BC6 CRC64;

Query Match 19.6%; Score 689; DB 4; Length 236;
 Best Local Similarity 62.7%; Pred. No. 1.1e-35;
 Matches 133; Conservative 28; Mismatches 51; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDR 519
 DB 24 IOMTQSSSSLSASGVDVTITCRASQDISYLAWFQKQPKAKPSLLYGASSLQSGVQSK 83
 QY 520 FSGSGYGTDFLTITSSVOAEDAAVYFCQDYNSPPTFGGKTLEIKRADAAPTIVSIPPPS 579
 DB 84 FSGSGYGTDFLTITSSLOPEDFATYVCQYKSYPTFGGKTLEIKRTVAAPSVFIPPPS 143
 QY 580 SEQLTSGASVVCFLNNFYKDIIVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLT 639
 DB 144 DEQLKSGTASVVCFLNNFYKDIIVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLT 203
 QY 640 TKDYERHNSYTCEATHKTSPIVKSFNRNE 671
 DB 204 SKADYKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 31
 Q72351
 ID Q72351 PRELIMINARY; PRT; 482 AA.
 AC Q72351;
 DT 01-OCT-2003 (TremBLrel. 25, Created)
 DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
 DE Hypothetical protein DKFZp686N02209.
 GN DKFZp686N02209.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BX38118; CAD98026.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901DIA034 CRC64;

Query Match 19.5%; Score 686.5; DB 4; Length 482;
 Best Local Similarity 28.3%; Pred. No. 4.1e-35;
 Matches 191; Conservative 75; Mismatches 161; Indels 249; Gaps 18;

QY 1 EVQLQQSGDILVKGASVKISKASGYFTGYHHWVKQSPCKGLEWIGRINPNNGVTLY 60
 DB 20 QAQVVEGSGVQVQGRSLRSLSCIASGFSGSAMHWRQIPFGKLEWAVISYDGNHKL 79
 QY 61 NQKFKDKATLVTKSTTAYMELRSLTSDSAVYCAR-----STMITNYV-----M 107
 DB 80 SDSVKGRFTISRDNSKSLFLHVNLSLTADTAIYCARDFHSKTSIFGLIPLYFYVSAM 139
 QY 108 DYWGQGTSTVSSAKTTPPVVPLAPGSAQNSMVTLCGLVKGYFPBPVTVVNSSL 167
 DB 140 DTWGRGTTIVSSAGTKGSPVFLAPSKTSKSGTAALGCLVKDYFPBPVTVVNSGALT 199
 QY 168 SGVHTFPAVLQSD-LYTLSSSVTVPSSTWSPSTVTCNAVHPASSTKVDKTVPRDSGSPS 226
 DB 200 SGVHTFPAVLQSGGLYSVSSVTVPSLSLGTQYTCNVNHPKSNITKVDKKVEPKSC----- 255
 QY 227 EKSEIEINEDLKRKSELOCTALGNLQIYYYNKSAITSSEKSAQOFLNTLLFKGFFGH 286
 DB 256 -----DKHTTCCPCPAPPELLGSPSVF--LFPFK 281

QY 287 PWYNDLLVLDLGLSTAATSEYEGSSVDLYGAYYGYOCAGGTNKTACTACMYGGVTLHDNNRLTE 346
 DB 282 P--KDTLM-----ISRTPEVT-CVVVDVS-----HE 304
 QY 347 EKKVPINLWIDGKQTTVPIDVKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKQVR 406
 DB 305 DPVKFNWYVDG----VEVHNNAKTPREEQ-----YNSTY---RVVS 339
 QY 407 GLIIVFHSSEGSTSVSDLEDAQGGYPTDILLRIYRONTTISSTLSLSLYLYTTSIVMTQTP 466
 DB 340 VLTVLHLDWLNKGEY----- 354
 QY 467 TSLVLSAGDRVTITCKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDRFSGSYG 526
 DB 355 -----KCKVS-----NKALPAP---IEKT-SKAKGP- 378
 QY 527 TDFLTITSSVOAEDAAVYFCQDYNSPPTFGGKTLEIKRADAAPTIVSIPPSSEQLTSG 586
 DB 379 -----REPOVYTLPPSDELTKN 396
 QY 587 GASVVCFLNNFYKDIIVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLTITLK 641
 DB 397 QVSLTCLVKGFYPSDIAVWESNGQFENNYKTPPVLD-----DGSFFLYSKLTVDK 449
 QY 642 DEYERHNSYTCEATHK 657
 DB 450 SEWQGGNVFSCSVME 465

RESULT 32
 Q8NEKO
 ID Q8NEKO PRELIMINARY; PRT; 239 AA.
 AC Q8NEKO;
 DT 01-OCT-2002 (TremBLrel. 22, Created)
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC030814; AAH30814.1; -;
 DR PIR: S23638; S23638.
 DR PIR: S34091; S34091.
 DR PIR: S40357; S40357.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00407; IgC1; 1.
 DR SMART: SM00406; IG; 1.
 DR PROSITE: PS00835; IG-LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Query Match 19.0%; Score 669.5; DB 4; Length 239;
 Best Local Similarity 59.4%; Pred. No. 1.8e-34;
 Matches 129; Conservative 32; Mismatches 51; Indels 5; Gaps 1;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSV-----SNDVAVYQKQPGSKLLISYTSRYA 514
 DB 22 IVMTQSFSLPVTGPEPASISCRSSQSLHSDGYNLDWYLVKQPGSPQLLYVLSNRAS 81
 QY 515 GVDRFSGSGYGTDFLTITSSVOAEDAAVYFCQDYNSPPTFGGKTLEIKRADAAPTIVS 574

Db 82 GVPDRFSGSGGDFTLTKISKVEAEVDGIYCMQGLQTPQTGGQKVKIKRTVAAPSVF 141
QY 575 IFPPSSSEQLTSGGASVVCFLNFPKDIINVKKIDGSEBQNGVLNSWTDQDSDKSTYSMS 634
Db 142 IFPPSEQLKSGTASVCLLNFPYKQVQWQVNTLQSGNSQESVTEQDSDKSTYSLS 201
QY 635 STLTCLKDEYERHNSVTCATHKTSTSPIVKGFNRNE 671
Db 202 STLTCLKADYERKHVYACEVTHQGLSPVTKSPFNRC 238
RESULT 33
Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC053984; AAH53984.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match 18.6%; Score 666.5; DB 4; Length 470;
Best Local Similarity 28.6%; Pred. No. 7.2e-34;
Matches 190; Conservative 66; Mismatches 170; Indels 239; Gaps 18;
QY 1 EVOLQSGDPLVKPGASVKISKAGSYSTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 20 EVQLVESGGGLVQPGGSLRLSASGFTLNNYDMHWVRQGIKGLWVSKIG-TAGDRY 78
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYYCARST--MITYVMDYWGQGTSTVTV 118
Db 79 AGSVKGRFTISRNKADSLYLNQWLSRVGDAVYYCARGAWFLGAFDINGQGTMTV 138
QY 119 SSAKTTTPSVYPLAPGSAATQSMVTGLCLVKGYPFPEVTVTWNSGSLSSGVHTTPPAVLQ 178
Db 139 SSASTKGPSVFPPLAPGSKSTSGTAAAGCLVKGVDYFPEVTVSWNSGALTSQWHTFPAVLQ 198
QY 179 SD-LYTLSSVTVPSSTWPSSEVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237

Db 199 SSGLYSLSSVTVFSSSLGTQTYICNVNHNKSNKVDKVEPKSC----- 243
QY 238 RKSELOQTALCNLKOIYYNSKAITSEKSAOFLNTLLPKGFFTCGHPWYNDLLVDLG 297
Db 244 -----DKTHTCPPTCFAPELGLGSPSVF--LPPPKP--KDTLM--- 275
QY 298 STAATSEYEGSVLDYGAIVYQACAGTPNKACMGVGLHDNNRLTEKKVPINLWID 357
Db 276 -----ISRTPEVT--CVVVDVS-----HEDEPVKFNWYVD 303
QY 358 GKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVORGLIIVFHSSEGS 417
Db 304 G-----VEVHNAKTPREEQ-----YNSTY-----RVVSVLTVLHQDWLN 338
QY 418 TVSYDLFDAGQYPTDILLRIYRDNVTISSTLSLSLYLTTISVMTQPTSLVLSAGDRV 477
Db 339 GKEY----- 342
QY 478 TITCKASQSVSNDAVYQKQPGQPKLLISYTSRYAGVDPFRFSGSGYGTDFTLTISSVQ 537
Db 343 --KCKVS-----NKALPAP---IEKTISKAKGQP----- 366
QY 538 AEDAAVFCQDYNSPPTFGGTTKLEIKRADAPTIVSIFPPSSSEQLTSGGASVVCFLNFP 597
Db 367 -----RBPQVYTLPPSRDELTKNOVSLTCLVKGF 395
QY 598 YPKDINVKWKIDGSEKQ-----GVLSWTDQDSDKSTYSMSLTILTKDEYERHNSYTC 652
Db 396 YPSDIAVEMESNGQPNENYKTPPVLDS-----DGSFLYSLKLTVDKSRWQGNVFS 448
QY 653 EATHK 657
Db 449 SVMHE 453
RESULT 34
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025985; AAH25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SMC0406; IGv; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 18.8%; Score 662.5; DB 4; Length 473;
Best Local Similarity 26.8%; Pred. No. 1.3e-33;
Matches 183; Conservative 78; Mismatches 141; Indels 281; Gaps 19;

Query Match	18.4%; Score 648; DB 11; Length 614;
Best Local Similarity	28.9%; Pred.No.1.5e-32;
Matches	202; Conservative 91; Mismatches 205; Indels 200; Gaps 28;
Qy	1 EVQLQQSGPDLVKPGASVKISKCKASGYSTFYGMHWKQSPGKLEWIGRLNPNNGVTLY 60
Db	20 QVQLQQSGPELVKPGASVKISKCKASGYAFSSWMNVKQRPKGKLEWIGRYVPGDGTNY 79
Qy	61 NQKFKDATTLDKSSSTAYMELASLTSEDSAVTYCARSTMITNYMDYWGQGTSTVTS 120
Db	80 NGKFKGATLTADKSSSTAYMQLSSLTSEDSAVTYFCARD-YGSSYRAYWGQGLTVTSA 138
Qy	121 AKITPPSVYIPLAP-GSAAQTNSTMVTLGLVKGYPEPVVTW-----NSGSLSSGVHITPPAV 176
Db	139 ESQSPFNPFVLSCEPLSKDNLVAMGLARDFLPSTISFTWYQNNAEVIQIRTEPTL 198
Qy	177 LQSDLYTLSSSVTV-PSS--TWPSSETVCNAH-----PA---SSTKVDKKIIVP 219
Db	199 RTGKYLIATQVLLSPKSLLEGSDEYLVCKIHGGKKNKDLHVPVPAVMNPVNVFVPP 258
Qy	220 RDS-GGPFSEKSEENEDLRKKSLOGTALGNLQIYYYNASKAITSSEKSGADQLTNTLL 278
Db	259 RDGFSGAP-----RKSKL-----ICEATNFTPKPITVS-----287
Qy	279 FKGEFTGHPWYND-LIVDLGSLTA--ATSEVEGSSVDLYGAYYGQACAGGTENKTACWYG 335
Db	288 -----WLKDGKLVESEFTTDPVTIENKGSPPQTY-----316
Qy	336 VTLHDNNRLTEKKVPINLMDGQTVTPIDKVKTSKEVTVQELDLQAHYHLHGKFLY 395
Db	317 -----KVIST--LTISEID-----WL 330
Qy	396 NSDSFGKVQGLTVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTIGSTLSLSLYL 455
Db	331 NLNVYTCRDVHRGLTFLKNVSSCA-----ASPSTDI-----362
Qy	456 YTTISVMTQPTSLVLSAGDRVITCKASQSVND-----VAMYQKPGQSKLLISYTSR 512
Db	363 -----LATPIPSFADIFLSKSANLTCVLSNLAIVETLINISWASQS-GEPIETKIKIMESH 417
Qy	513 YAGVPEDESGSGYGTDTFTLISSVQAEQ---AAVYFC---QODYNSPPTFGGQTKLEIKR 566
Db	418 PNGT---FSAKG-----VASVCVDEMMNRKEFVCTVTHRDLPS-----QKKFISK 460
Qy	567 ADAA-----PVSIFPPPSSEQLT-SGGASVYCVFLNFPKDIVNKWKIDGS--ERQNGVLN 619
Db	461 PNEVHKHPAVAYLLPPAREQLNRESATVTCLVKGFSPADISVQWLQRGQLLPQEKVYTS 520
Qy	620 SWTDDQSKOSTYMSGSTLTITKQIEYERHNSYTCETHK 657
Db	521 AMPPECAPGAFYTHSILTVTEEWNSGETYTCVWSHE 558

```

RESULT 37
QBNA49          PRELIMINARY;          PRT;      521 AA.
ID
AC      QBNA49;
CT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hom
OX      NCBI_TaxId=9606;
[1]
SEQUENCE FROM N.A.
RP      TISSUE=Primary B-Cells;
RC      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RR      EMBL; BC033178; AAH33178.1; -.
DR      PIR; A60764; A60764.
DR      InterPro; IPR007110; IQ-like.

```

[illegible]


```

Db 269 GSDASIT-----CTLNG-----280
QY 357 DGKQTTVPIDKVKTSKEVTVOQLDLQARHLYHGKFGVNSDFGKVGORGLIVFHSBEG 416
Db 281 -----280
QY 417 STVSVDLFAQGOYPTLLRIYRDNTTISSTLSISLYLTSIVMTQPTSLLYSAGDR 476
Db 281 -----LRPEG-----AVFTWEP-----TGKDA 299
QY 477 VTTCASOSVNDVAVYQKQKQKQKLLISYTSRYAGVPRFSGSGYGTDTLTISV 536
Db 300 V-----QKKAQVNSCQCY-----VSSVLPGCAERWNS---GASFCKTCTVTP 338
QY 537 QASDAVYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGG-ASYVCFLN 595
Db 339 ESTLTGTTAKVTNTP-----PQHLPLPPELALNELVSTCLVR 382
QY 596 NFYPKDKVKKIDGSRQNG-----VLNSWTDQSKDSTYSMSSTLTTLTKDYERHNSYT 651
Db 383 AFPKQVLRVW-LHGNEELSPESYLVEPLKPEGEGATVLTSLVLRVSAEIKWQGDQYS 441
QY 652 CEATHK 657
Db 442 CMVGHE 447

RESULT 40
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7 AC Q7TCM2 PRELIMINARY; PRT; 243 AA.
AC Q7TCM2;
DT 01-OCT-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAR18315.1; -.
DR MGD; MGI:96448; IGH-6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MEC.
DR InterPro; IPR003596; Ig_V.
DR Fram; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 17.6%; Score 618.5; DB 11; Length 613;
Best Local Similarity 28.1%; Pred. No. 1.1e-30;
Matches 196; Conservative 90; Mismatches 211; Indels 201; Gaps 28;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSTGYMHVWVQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQSGELVKPGASVKISCKATGTFSSYIEWVKORPGHLEWIGELIPGSGSTNY 79
QY 61 NQKFKDKATLVDSKSTTAYMELRLTSDSASVYCARSTMTNYMDYWGOGTSYTVSS 120
Db 80 NEKFKGKATFTADTSNTAYMQLSSLTSDSASVYCAR-RLGRWYFDVWGAGTIVTVSS 137
QY 121 AKTTPSVVPLAP-GSAAQNTSMVTLGCLVKGYFPEPVTVW---NSGSLSGVITFPVAV 176
Db 138 EQSFFNPVPLVSCSEPLSKDLNVAWGCLARDFLPSTISFTWYQNTEVIGIIRFPTL 197

```

```

QY 177 LQSDLYTLSSSVTV-PSS--TWPSETVTCNVAH-----PA--SSTKVKKIVP 219
Db 198 RTGKYLATSVLLSPKSIILEGSDEYLVCKIHYGGKRDHLVPIPAVAEMNPVNVFVPP 257
QY 220 RDS-GGPSEKSEEBINEKDLRKSELOQTALGNLQIYYIYNSKAITSEKSAQDLTTL 278
Db 258 RDGFGSDAP-----RKSKL-----ICEATNFTPKPITVS-----286
QY 279 PKGFTGHPWYND-LLYDLQSTA--ATSEYEGSSVDLYGAYYQOCAGGTNKTACMYGG 335
Db 287 -----WLDGKLVESGFTTDPVTIENKGSPPQFY-----315
QY 336 VTLHNNRLTEBKVKPYNLMDGKQTTVPIDKVKTSKEVTVOQLDLQARHLYHGKFGY 395
Db 316 -----KVIST--LTISEID-----WL 329
QY 396 NSDFGKVGORGLIVFHSBEGSTVSYDLFAQGOYPTLLRIYRDNTTISSTLSISLYL 455
Db 330 NLNYTTCRVDRHGLTFLKNVSSSTCA-----ASPSTDI-----361
QY 456 YTTISVMTQPTSLVLSAGDRVTITCKASQSVND--VAWYQKQKQKQKLLISYTSR 512
Db 362 ----LTFTIPESFADIPLSKANLTLVSNLATYETLINISWASQ--GEPLTKIKINESH 416
QY 513 YAGVDPFRSGSGYGTDTLTISVQAE-----AAVYFC---QQDYNPPTFGGKTKLEIKR 566
Db 417 PNGT----PSAKG-----VASVCVEDMNNRKEFVCTVTHRDLPSP-----QKKTISK 459
QY 567 ADAA-----PTVSIFFPPSSEQLT-SGGASVVCFLNFPKDNVKNKIDGS--EQNGVLN 619
Db 460 PNEVHKHPPAVYLLPPAREQNLRESATVCLVKGSPADISVQWLQRLPQKLVTS 519
QY 620 SWTDQSKDSTYSMSSTLTTLTKDYERHNSYTCEATHK 657
Db 520 APMEPEGAPGYFTHSILTVEEENSGEYITCVVGHE 557

RESULT 41
Q7TCM2 PRELIMINARY; PRT; 243 AA.
ID Q7TCM2 AC Q7TCM2;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAE00495.1; -.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;

Query Match 17.2%; Score 606; DB 11; Length 243;
Best Local Similarity 28.0%; Pred. No. 1.9e-30;
Matches 158; Conservative 31; Mismatches 48; Indels 328; Gaps 7;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSTGYMHVWVQSPGKLEWIGRINPNNGVTLY 60
Db 1 QVQLQSGSELVPGASVKLSCKASGYTFTTYMHVVKQRHGGGLEWIGNIPGSGITNY 60
QY 61 NQKFKDKATLVDSKSTTAYMELRLTSDSASVYCARSTMTNYMDYWGOGTSYTVSS 120
Db 61 DEKFKNKGILTVDTSSTAYMHLSSLASDSASVYICARG----GRGLDVWGAGTTLTVSS 116

```



```
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein_481
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match
  17.1%; Score 602.5; DB 11; Length 488;
Best Local Similarity 27.5%; Pred. No. 8e-30;
Matches 184; Conservative 73; Mismatches 165; Indels 247; Gaps 21;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKLEWIGRIHPNNGVTLY 60
Db 20 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKLEWIGRIHPNNGVTLY 79

QY 61 NQKFKDQATLVDSSTTAYMELRLTSEDSAVYYCARSTMTINYYM-----DYWGQGTSLV 116
Db 80 NQKFKGKATLVDSKSSIAVMQLNLTSDSAVYYCARGPVYYSFSDRGDYWGQGTSLV 139

QY 117 TVSAKTPPSVYPLAPGSAQTNSMTGLCLVKGYPPE-PVTVTW-NSGSLSSGVHTPL 174
Db 140 TVSAEPAREPTIYPLFPQALSSDPVI-IGCLIHDFPFGSTMTVWTKGSKGDIITVNPFP 198

QY 175 AVLQSDLYTLSSSVTPSPSTWP-SETVTCTNVAHPASSTKVDKIVPRDSGGPSEKSEIN 233
Db 199 ALASGGRYTWSSQTLTIPAVECPGEGSVKCSVQH-----DSNPVQELN 240

QY 234 EKDLRKSELOQTALGNLQIYYNKAITSSEKADQFLNTLLFKGFTGHPWVNDLL 293
Db 241 V-----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL 273

QY 294 VDLGTAATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVGTLDHNNRLTEKKVPIN 353
Db 274 --LGDASIT-----CTLNG-----286

QY 354 LWDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQGLIVFHS 413
Db 287 -----286

QY 414 SEGSTVSYDLFDAQGGYPTLLRIYRDNTTISLSISLYLTYTIVMTQPTSLLSVA 473
Db 287 -----LQRPALDILL-----AVFTWEP-----TG 302

QY 474 GDRVTITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDTPLTI 533
Db 303 KDAV-----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTV 341

QY 534 SSVQAEADAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIIPPSSBQLTSGG-ASVVC 592
Db 342 TPESDPTLTGTIAKVTNTFP-----PQVHLLPPPSSEELALNELVSLTC 385

QY 593 FLNNFVKDINVKWIDGSRONG-----VLNSWTDQSDKSTYSMSSTLTLTKDEVERHN 648
Db 386 LVAFAPKPEVLVLRW-LHGNEELSPESYLVEPLKEPGEGATTILVTSVLVSAEIKWQGD 444

QY 649 SYTCEATHK 657
Db 445 QYSCMVGHE 453

RESULT 44
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
```

```
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; --
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match
  16.6%; Score 583; DB 11; Length 481;
Best Local Similarity 26.9%; Pred. No. 1.3e-28;
Matches 179; Conservative 73; Mismatches 167; Indels 246; Gaps 21;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKLEWIGRIHPNNGVTLY 60
Db 20 QVLLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKLEWIGRIHPNNGVTLY 79

QY 61 NQKFKDQATLVDSSTTAYMELRLTSEDSAVYYCARSTMTINYYM-----DSNPVQELN 120
Db 80 NEKFKGKATLVDSKSSIAVMQLNLTSDSAVYYCARGPVYYSFSDRGDYWGQGTSLV 136

QY 121 AKTTPSYVYPLAPGSAQTNSMTGLCLVKGYPPE-PVTVTW-NSGSLSSGVHTFPVLQ 178
Db 137 EPAREPTIYPLFPQALSSDPVI-IGCLIHDFPFGSTMTVWTKGSKGDIITVNPFPALAS 195

QY 179 SDLYTLSSSVTPSPSTWP-SETVTCTNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
Db 196 GGRYTWSSQTLTIPAVECPGEGSVKCSVQH-----234

QY 238 RKSELOQTALGNLQIYYNKAITSSEKADQFLNTLLFKGFTGHPWVNDLLVDLG 297
Db 235 -----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL--LG 268

QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVGTLDHNNRLTEKKVPINLWID 357
Db 269 SDASIT-----CTLNG-----279

QY 358 GKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQGLIVFHSSEGS 417
Db 280 -----279

QY 418 TVSYDLFDAQGGYPTLLRIYRDNTTISLSISLYLTYTIVMTQPTSLLSAGDRV 477
Db 280 -----LQRPALDILL-----AVFTWEP-----TGKDAV 299

QY 478 TITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDTLTITSSVQ 537
Db 300 -----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTVTHPE 338

QY 538 ABDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIIPPSSBQLTSGG-ASVVCFLNN 596
Db 339 SDTLTGTTIAKVTNTFP-----PQVHLLPPPSSEELALNELVSLTCLVRA 382

QY 597 FYPKDINVKWIDGSRONG-----VLNSWTDQSDKSTYSMSSTLTLTKDEVERHNSYTC 652
Db 383 FNPKEVLVLRW-LHGNEELSPESYLVEPLKEPGEGATTILVTSVLVSAEIKWQGDQISC 441

QY 653 EATHK 657
Db 442 MVGHE 446

RESULT 45
Q8VCV5 PRELIMINARY; PRT; 481 AA.
ID Q8VCV5
AC Q8VCV5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
```



```
Db 352 -----TF-----PPQVHLLPPPEELALNELLSLCLVRA 381
QY 597 FVPKDNVWKIDGSRQNG---VLNSWTDQDSKDSITYSMSTLTTLTKDEYERHNSYTC 652
Db 382 FNPKEVLVW-LHGNEELSPESYLVEPLKEPGEAGATTYLVLSVLRVSAETWKQDQSC 440
QY 653 EATHK 657
Db 441 MVGHE 445

RESULT 47
Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-V0558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAL18322.1; -.
DR MGD; MGI:96486; Igh-V0558.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_V.
DR Pfam; PF00047; Igh; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGH_LIKE; 4.
DR PROSITE; PS00230; IGH_MHC; 2.
DR Hypothetical protein.
KW SEQUENCE 489 AA; 53208 MW; CC85B1194DAFEF2C CRC64;

Query Match 16.0%; Score 565; DB 11; Length 489;
Best Local Similarity 26.3%; Pred. No. 1.8e-27;
Matches 176; Conservative 76; Mismatches 170; Indels 248; Gaps 21;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWYKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 KVLQSGDAELVKPGASVKLSCKASGYTFSDYFIHWIKQRSGGLEWIGWFPNGSGIKF 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYVCARSTMITNY-----VMDYWGQGT 115
Db 80 NEKFKDKATLTADKSTTVYMDLSRLTSDSAVYFCARHEDRGNDYDGLAWFYWGQGT 139
QY 116 VTSSAKTTPPSVYPLAPGSAQTNSMTLGLCLVKGYPPE-PVTVW-NSGSLSSGVHTF 173
Db 140 VTSSAPAREPTIYPLTFQALSSDVI-IGLLIHDYFPGTMTVWGSKDITTVNPP 198
QY 174 PAVLQSDLYLTSSSVTPSSTWP-SFTVTCNVAHPASSTKYDKIVPRDSGSPSESEI 232
Db 199 PALASGRVTMSQLTLPAVECEGESVKCSQVH-----DSNPVQEL 240
QY 233 NEKDLKKSELOGTALGNLKIYYNSKAITSSSEKSAQFLNTLLFKGFTTGFHPYNDL 292
Db 241 NV-----NCPGIC---SPPTTPPPSCQPSLS-----LQRALEDL 273
QY 293 LVDLGSTAATSEVGSVDLYGNAYYQCAGGTPTKACMYGVTLDNNRUTEKKVPI 352
Db 274 L--LGSASAIT-----CTLNG----- 287
QY 353 NLWIDGKQTTPIDKVKTSKKEVTVQELDQARHYLHGKFGLYNSDSFGKVQORGLIVFH 412
Db 288 ----- 287
```

```
QY 413 SSEGSTVSYDLFDAQGVDPDTLLRIYRDNTTISSTLSLSISLYTTSIVMTQPTSLIVS 472
Db 288 -----LRDEG-----AVTWEP-----T 302
QY 473 AGDRVTTICKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYCTDFTLT 532
Db 303 GKDAV-----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCT 341
QY 533 ISSVQAADAAVYFCQDYNPPTFGGCTKLEIKRADAAPTIVSIPPPSEQLTSGG-ASVV 591
Db 342 VTHPESDTLTGTTIAKVTNTFP-----PQVHLLPPPEELALNELSLT 385
QY 592 CFLNNFVKDINVKWIDGSRQNG---VLNSWTDQDSKDSITYSMSTLTTLTKDEYERH 647
Db 386 CLVRAFNPKEVLVW-LHGNEELSPESYLVEPLKEPGEAGATTYLVLSVLRVSAEIKWQ 444
QY 648 NSYTCEATHK 657
Db 445 DQYSCMVGHE 454

RESULT 48
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAL15760.1; -.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh_V.
DR Pfam; PF00047; Igh; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGH_LIKE; 5.
DR PROSITE; PS00290; IGH_MHC; 3.
DR Hypothetical protein.
KW SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 15.9%; Score 561; DB 4; Length 597;
Best Local Similarity 26.2%; Pred. No. 4.3e-21;
Matches 183; Conservative 104; Mismatches 214; Indels 198; Gaps 28;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWYKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 EVQLLEGGGLVQPGGSLRLSCAASGFSYFAMNVRQAPGKLEWVAISGSGGTYT 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYVCARS---TMITNYM-DYWGQGT 115
Db 80 ADVKGRFTISRDNRSRDTLYLQMNLSRAEDTAVYICARDPRGYSASGNYTREDYWGQGT 139
QY 116 VTSSAKTTPPSVYPL--AFGSAQAQTNSMTLGLCLVKGYPPEPVTVW---NSGSLSSGV 170
Db 140 VTSSGASAPTLFPLVSCNSPDSSTSS-VAVGCLAQDFLPDSITFSWKYKNNSDISS-T 197
QY 171 HTFPAVQLSDLYLTSSSVTPVPS---TWPSETVCNVAHPASSTKYDKIVPRDSGSPSE 227
Db 198 RGFSVLRGKKYAAATSQVLLPFSKDWMOGTDEHVVCVKQHP-NGNKEKNVPLPIAELPPK 256
QY 228 KSEINEKDLKKSELOGTALGNLKIYYNSKAITSSSEKSAQFLNTLLFKGFTTGH 287
Db 257 VSVFVPRD-----GFF-GNP 271
```

```
QY 288 WYNDLLVGLGTAATSEYEGSSVDLYGAYICYQCAGGTGPNKTCACMGVGLTHDNNRLTBE 347
DB 272 RKSLIC-----QATGESP-----285
QY 348 KKVPIVNIWDGQ--TVPIDKVTSKKE-----VTQELDLQARVYHKGFL 394
DB 286 RQIQVWMLREGQVSGVTTDQVQAEKESGPTTYKVTSLTKESD-----W 333
QY 395 YNSDSFGKQVGLVIFHSSEGSVTVSLDPAQOQYPTLLRIYRNTTSSISLSISLY 454
DB 334 LSQSMFTCRVDHRLGTLFOQRASSWCVD-----OPTAIRVF-----AIPPSAFSL- 380
QY 455 LYTTSIVNTOPTSLLSVAGDRVTITCKASOSVNDVAVYQOQPGQPKLLISYTSRYA 514
DB 381 --TKSTKLTCLVLDL--TTYDSVTI-----SWTRQN-GEAVK--THTNISES 420
QY 515 GVPDRFSGSGYGTDTLTISVQAEADAIVFCODYNSPTF-----GGGTKLEIK 565
DB 421 HPNATFSAVG-----EASI--CEDWNSGERFTCTVTHDLPPLKOTIS 463
QY 566 RADA--PTVSIFPPSSSEQLT-SGGASVVCFLNFPYKDIYKWKIDGS--ERQNGVL 618
DB 464 RPKGVALHRPVDYLLPAREQLNRESATITCLVTGFSPADVFQVMQGOPLSPKVT 523
QY 619 NSWTQDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHK 657
DB 524 SAPMPEQAPGRYFAHSILTVSEBWNVTGETYTCVVAHE 562

RESULT 49
Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC Q7SZ36;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farley J., Heltan E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054155; AAH54155.1; -.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47B8D0D2639CB436 CRC64;

Query Match 15.6%; Score 548; DB 13; Length 237;
Best Local Similarity 48.6%; Pred. No. 8e-27; Indels 6; Gaps 2;
Matches 105; Conservative 42; Mismatches 63;

QY 460 IVMTQPTSLLSVAGDRVTITCKASQSVSND-----VAVYQOQPGQPKLLISYTSRYAG 515
DB 22 IVLTQSPDYVSVPGETVTLTKASSVAIGSTVYLHWYQKSGVQPKLLIYLANRHTG 81
QY 516 VPDPSGSGYGTDTLTITSSVQAEADAIVFCODYNSPTFEGGTGKLEIKADAAPTYSI 575
DB 82 TPERISGSGSGTDTLTISRMEADAADYCCQGRSDLTFTGKTRVELKENDAKPAVFI 141
QY 576 PPSSEQLTSGGASVVCFLNFPYKDIYKWKIDGSRQNGVLSWTDQDSKSTYSMS 635
DB 142 FXPSDEQYKEGNPTAVCLINFFPREDLTVTWKVDSDVSDTSDPMQESDSTYSQSS 201
QY 636 TLTKDEYERHNSYTCEATHKSTSPIVKSFNNE 671
DB 202 MLTLTKDWKADKPECLVQHK--TAQLTQSFQSKQ 235

RESULT 50
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, and Lymph;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR EMBL; BC001872; AAH01872.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 15.5%; Score 545; DB 4; Length 597;
Best Local Similarity 25.9%; Pred. No. 4.4e-26;
Matches 182; Conservative 103; Mismatches 213; Indels 204; Gaps 29;

QY 1 EYVLOQSGPDLKPGASVKISCKASGYSTGYVHWKQSPKGLWIGRINPNNGVLY 60
DB 20 QVLOQWAGLKPSETLSLTGVTGGSGFYGSWIRQPPQKGLWIGRIN-HSGITNY 78
QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSEDASVYVCARSTMT-----NYVMYWGQ 112
DB 79 NPSLKSRTVISVDTSKQLSLKSSVNAADAVVYCAR--VITRASPGTDGRYGDVWGQ 136
```


RC STRAIN-C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to 4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB067785; BAB63270.1; -;
DR PIR: F28833; F28833.
DR PIR: F33932; F33932.
DR PIR: PH1105; PH1105.
DR PIR: PH1108; PH1108.
DR PIR: PH1114; PH1114.
DR PIR: PH1118; PH1118.
DR PIR: PH1119; PH1119.
DR PIR: PH1125; PH1125.
DR PIR: PH1126; PH1126.
DR PIR: PH1128; PH1128.
DR PIR: PH1129; PH1129.
DR PIR: PH1131; PH1131.
DR PIR: PH1134; PH1134.
DR PIR: PH1137; PH1137.
DR PIR: PH1139; PH1139.
DR PIR: PH1142; PH1142.
DR PIR: PH1144; PH1144.
DR PIR: PH1147; PH1147.
DR PIR: PH1149; PH1149.
DR PIR: PH1150; PH1150.
DR PIR: PH1151; PH1151.
DR PIR: PH1152; PH1152.
DR PIR: PH1153; PH1153.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FT NON_TER 145
FT SEQUENCE 145 AA; 16081 MW; ECDBA1A35E05B8AA CRC64;
SQ
Query Match 15.0%; Score 527; DB 11; Length 145;
Best Local Similarity 74.8%; Pred. No. 8.6e-26;
Matches 98; Conservative 15; Mismatches 18; Indels 0; Gaps 0;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYHHVWKQSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLQPGAEIVKPGASVKLSCKASGYTFTSYHHVWKQRFGRGLEWIGRIIDPNSSGTTY 60
QY 61 NQKFKDKATLVDKSSTAYMELSLTSEDSAVYVCARSTMITNYVMDYWGQGTSTVVS 120
Db 61 NEKFKSKATLVDKSSTAYMELSLTSEDSAVYVCARSDYDYDYMDYWGQGTSTVVS 120
QY 121 AKTTTPPSVYPL 131
Db 121 ESQSPPNVFPL 131
RESULT 61
Q96EYO PRELIMINARY; PRT; 613 AA.
AC Q96EYO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC011857; AAH11857.1; -;
DR PIR: S15590; S15590.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 5.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67273 MW; 31214203PB8421E7 CRC64;
Query Match 14.9%; Score 525.5; DB 4; Length 613;
Best Local Similarity 25.6%; Pred. No. 7.7e-25;
Matches 178; Conservative 101; Mismatches 221; Indels 195; Gaps 28;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYHHVWKQSPGKGLWIGRIINPNNGVTLY 60
Db 20 QVQLQSGPGLVKPSETLSLTCTVSGGSISSYYKSWIRQPKAGKLEWIGRIY-TSGSTNY 78
QY 61 NQKFKDKATLVDKSSTAYMELSLTSEDSAVYVCARSTM-ITNYVMDYWGQGTSTVVS 119
Db 79 NPSLSRVMTMSVDTSKQFSLKLSVTAADTAVYVCASQPWELPTVGLFYWGQGTSTVVS 138
QY 120 SAKTTPPSVYPL--APGSAAGTNSMTGLCLVKGYFPEPVTVTW--NSGSLSGVHTFP 174
Db 139 SGASAPTLFPLVSCENSPDTSS-VAVGCLAQDFLPDSITFSWKYKNSSDISS-TRGFP 196
QY 175 AVLQSDLYTLSSSTVPS--TWPSETVTCNVAPASSTKVDKKIVPRDSGGGSEKSEE 231
Db 197 SVLRGGKYAATQVLLPSKQVNVQGTDEHVCKVQHP-NGNKEKQVPLEVIAELPKVSFV 255
QY 232 INEKDLRKSELOGTALGNLKIYYNKAITSSEKSDAQFLTLLPKGFPTGHPWVND 291
Db 256 VPRD-----GFP-GNPRKSK 270
QY 292 LLVDLGLSTAATSEYEGSSVDLYGAYGYCAGGTPNKTACMYGVTLHDNRLTEEEKVP 351
Db 271 LIC-----QATGFSF-----RQIQ 284
QY 352 INLWIDGK--TTVIDKVKYSKE-----VTVQLDLQARHVLHGKFLGNSD 398
Db 285 VSWLRGKGVGSGVTTDQVQAEAKSGSTTYKVTSLTKESD-----WLSQS 332
QY 399 SFGGKQVQRLIVFHSSEGSTVSYDLFDAQGVDPDLLRIYRDNITTSISLSISLYTT 458
Db 333 MTCRVDRGLTFQNVASSMCPD-----QDTAIRVF---AIPSFASIFL---TK 377
QY 459 SIWMTQTPTSLVSAGDRVTITCKASQSVSNVDVAVYQKPGQSPKLLISYISSRYAGVPD 518
Db 378 STKLTLCLVTL--TTVDSVTI-----SWTRQN-GEAVK---THTNISHPNA 419
QY 519 RPSGSGYGTDFLTLTSSVQAEADAAYVFCQDYNPSPTF-----CGGTKLEIKRADA 569
Db 420 TFSAVG-----EASI--CEDDWNSSERFCTVTHTDLSPLKQTSIRPKG 462
QY 570 A-----PTVSIFPPSSSEQLT--SGGASVVCFLNNFYPRDINVKWKIDGS--ERQNGVLSWT 622
Db 463 VALHRPDVYLLPPAREQLNLRSAITCLVTGFSADVFQVQWQRPQLSPKPYVTSAPM 522
QY 623 DQSKDSTYSMSSTLTTLTKDEYERHNSYTCETHK 657
Db 523 PEPQAFGRYFAHSILTVSEEWNTGTETVTCVVAHE 557
RESULT 62
Q9BRVO PRELIMINARY; PRT; 500 AA.
AC Q9BRVO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.

RC	STRAIN=C57BL/6;
RA	Kozono Y., Kozono H., Azuma T.;
RB	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RC	Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RD	Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RE	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RF	ENBL; AB067790. BAB63275.1; -.
RG	PIR; F28833; F28833.
RH	PIR; F33932; F33932.
RI	PIR; PH105; PH1105.
RJ	PIR; PH108; PH1108.
RK	PIR; PH114; PH1114.
RL	PIR; PH118; PH1118.
RM	PIR; PH119; PH1119.
RN	PIR; PH125; PH1125.
RO	PIR; PH126; PH1126.
RP	PIR; PH128; PH1128.
RQ	PIR; PH129; PH1129.
RR	PIR; PH131; PH1131.
RS	PIR; PH134; PH1134.
RT	PIR; PH137; PH1137.
RU	PIR; PH139; PH1139.
RV	PIR; PH142; PH1142.
RW	PIR; PH144; PH1144.
RX	PIR; PH147; PH1147.
RY	PIR; PH149; PH1149.
RZ	PIR; PH150; PH1150.
SA	PIR; PH151; PH1151.
SB	PIR; PH152; PH1152.
SC	PIR; PH153; PH1153.
SD	InterPro; IPR007110; Ig-like.
SE	InterPro; IPR003596; Ig_v.
SF	Pfam; PF000047; ig; 1.
SG	SMART; SM00406; IgV; 1.
SH	PROSITE; PS50835; IG_LIKE; 1.
SI	NON_TER 1
SJ	NON_TER 143
SK	SEQUENCE 143 AA; 15868 MW; 139B2E966B81E07F CRC64;

```
Query Match      : 14.6%; Score 514; DB 11; Length 143;
Best Local Similarity 74.0%; Pred. No. 5.5e-25;
Matches          97; Conservative 15; Mismatches 17; Indels 2; Gaps 1

QY    1 EVLOQSGLVKPGASVKLSCKASGVSFTCYVHHWTKSPGRGLEWIGRIINPNCVTLY 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1 QVOLOQPAGELVKPGASVKLSCKASGVTFSTYNHHWTKRPRGLEWICRIDNSGGTY 60
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY    61 NOKFKDKATLTVDKSGSTTAYMELRSITSDESADVVCARSTMITNYMDYWGQGSTVTSS 120
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     61 NEKFPSKATLTVDKPSSTAYMQLSLTSDESADVVCAR--WDEDYAMDYWGQGSTVTSS 118
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY    121 AKTPPSVYPL 131
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     119 ESOSFPNVFPL 129
       :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 67	Q8WU38	PRELIMINARY;	PRT;	573 AA.
ID	Q8WU38			
AC	Q8WU38;			
DT	01-WAR-2002 (TrEMBLrel. 20, Created)			
DT	01-WAR-2002 (TrEMBLrel. 20, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Hypothetical protein.			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI	TaxID=9606;			
RN	[1]_			
RP	SEQUENCE FROM N.A.			
RC	ISSUE=10ns11;			
RA	Strausberg R.;			
RL	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			

DR ENBL; BC021276; AAH21276.1; -.
DR FIR; S21205; S21205.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
DR Hypothetical protein. KW
SQ SEQUENCE 573 AA; 62967 MW; PF007234403AAC530 CRC64;

Query Match 14.6%; Score 514; DB 4; Length 573;
Best Local Similarity 27.8%; Pred. NO. 3.7e-24;
Matches 157; Conservative 85; Mismatches 201; Indels 122; Gaps 18

```

Qy 1 EVLOQSGPDLVPGASVKISCKASGYSTFGYYMHVWYKSPGKLEWIGRIINPNNGVTLY 60
Db 20 EYQLVESGGGLVQPGSRLLRLSCAASGFTFDYAMHWVRQAPGKLEWVGSIWNSSGICY 79
Qy 61 NQPKDKATLIVDKSSITAYMELRSLTSEDSAVYYCAR----STMITNYMVD:WQGTSV 116
Db 80 ADSVKGRTITGRDNAKNSLYLQMNLSRAEDTALYYCAKSGSGYIGYYGMVDWQGQTVT 139
Qy 117 TVSSAKTTTPPSVYIPLPGSA-AQTNSSVTLGLGVKGFPEPVTVTWNSGLSGGVHTPPA 175
Db 140 TVSSAPTAPDVPIISGCHRPKDNSPVVLACLTIGYHPTSVTVTWYMGTSQPOPTTPE 199
Qy 176 VLQSLDYTLSS-VTVPSSTWSPSTVTCNVAPAS-----STKVDKKIYF---- 219
Db 200 IQRRDSYNTSSQLSTPLQWRQGEYKCVVQHTASKSKKEIPRPWPSPKQAASSVFTAQP 259
Qy 220 -----RDSGGPSEKSEINEKDLRKSELOGTALGNLQI--YYNKA 261
Db 260 QAEGSLAKATTAPATTNTGRGEEKKEKEEQRERETKTPECSHTQPLGVILLTPA 319
Qy 262 ITSSEKSAQQLTNTLFLKGFFTCHPWYNLLVDLGSSTAATSEYEGSSVDLGYGVQC 321
Db 320 V-----QDLWLRDKATFTCFVGS-----DLKAHLTWEV 349
Qy 322 AGGTENKTACMYGV-----TLHDNNRLTEBK--VPINLWIDGKQTTVPIDKVK-TSKK 373
Db 350 AGKVPT-----CGVEEGLLERHNSGQSQHSRLTLPRSLMNAGTSVTCITLNHPSLPQR 403
Qy 374 EYTVQELDLQARHYLHGKFGLYNSDFGCKVQKGLVVFHSS-GSTVSVDLFDAGQVPD 432
Db 404 LMAUREPAAQ-----PVKLSLNLASSDPPEAASWLLCEVSGFPSP 445
Qy 433 TLLRIY-RDNTTISSTLSI-----SLYLTSTIVMTQTPTSLVYAGDRVTTITCKA 483
Db 446 NILLMWLEQREVNISGFARPPQPGSTTTFWMSVLVPAPPS-----POPATYTCV 500
Qy 484 SOSVSNVDVWYQQKGPQSKLLISY 508
Db 501 SHEDSRTLL-----NASRLEVS 519

```

RESULT	68	
Q9QXE9		
ID	Q9QXE9	PRELIMINARY;
AC	Q9QXE9;	PRT; 117 AA.
DT	01-MAY-2000	(TrEMBLrel. 13, Created)
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)
DE	Immunoglobulin heavy chain V-D-J region (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Clemens A., Rademakers A., Specht C., Koelsch E.;	
RL	Submitted (SFC-1997) to the EMBL/GenBank/DBJ databases.	

Db 118 ESQSPFNVPFL 128

RESULT 70
Q924P6 PRELIMINARY; PRT; 143 AA.

ID	Q924P6	PRELIMINARY;	PRT;	143 AA.
AC	Q924P6;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	VIH86.2-D-J-C mu protein (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;			
RA	Kozono Y., Kozono H., Azuma T.;			
RA	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals			
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-			
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP).";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AB069919; BAB63935.1; -.			
DR	PIR; F33932; F33932.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003596; IG_v.			
DR	PIfam; PF00047; IG; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKES; 1.			
FT	NON TER 1			
FT	NON TER 143			
SEQ	SEQUENCE 143 AA; 15714 MW; 523385316C345A93 CRC64;			
	Query Match 14.4%; Score 507; DB 11; Length 143;			
	Best Local Similarity 73.3%; Pred. No. 1.5e-24;			
	Matches 96; Conservative 16; Mismatches 17; Indels 2; Gaps			
QY	1 EVQLQQSGDPLVPGASVRIKSCASGYFTGYHHVYKQSPGKLEWIGRIPLNNGV			
DB	1 QVQLQQPGTELVPFGASVKLSCTASGYFTSYHHVYKQSPGKLEWIGRIPLNNGV			
QY	61 NQKPKDQATVDSKSTTAYMELSLTSDSAVYICARSTMTINYYMDYMGQTSVTV			
DB	61 NEKPKTATVDSKSTTAYMELSLTSDSAVYICAR--RLGGVMDYMGQTSVTV			
QY	121 AKTTPSPVPEL 131			
DB	119 ESQSPFNVPFL 129			
	Q924R2 PRELIMINARY; PRT; 140 AA.			
ID	Q924R2			
AC	Q924R2;			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	VIH86.2-D-J-C mu protein (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10090;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;			
RA	Kozono Y., Kozono H., Azuma T.;			
RA	"Direct Estimation of Relative Affinity by Flow Cytometry Reveals			
RT	Affinity Maturation of B Cell Antigen Receptors in Response to (4-			
RT	Hydroxy-3-Nitrophenyl)Acetyl (NP).";			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AB067788; BAB63273.1; -.			

DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON_TER 140 140
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15361 MW; 60739B790FC6AF24 CRC64;

Query Match
Best Local Similarity 14.4%; Score 506.5; DB 11; Length 140;
Matches 96; Conservative 14; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVLOQSGDLVKPGASVKISCKASYFTGYMHWKSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLQPGAEVLPKPGASVKISCKASYFTGYMHWKSPGKLEWIGRINPNNGVTLY 60

QY 61 NQKFKDKALTVDKSSTTAYMELRLSITSDSAVYICARSTMTINMYMDYVWGGTSVTYSS 120
DB 61 NEKFKSKALTVDKSSTTAYMELRLSITSDSAVYICARSTMTINMYMDYVWGGTSVTYSS 115

QY 121 AKTTPPSVPL 131
DB 116 EQSQSFNVEPL 126

RESULT 72
Q8WY24 PRELIMINARY; PRT; 497 AA.
AC Q8WY24;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNC66 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S.; Shao X.; Cao J.; Geng L.; Fang Y.; Dong Q.;
RT "Identification and characterization of SNC66, a Ig-like gene which is
RT down-regulated in colorectal cancer".
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A283666; AAL36987.1; -
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A66325 CRC64;

Query Match
Best Local Similarity 14.4%; Score 506; DB 4; Length 497;
Matches 163; Conservative 79; Mismatches 178; Indels 256; Gaps 20;

QY 3 QLQSGDLVKPGASVKISCKASYFTGYMHWKSPGKLEWIGRINPNNGVTLYNQ 62
DB 22 QLESGAEVLPKPGASVKISCKASYFTGYMHWKSPGKLEWIGRINPNNGVTLYNQ 62

QY 63 KFKDKALTVDKSSTTAYMELRLSITSDSAVYICARSTMTINMYMDY----WQGGTSVT 117
DB 82 KFGRLTFSRDTSINTAYMELRLSITSDSAVYICARSTMTINMYMDY----WQGGTSVT 141

QY 118 VSSAKTTPPSVPLAPGSAQAQNSMTLGLVAVYVPEPVTWNSGSLSSGVHTTTPAV 176
DB 142 VSSAKTTPPSVPLAPGSAQAQNSMTLGLVAVYVPEPVTWNSGSLSSGVHTTTPAV 200

QY 177 --LQSDLYTLSSSVTVFSS--TWPSETVTCNVAH---PASSTKVDKTI-----VPRDSGGP 225
DB 201 QDASGLYTLSSSVTVFSS--TWPSETVTCNVAH---PASSTKVDKTI-----VPRDSGGP 260

QY 226 SEKSEENEDLRKKSLOGTALGNLQIYYNSKAITSEKSDAQPLTWLLEKGFPTG 285
DB 261 TPSPSCCHPRLSLHRLPALELLG-----SEANLTCTL-----TG 295

QY 286 HPVNDLLVLDGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 296 -----LRD--ASGVTFWTWPS-----GKSVAQGPPEPDLGCGYSVS----- 330

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYNSDSFGKVKQ 405
DB 331 -----SVLPSCAEPWNHGK----- 344

QY 406 RGLVHFHSSGTSYDLFDAQGOQVPTLLRIYRDNLTISSTLSLSLYLYTTSIVMTQT 465
DB 345 ----- 344

QY 466 PTLVLLSAGDRVTITCKASQSVNDVAVYQKQKPKLLISYTSRYAGVDRFSGSGY 525
DB 345 -----TFTCTA-----AYPESK----- 356

QY 526 GTDFTLTISVQAEADAAYFCQDYNSSPTFGGKTKLEIKRAADAAPTYSIFPPSSEQLTS 585
DB 357 -TPTATILP-----KSGNTF-----RPEVHLLPPPESEAL 386

QY 586 GG-ASVVCFLNNFYKPDINVKWKIDGSRQNGVLSNWTQDQSKD---STYSMSSTLTLT 641
DB 387 NELVTLTCLARGFSPKDLVRLVWLGSGQLPREKYLTVASRQEPGQGTTFITAVTILVAA 446

QY 642 DEYERHNSYTCEATHK 657
DB 447 EDWKKGDTFSCMGVGE 462

RESULT 73
Q924R8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RA Kozono Y.; Kozono H.; Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals

DE	CN 8 scfV.
GN	CN 8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCHI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Balb/c; TISSUE=Spleen;
RX	MEDLINE=20183931; PubMed=10706631;
RA	Shinozawa H., Demura T., Fukuda H.;
RT	"Isolation of a vascular cell wall-specific monoclonal antibody
RT	recognizing a cell polarity by using a phage display subtraction
RT	method.";
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR	EMBL; AB016341; BA888633.1; -
DR	PIR; A33933; A33933.
DR	PIR; S19112; S19112.
DR	HSP; P01607; IREI.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig.V.
DR	Pfam; PF00047; Ig; 2.
DR	SMART; SM00406; IGv; 2.
DR	PROSITE; PSS0835; IG LIKE; 2.
SQ	SEQUENCE 298 AA; 31867 MW; EOF96B8A17004317 CRC64;
	Query Match 14.3%; Score 503.5; DB 11; Length 298;
	Best Local Similarity 23.7%; Pred.No. 6.9e-24;
	Matches 136; Conservative 42; Mismatches 70; Indels 325; Gaps 6;
QY	1 EVOLQQSGPDLVKPGASVKISCKASGYFTGYYMHWKQSPGKGLEWIGRNPNNGVTLY 60
DB	: :
DB	40 QVKLQQSGGLVKPGSLKLSCAASGDFRYMWSWRQAPGKGLEWIGEINPDSTINY 99
QY	61 NQPKKATLTVDKSSITAYNEILRSITSERSAVYICARSTMITNYMDYMGQGTSTVSS 120
DB	: :
DB	100 TPCLKDFFISRDNAKNTLYLQMSKVRSEDTALYCARYGHSA--YMQGGTTTVTS- 156
QY	121 AKTTPPSVYPLAPGSAAQTNSMTVLGCLVGYPPEPTVTWNSSGLSSGVHTFPFVLQSD 180
DB	: :
DB	157 -----SGGGSG----- 163
QY	181 LYTLSSTVPSTWPSETVTCNVHPASTKVDKKIVPRDSGGSPSKSEINEKLRKK 240
DB	: :
DB	164 -----GGGS----- 167
QY	241 SELQGTALGNLKQIIYYNSKAITSSEKSADQLTNLLFKGFFTGHPYNDLLVDLGSTA 300
DB	: :
DB	168 ----- 167
QY	301 ATSEYEGSSVDLYAGYGYCAGGTPNKTKACWGGVTLDHNNRLTEKKVPINLWDKGK 360
DB	: :
DB	168 -----GG----- 169
QY	361 TTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKQVQRGLIVFHSSSEGSTVS 420
DB	: :
DB	170 -----GG----- 171
QY	421 YDLFDAQGYPDILLRIYRDNNTISLSLSLVYTTISVMQTPTSLIVSAGDRVIT 480
DB	: :
DB	172 -----SDIELTQPASLASVGETVTIT 194
QY	481 CKASQSYNSDVAWYQOKPGOSP KLLISYTSRVAGVDPFRSGSGYGTFDLTITSSVOAED 540
DB	: :
DB	195 CRASGNHNFLAWYQOKGKSPQLLYVNAKTLADVFSRFSGSGSGFYQSLKNSLPED 254
QY	541 AAVYFCQDYNSPPTFGGKTLEIKRADAAPTV 573
DB	: :
DB	255 FGSIYCCHFWTTPYTFGGGKTLEIKRAAGAAPV 287

Search completed: August 12, 2004, 13:32:24
Job time : 71.4605 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 84.4429 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQSGPDLVKPGASVKI.....EATHKTSPIVKSFNRES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseqp_29Jan04:*

- 1: Genesecp1980s:*
- 2: Genesecp1990s:*
- 3: Genesecp2000s:*
- 4: Genesecp2001s:*
- 5: Genesecp2002s:*
- 6: Genesecp2003as:*
- 7: Genesecp2003bs:*
- 8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3522	100.0	672	6	ABP58454
2	1644	46.7	573	4	AA654459
3	1218	34.6	233	6	ABP58455
4	1130	32.1	233	6	ABP58457
5	1113	31.6	245	2	AAW35375
6	1107	31.4	233	6	ABP58456
7	1107	31.4	237	4	AAU14103
8	1107	31.4	257	6	ABO10288
9	1096.5	31.1	720	4	AA655572
10	1093	31.0	230	4	AA673339
11	1091	31.0	245	2	AAW35374
12	1072	30.4	248	6	ABU79072
13	1069	30.4	592	4	AA63838
14	1069	30.4	595	2	AAW36003
15	1059.5	30.1	464	2	AAW6088
16	1055.5	30.0	445	2	AAW6085
17	1048	29.8	230	2	AAW45012
18	1044	29.6	230	5	AAW62235
19	1035	29.4	230	2	AAW33204
20	1028	29.2	537	5	AAE18377
21	1028	29.2	537	5	ABG76352
22	1025.5	29.1	464	3	AAW33041
23	1025.5	29.1	464	3	AAW33041
24	1025.5	29.1	464	3	AAW33087
25	1025.5	29.1	464	5	ABB74912

26	1025.5	29.1	464	5	ABB74866
27	1024.5	29.1	613	5	AAE18380
28	1024.5	29.1	613	5	ABG76355
29	1023.5	29.1	456	5	AAE18370
30	1023.5	29.1	456	5	ABG76345
31	1023.5	29.1	493	5	AAE18379
32	1023.5	29.1	493	5	ABG76354
33	1023.5	29.1	510	5	AAE18378
34	1023.5	29.1	510	5	ABG76353
35	1022.5	29.0	438	5	AAE18372
36	1022.5	29.0	438	5	ABG76347
37	1018	28.9	206	2	AAV39452
38	1018	28.9	465	2	AAW65758
39	980.5	27.8	711	2	AAW85692
40	979.5	27.8	223	7	ADE06766
41	977.5	27.8	626	3	AAW55081
42	972.5	27.6	243	2	AAW86002
43	972.5	27.6	243	2	AAW42294
44	972.5	27.6	243	2	AAW27407
45	972.5	27.6	243	4	AAW83835
46	970	27.5	214	2	AAW44176
47	967.5	27.5	488	2	AAW86004
48	967.5	27.5	488	4	AAW83836
49	967.5	27.5	488	6	ABU07262
50	967.5	27.5	488	6	ABU07253
51	966.5	27.4	209	6	ABP95772
52	966.5	27.4	209	6	ABP95771
53	966	27.4	468	2	AAW13061
54	961.5	27.3	225	2	AAW40385
55	960	27.3	212	2	AAW15932
56	960	27.3	233	2	AAW13203
57	953.5	27.1	223	2	AAW53802
58	953	27.1	220	2	AAW53802
59	951.5	27.0	469	2	AAW40384
60	948	26.9	214	3	AAU78253
61	948	26.9	233	6	ABP58458
62	948	26.9	257	4	AAU14104
63	948	26.9	257	6	ABO10269
64	948	26.9	257	6	ADW44368
65	945	26.8	234	6	AAO29870
66	944.5	26.8	209	6	ABP96752
67	944.5	26.8	209	6	ABP96751
68	944.5	26.8	239	2	AAW76087
69	944	26.8	233	2	AAW06738
70	942	26.7	233	2	AAW45011
71	941.5	26.7	219	2	AAW76086
72	941	26.7	233	2	AAW35373
73	941	26.7	233	4	AAW67338
74	938	26.6	234	5	AAU72802
75	935	26.5	257	6	ABU79068
76	933	26.5	222	2	AAW15934
77	933	26.5	233	5	ABB76234
78	932.5	26.5	218	7	ADD05274
79	931	26.4	223	1	AAW40031
80	925	26.3	257	5	ABB79501
81	925	26.3	257	6	ABU10081
82	925	26.3	257	6	ABU62324
83	925	26.3	257	7	AAE37676
84	921	26.1	233	3	AAW54463
85	921	26.1	233	5	ABB79502
86	921	26.1	233	5	ABU10082
87	921	26.1	233	7	ABU62325
88	921	26.1	233	7	AAE37677
89	919.5	26.1	219	2	AAW44495
90	917.5	26.1	219	6	ABP96777
91	917.5	26.1	219	6	ABP96778
92	917	26.0	233	6	ABU10099
93	916.5	26.0	238	2	AAW31752
94	916.5	26.0	238	2	AAW71889
95	916.5	26.0	238	3	AAW12909
96	916	26.0	454	5	ABB76124
97	916	26.0	462	5	ABB76126
98	915.5	26.0	254	2	AAW30123

99 915.5 26.0 254 2 AAY30121 Murine an
100 915 26.0 238 2 AAW83042 Anti-Pas

ALIGNMENTS

RESULT 1
ABP58454
ID ABP58454 standard; protein; 672 AA.
XX AC ABP58454;
XX 14-APR-2003 (first entry)
XX Engineered superantigen for human cancer therapy.
DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW Cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
XX Homo sapiens.
OS Staphylococcus sp.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
XX 1. 120
XX /note= "574 variable heavy chain"
FT Misc-difference 41 /note= "wild-type His substituted by Pro"
FT Misc-difference 44 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 69 /note= "wild-type Ile substituted by Thr"
FT Misc-difference 113 /note= "wild-type Val substituted by Gly"
FT Region 121. .222
FT /note= "C242 constant heavy chain"
FT Region 226. .458
FT /note= "SEA/E-120"
FT Misc-difference 245 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 246 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 249 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 252 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 304 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 306 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 308 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 309 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 452 /note= "wild-type Asp substituted by Ser"
FT Region 459. .565
FT /note= "574 variable light chain"
FT Misc-difference 469 /note= "wild-type Phe substituted by Ser"
FT Misc-difference 504 /note= "wild-type Thr substituted by Lys"
FT Misc-difference 522 /note= "wild-type Ile substituted by Ser"
FT Misc-difference 532 /note= "wild-type Phe substituted by Leu"
FT Misc-difference 536 /note= "wild-type Thr substituted by Ser"
FT Misc-difference 537 /note= "wild-type Leu substituted by Val"
FT Misc-difference 542

FT Region /note= "wild-type Leu substituted by Ala"
FT 566. .672
FT /note= "C242 constant light chain"
XX WO2003002143-A1.
XX 09-JAN-2003.
XX 19-JUN-2002; 2002WO-SE001188.
XX 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Brlandsson E, Antonsson P, Walse B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX receptor and four regions to determine binding to class II major
XX histocompatibility complex, antibody to cancer associated cell surface
XX structure.
XX Claim 12; Fig 10; 102pp; English.
XX The present sequence is a conjugate of a bacterial superantigen and an
XX antibody moiety, and has been designed to target and destroy cancer
XX cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
XX was derived from staphylococcal enterotoxin E (SEE) by the incorporation
XX of the following amino acid substitutions to reduce seroreactivity whilst
XX maintaining production levels and biological activity: R20G, N21F, S24G,
XX R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
XX Fab moiety of the tumour reactive antibody 5T4. Substitutions were made
XX in the 5T4 sequence to obtain higher yields: in the heavy chain, H41P,
XX S44G, I49T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
XX T77S, L78V and L83A. An expression vector comprising DNA encoding the
XX conjugate can be used to transform host cells for recombinant production
XX of the conjugate. The conjugate is useful for treating cancer, including
XX cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
XX cervix and prostate (claimed)
XX SQ Sequence 672 AA;
Query Match 100.0%; Score 3522; DB 6; Length 672;
Best Local Similarity 100.0%; Pred.No. 3e-201;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLOQSGDPLVKPGASVKISCKASGYGFTGYMHVWVKQSPCKGLEWIGRINPNNGVTL 60
DB 1 EVLOQSGDPLVKPGASVKISCKASGYGFTGYMHVWVKQSPCKGLEWIGRINPNNGVTL 60
QY 61 NQKPKDKATLTVDKSTTAYMELRLTSEDSAVVYCARSTMITNYMDYWGCGTSTVYSS 120
DB 61 NQKPKDKATLTVDKSTTAYMELRLTSEDSAVVYCARSTMITNYMDYWGCGTSTVYSS 120
QY 121 AKTTTPSVYPLAPGSAQTNSMVTGLVKGFPEPVTWNSGLSSGVHTFPVAVLQSD 180
DB 121 AKTTTPSVYPLAPGSAQTNSMVTGLVKGFPEPVTWNSGLSSGVHTFPVAVLQSD 180
QY 181 LYTLSSTVTPSSTWPFSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
DB 181 LYTLSSTVTPSSTWPFSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
QY 241 SELQGTALGNLKOIYYNSKAITSEKADQPLTNLLPKGFPTGHPWYNDLLVDLGSTA 300
DB 241 SELQGTALGNLKOIYYNSKAITSEKADQPLTNLLPKGFPTGHPWYNDLLVDLGSTA 300
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVVTLHDNNRLTEKKVPINLWIDGKQ 360
QY 361 TTVPIDKVTSKKVTVOELDLQAHYHGRFGLNSDSFGKVGORGILVHSSSEGSTVS 420

Db 361 TTVPIDKVKTSKEVTVOQLDLQARHLYHGKFGLYNSDSFGKQVQGLIVPHSSEGSTVS 420
 QY 421 YDLFDAGGYPDLIRIYEDNTTISSTLSISLYITTSIVMTOTPTSLIYNSAGDRVTIT 480
 Db 421 YDLFDAGGYPDLIRIYEDNTTISSTLSISLYITTSIVMTOTPTSLIYNSAGDRVTIT 480
 QY 481 CKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDFSGSGYGTDFTLTISSVQAE 540
 Db 481 CKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDFSGSGYGTDFTLTISSVQAE 540
 QY 541 AAVYFQQDYNSPPPTFGGKTKLEIKRADAAPTIVSIPPSSEOLITGGASVVCFLNFPYK 600
 Db 541 AAVYFQQDYNSPPPTFGGKTKLEIKRADAAPTIVSIPPSSEOLITGGASVVCFLNFPYK 600
 QY 601 DINVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLTITKDEYERHNSYTCETHKST 660
 Db 601 DINVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLTITKDEYERHNSYTCETHKST 660
 QY 661 SPIVKSFRNES 672
 Db 661 SPIVKSFRNES 672

RESULT 2
 AAG64459
 ID AAG64459 standard; protein; 573 AA.

XX AAG64459;
 AC
 DT 21-SEP-2001 (first entry)
 XX Mouse 6D9 catalytic antibody.
 DE Mouse 6D9; catalytic antibody; esterase activity.
 XX Mouse; 6D9;
 XX Mus sp.

Key Location/Qualifiers
 FT Misc-difference 28 /note= "Encoded by GCCTGA"
 FT Misc-difference 35 /label= unknown
 FT /note= "Encoded by TNT"
 FT Misc-difference 46 /note= "Encoded by GAGTAA"
 FT Misc-difference 329 /note= "Encoded by GAGTAA"
 FT Misc-difference 572 /note= "Encoded by TGTAA"
 FT Misc-difference 572 /note= "Encoded by TGTAA"
 XX
 PN JP2001128681-A.

XX 15-MAY-2001.
 XX 04-NOV-1999; 99JP-00314259.
 XX 04-NOV-1999; 99JP-00314259.
 XX (NIBS) JAPAN TOBACCO INC.
 PA (SEIB-) SEIBUTSU BUNSHI KOGAKU KENKYUSHO KK.
 PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.
 XX WPI; 2001-373026/39.
 DR N-PSDB; AAH47858.
 XX A new catalytic antibody.

Claim 3; Page 14-17; 18pp; Japanese.

The present sequence is that of the mouse 6D9 catalytic antibody. The invention relates to an antibody in which 1 to 9 amino acids are replaced, deleted, inserted and/or added to substantially increase its catalytic esterase activity

XX Sequence 573 AA;
 SQ
 Query Match 46.7%; Score 1644; DB 4; Length 573;
 Best Local Similarity 51.2%; Pred. No. 1.4e-89;
 Matches 353; Conservative 52; Mismatches 78; Indels 206; Gaps 11;
 QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPANGVTLY 60
 Db 71 QVQLLEGGGLVKGSGSLKLSCAASGFTFNYSAMSWRQTPEKELEWVVIS-SGGSIIY 129
 QY 61 NQKPKDKATUTVDKSTTAYMELRSLTSDSASVYICARSTMTNY-----VMDYWGQGT 114
 Db 130 LDSYKGFVSRDNRNLIYLTQMTSLASEDTAMVFCAR---VSHYDGRDWRDYDVMWAGT 186
 QY 115 SVTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSGVHTFP 174
 Db 187 SVTVSSAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSGVHTFP 246
 QY 175 AVLQSDLYTLSSSVTPSPSTWPTSETVTCNVAHPASSTKVDKIVPRDSGSPSEKSEINE 234
 Db 247 AVLQSDLYTLSSSVTPSPSTWPTSETVTCNVAHPASSTKVDKIVPRD-----293
 QY 235 KDLKKSELOQTALGNLKQIYYNSKAITSEKSDQFLTNLLFKGFTGHPWYNLLV 294
 Db 294 -----CTSEAST-----301
 QY 295 DLGSTAATSEYEGSSVDLYGAVYGYQAGGTPNKACMYGVTLHDNNRLTEKKVPINL 354
 Db 302 -----TVSKTENLSSGSSVIEFRAGY-----LFF 326
 QY 355 WIDG-KQTTVPIDKVKTSKEVTVOQLDLQARHLYHGKFGLYNSDSFGKQVQGLIVPHS 413
 Db 327 WMEAMKQSTI-----336
 QY 414 SEGSTVSYDLFDAGGYPDLIRIYEDNTTISSTLSISLYIT-----TSIVMTOTPT 467
 Db 337 -----LILLILLTPTVKMAELVMTOTPL 362
 QY 468 SLVYSGAGRVITCKASQSV--SND---VAVYQKQSPKLLISYTSRYAGVDPDFSG 522
 Db 363 SLVYSLGDAQSISCRSSQTIYHNSGDTYLDWFLQKQSPKLLIYKVSNEFSGVDPDFSG 422
 QY 523 SGYGTDFTLTISSVQAEAAVYFCQDYNSPPPTFGGKTKLEIKRADAAPTIVSIPPSSEQ 582
 Db 423 SGYGTDFTLTISSVQAEAAVYFCQDYNSPPPTFGGKTKLEIKRADAAPTIVSIPPSSEQ 482
 QY 583 LTSGASVVCFLNFPYKIDNVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLTITKD 642
 Db 483 LTSGASVVCFLNFPYKIDNVKWKIDGSRQNGVLSWTDQDSKDYTSMSSTLTITKD 542
 QY 643 EYERHNSYTCETHKSTSTPIVKSFRNE 671
 Db 543 EYERHNSYTCETHKSTSTPIVKSFRNE 571

RESULT 3
 ABP58455
 ID ABP58455 standard; protein; 233 AA.

XX AC ABP58455;
 XX AC ABP58455;
 DT 14-APR-2003 (first entry)
 DE Engineered superantigen SEA/E-120 for human cancer therapy.
 XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-120; mutant; mutein.
 OS Staphylococcus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FH

FT Misc-difference 20 /note= "wild-type Arg substituted by Gly"
 FT Misc-difference 21 /note= "wild-type Arg substituted by Gly"
 FT Misc-difference 24 /note= "wild-type Asn substituted by Thr"
 FT Misc-difference 24 /note= "wild-type Ser substituted by Gly"
 FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
 FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 81 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 83 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
 FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
 FT
 PN WO2003002143-A1.
 XX
 XX 09-JAN-2003.
 PD
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 XX 28-JUN-2001; 2001SE-00002327.
 PR
 XX (ACTI-) ACTIVE BIOTECH AB.
 PA
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 PT
 XX
 XX Claim 8; Fig 2; 102pp; English.
 PS
 XX The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
 CC enterotoxin E (SEE), by the incorporation of the following amino acid
 CC substitutions to reduce seroreactivity whilst maintaining production
 CC levels and biological activity: R20G, N21T, S24G, R27K, K79P, K81E, K93S
 CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
 CC tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
 CC designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 XX Sequence 233 AA;

Query Match 34.6%; Score 1218; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1e-64;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 405
 DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 458
 DB 181 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 233

Query Match 32.1%; Score 1130; DB 6; Length 233;
 Best Local Similarity 91.4%; Pred. No. 1.8e-59;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 405
 DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 458
 DB 181 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 233

Query Match 32.1%; Score 1130; DB 6; Length 233;
 Best Local Similarity 91.4%; Pred. No. 1.8e-59;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 405
 DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDQARHLYHGKFLYNSDSFGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 458
 DB 181 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISSTLSISLYTT 233

Db 181 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNKNTINSENHIALVLYTT 233

RESULT 5

AAW35375

ID AAW35375 standard; peptide; 245 AA.

XX AC AAW35375;

XX DT 20-APR-1998 (first entry)

XX DE Staphylococcus enterotoxin SEE modified superantigen.

XX KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;

XX KW cancer; infection; autoimmune disease; antibody; modified.

XX OS Staphylococcus sp.

XX FH Key Location/Qualifiers

FT Misc-difference 20

FT /label= R20G

FT /note= "wild-type Arg is replaced by Gly"

FT Misc-difference 21

FT /label= N21T

FT /note= "wild-type Asn is replaced by Thr"

FT Misc-difference 24

FT /label= S24G

FT /note= "wild-type Ser is replaced by Gly"

FT Misc-difference 27

FT /label= R27K

FT /note= "wild-type Arg is replaced by Lys"

PN WO9736932-A1.

XX 09-OCT-1997.

XX 26-MAR-1997; 97WO-S5000537.

XX 29-MAR-1996; 96SE-00001245.

PR 12-AUG-1996; 96US-00695692.

XX (PHAA) PHARMACIA & UPJOHN AB.

XX Antonsson P, Hansson J, Bjoerk P, Dohlisten M, Kalland T;

PI Abrahamsen L, Forsberg G;

XX WPI; 1997-503052/46.

XX Conjugate of target seeking moiety and modified superantigen - useful for

PT activating the immune system to treat cancer, viral infections, parasitic

PT infestations and autoimmune diseases.

XX Claim 5; Page; 58pp; English.

XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-

CC type SEE superantigen is modified to be used in a novel conjugate. The

CC novel conjugate comprises a target seeking moiety and a modified wild

CC type superantigen. This modified superantigen retains its ability to

CC activate a subset of T cells, even though 1 or more wild-type amino acid

CC residues in at least 1 region which functions in determining binding to T

CC cell receptor (TCR) and activation of a subset of T cells has/have been

CC replaced. Such a modified superantigen can optionally be used as part of

CC a conjugate with a target seeking moiety, for activating the immune

CC system to treat a mammalian disease. A pharmaceutical composition can be

CC prepared comprising a modified antibody (preferably a Fab fragment fused

CC to a peptide moiety providing activation of T cells in Vbeta specific

CC manner) in which cysteines providing for interchain cysteine linkages in

CC the native antibody have been replaced (preferably by serine residues) to

CC prohibit cysteine formation. The modified wild-type superantigen is used

CC for treating cancer, viral infections, parasitic infestations and

CC autoimmune disease. The modified wild type superantigen has a lower

CC immunogenicity and reactivity with neutralising antibodies and has fewer

CC side-effects when used as a drug, compared to wild type superantigen.

CC Note: This sequence is not provided in the specification. It has been

CC created by modifying the wild-type SEE superantigen sequence in Pages 38-

CC 39 of the specification

XX SQ Sequence 245 AA;

Query Match 31.6%; Score 1113; DB 2; Length 245;

Best Local Similarity 86.9%; Pred. No. 1.9e-58;

Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;

QY 226 SEKSEINEKDLRKSEHQGTALGNLKOIYYNKAITSSEKSDQFLNTLLFKGPFPTG 285

DB 1 SEKSEINEKDLRKSEHQGTALGNLKOIYYNKAITSSEKSDQFLNTLLFKGPFPTG 60

QY 286 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 345

DB 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 120

QY 346 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDLOARHYLHGKFGLYNSDSFGGKVQ 405

DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDLOARHYLHGKFGLYNSDSFGGKVQ 180

QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNKNTINSENHIALVLYTT 453

DB 181 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNKNTINSENHIALVLYTT 240

QY 454 YLYTT 458

DB 241 YLYTT 245

RESULT 6

ABP58456

ID ABP58456 standard; protein; 233 AA.

XX AC ABP58456;

XX DT 14-APR-2003 (first entry)

XX DE Staphylococcal enterotoxin E.

XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;

XX cytotstatic; vaccine.

XX OS Staphylococcus sp.

XX PN WO2003002143-A1.

XX 09-JUN-2003.

XX 19-JUN-2002; 2002WO-SE001188.

XX 28-JUN-2001; 2001SE-00002327.

XX (ACTI-) ACTIVE BIOTECH AB.

XX Forsberg G, Erlandsson E, Antonsson P, Walse B;

XX WPI; 2003-201467/19.

XX Conjugate for therapy, has bacterial superantigen with a region in T-cell

XX receptor and four regions to determine binding to class II major

XX histocompatibility complex, antibody to cancer associated cell surface

XX structure.

XX Example 3; Fig 4; 102pp; English.

XX The present sequence is the protein sequence of staphylococcal

XX enterotoxin SEE. The invention provides novel conjugates (see ABP58454)

XX for human cancer therapy. These comprise an engineered bacterial

XX superantigen, such as novel SEA/E-120 (see ABP58455), which is based on

XX SEE, and an antibody moiety, such as tumour reactive antibody 5F4. The

XX superantigen is engineered to reduce seroreactivity whilst maintaining

CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
XX
SQ Sequence 233 AA;

Query Match 31.4%; Score 1107; DB 6; Length 233;
Best Local Similarity 89.7%; Pred. No. 4.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFNTLLFKGFTG 285
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFNTLLFKGFTG 60
QY 286 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 120
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 405
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 7
AAU14103
ID AAU14103 standard; peptide; 257 AA.
XX AAU14103;
XX
DT 21-NOV-2001 (first entry)
XX
DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX
KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
KW antifusogenic; antiviral; HIV transmission.
XX
OS Staphylococcus aureus.
XX
PN WC200151673-A2.
XX
PD 19-JUL-2001.
XX
PF 05-JUL-2000; 2000WO-US035727.
XX
PR 09-JUL-1999; 99US-00350841.
XX
PA (TRIM-) TRIMERIS INC.
XX
PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX
DR WPI; 2001-442157/47.
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.

XX Disclosure; Fig 41; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
CC E
XX
SQ Sequence 257 AA;

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 4.6e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFNTLLFKGFTG 84
QY 286 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 8
ABO10268
ID ABO10268 standard; protein; 257 AA.
XX ABO10268;
XX
DT 19-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin E.
XX
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
OS Staphylococcus aureus.
XX
PN US6518013-B1.
XX
PD 11-FEB-2003.
XX
PF 07-JUN-1995; 95US-00485546.
XX
PR 07-JUN-1993; 93US-00073028.
PR 07-JUN-1994; 94US-00255208.
PR 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
XX
XX WPI; 2003-465599/44.
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
XX Example; Fig 41; 716pp; English.
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of AILMOTIS,

CC 107X178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amino group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC protein from a pathogenic organism analysed for regions analogous to
CC DP107 or DP178
XX
SQ

Query Match 31.4%; Score 1107; DB 6; Length 257;
Best Local Similarity 89.7%; Pred. No. 4.6e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINERKDKKSELQGTALGNLQIYYNKAITSSEKSAQDFLTLFGFTG 285
DB 25 SEKSEINERKDKKSELQGNALSLRQIYYNEKAITENKESDDQFLENTLLFGFTG 84
QY 286 HPWYNDLLVDLSTATSEVSGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EEKKVPINLWDGKQTPVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQ 405
DB 145 EEKKVPINLWDGKQTPVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQ 204
QY 406 RGLIVFHSSEGSTVSDLEDAQGVPTLLRIYRDNLTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSDLEDAQGVPTLLRIYRDNLTISSTLSISLYLYTT 257

RESULT 9
AAG65572
ID AAG65572 standard; protein; 720 AA.

XX AAG65572;
AC AAG65572;
DT 30-NOV-2001 (first entry)
DE Amino acid sequence of a plasmid pFCAH9-B8d.
XX Gene library; immunoglobulin; antibody library.
XX Synthetic.
XX WO200162907-A1.
XX 30-AUG-2001.
XX 22-FEB-2001; 2001WO-JP001298.
XX 22-FEB-2000; 2000JP-00050543.
XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinochara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
XX N-PSDB; AAH47738.

PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.

XX Example; Fig 3-6; 181pp; Japanese.

CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries. The present sequence represents the amino
CC acid sequence of a plasmid pFCAH9-B8d

XX Sequence 720 AA;

Query Match 31.1%; Score 1096.5; DB 4; Length 720;
Best Local Similarity 37.9%; Pred. No. 6.7e-57;
Matches 256; Conservative 39; Mismatches 55; Indels 325; Gaps 9;

QY 1 EVQLQQSGPDLVKGASVKISCKASGYFTGYMHWVKQSPGKLEWIGINPNNGVTLY 60
DB 23 QVQLQQSGAELVKGASVKLSCTASGFINIKDTYMHVWKQRPKG----- 66
QY 61 NQKPKDKATLTVDKSSITAYMELRSLTSEDSAVVYCARSTMITNY---VMDYMGQGTSTV 117
DB 67 -----LTSEDTAVYCA-----CYDYGNFDYNGQGTSTV 95
QY 118 VSSAKTTPSPVPLAPGSAATQNSMVLGCLVKGYPEPVTVTWNSGSLSSGVHTPPAVL 177
DB 96 VSSASTKGPSVFPPLAPGSKTSSTGTAALGCLVKGYPEPVTVTWNSGSLSSGVHTPPAVL 155
QY 178 QSD--LYTLSSSTVPSSTWPSSETVTCNVAPASSTKVDKIVPRDSGGPSEKSEINEKD 236
DB 156 QSSGLYLSSTVTPSSSLGTQYICNVNHPKNTKVDKVEPK----- 199
QY 237 LRKKELOGTALGNLKOIYYNKAITSSEKSAQDFLTLFGFTGHPWYNDLLVDL 296
DB 200 ----- 199
QY 297 GSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWI 356
DB 200 -----SCHH----- 203
QY 357 DGKQTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQGLIVFHSSEG 416
DB 204 -----HHHMKVLLPTAAA-----GLUL----- 221
QY 417 STVSYDLFDAQGVPTLLRIYRDNLTISSTLSISLYLYTTISIVMTQTSTLLVSAGDR 476
DB 222 -----LAAQFAMATSDIELTQSPASLSASVGET 249
QY 477 VTITCKASQSVNDVAVYQKQSPKLLISYTSRAGVDFRPSGSGYGTDFLTITSSV 536
DB 250 VTITCRASGNIHNYLA----- 265
QY 537 QAEDAAVYFCQDYNSGPTFGGKTKLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNN 596
DB 266 -----KLEIKRADAAPTVSIFPPSSQLTSGGASVVCFLNS 301
QY 597 FYPKDNVKKIDGSRQNGVLSNWTDDSKSTYSVSSLTTLTKDEYEHNSYTCETH 656
DB 302 FYPKDNVKKIDGSRQNGVLSNWTDDSKSTYSVSSLTTLTKDEYEHNSYTCETH 361
QY 657 KTSTSPIVKSFNRNE 671
DB 362 KTSTSPIVKSFNRNE 376

RESULT 10
AAB67339
ID AAB67339 standard; peptide; 230 AA.
XX AAB67339;
XX AAB67339;

DT 23-APR-2001 (first entry)
 XX Staphylococcus aureus enterotoxin E protein.
 DE Tumour; cancer; immune; enterotoxin.
 XX Staphylococcus aureus.
 OS US6180097-B1.
 XX 30-JAN-2001.
 XX 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 PI WPI; 2001-158657/16.
 DR Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 XX in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 PS The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 230 AA;
 SQ Query Match 31.0%; Score 1093; DB 4; Length 230;
 Best Local Similarity 89.6%; Pred. No. 2.7e-57;
 Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 229 SEEINEXDLRKSELOGTALGNLQIYYNKAITSSEKSDAQFLTNLLPKGFTGHPW 288
 DB 1 SEEINEXDLRKSELOGTALGNLQIYYNKAITSSEKSDAQFLTNLLPKGFTGHPW 60
 QY 289 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEK 348
 DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEK 120
 QY 349 KVPINLWIDGKQTTVPIDKVTSKKEVTVOBLDQARHYLHGKGLYNSDSFGKVGORGL 408
 DB 121 KVPINLWIDGKQTTVPIDKVTSKKEVTVOBLDQARHYLHGKGLYNSDSFGKVGORGL 180
 QY 409 IVFHSSEGSTVSYDLFDAGQGPDTLLRIYRDNTTISTSLISLYLVT 458
 DB 181 IVFHSSEGSTVSYDLFDAGQGPDTLLRIYRDNTTINSENHLIDLYLVT 230
 RESULT 11
 ID AAW35374
 ID AAW35374 standard; peptide; 245 AA.
 XX AAW35374;
 AC AAW35374;
 XX 20-APR-1998 (first entry)
 DT
 XX

DE Staphylococcus enterotoxin SEE wild-type superantigen.
 XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody.
 XX Staphylococcus sp.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 20 /note= "can be mutated at this position"
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 XX WO9736932-A1.
 PN 09-OCT-1997.
 PD 26-MAR-1997; 97WO-SE000537.
 PF 29-MAR-1996; 96SE-00001245.
 XX 12-AUG-1996; 96US-00695692.
 PR (PHAA) PHARMACIA & UPJOHN AB.
 XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abraham L, Forsberg G;
 PI WPI; 1997-503052/46.
 DR Conjugate of target seeking moiety and modified superantigen - useful for
 XX activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX Claim 4; Page 38-39; 58pp; English.
 PS This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX Sequence 245 AA;
 SQ Query Match 31.0%; Score 1091; DB 2; Length 245;
 Best Local Similarity 85.3%; Pred. No. 3.9e-57;
 Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
 QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDAQFLTNLLPKGFTG 285
 DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDAQFLTNLLPKGFTG 60
 QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGQYPTDILLRIYRDNT-----TISTSLISL 453
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPTDILLRIYRDNTINSENHLIDLYTINSENHLID 240
QY 454 YLYTT 458
DB 241 YLYTT 245

RESULT 12
ABU79072
ID ABU79072 standard; protein; 248 AA.
XX AC ABU79072;
XX DT 18-JUN-2003 (first entry)
XX DE S. aureus SEE (staphylococcus enterotoxin E) protein.

XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX APC; antitumour.
XX OS Staphylococcus aureus.

XX US2002177551-A1.
XX 28-NOV-2002.
XX 30-MAY-2001; 2001US-00870759.
XX 31-MAY-2000; 2000US-0208128P.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2003-361759/34.
XX N-PSDB; ACA64698.

XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX to tumour associated lipids where the binding induces anergy or apoptosis
XX in T cells and antigen presenting cells.
XX Disclosure; Page; 167pp; English.

XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphoglycerolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX deleted), a construct useful in the treatment of cancer comprising a
XX superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
XX useful in the treatment of cancer (where an adaptor protein which
XX inhibits T cell activation by tumour associated antigens is deleted or
XX functionally deactivated), a composition useful in the treatment of
XX cancer (comprising a lipid raft conjugated to a superantigen), producing
XX (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX allowing tumour associated lipids to contact immunocytes, in which
XX receptors for the lipids are inactivated or deleted to produce a
XX tumouricidal immunocyte population, and administering the tumouricidal
XX activated immunocytes to the host), producing (M3) a tumouricidal APC

CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX Sequence 248 AA;
SQ Query Match 30.4%; Score 1072; DB 6; Length 248;
Best Local Similarity 90.2%; Pred. No. 5.3e-56;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQDLTWTLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQDLTWTLLFKGFTG 84
QY 286 HPWYNDLLVLDLGTATSEYEGSSVDLYGAYGYQACAGTPTNCTACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDLGTATSEYEGSSVDLYGAYGYQACAGTPTNCTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGQYPTDILLRIYRDNTTISSTSL 449
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGQYPTDILLRIYRDNTINSEN 248

RESULT 13
AAB83838
ID AAB83838 standard; protein; 592 AA.
XX AC AAB83838;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of an Ig-5T4 fusion protein.
XX Single chain antibody; SCFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder.
XX OS Synthetic.
XX Mus sp.
XX Key Location/Qualifiers
FH Key Misc-difference 503
FT Misc-difference 503 /note= "Met encoded by CTG"

XX PN WO200136486-A2.
XX PD 25-MAY-2001.
XX PF 13-NOV-2000; 2000WO-GB004317.
XX PR 18-NOV-1999; 99WO-GB003859.
XX PR 15-FEB-2000; 2000GB-00003527.
XX PR 02-MAR-2000; 2000GB-00005071.
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
XX PI Myers KA;
XX DR N-PSDB; AAF89733.
XX DR WPI; 2001-343805/36.
XX DR N-PSDB; AAF89733.
XX PT Use of single chain antibody capable of recognizing a disease associated
XX PT molecule for manufacturing a medicament for preventing and/or treating a
XX PT disease condition associated with disease associated molecule.
XX PS Disclosure; Fig 6; 118pp; English.
XX XX The specification describes the use of a single chain antibody (ScFv),
XX CC which is capable of recognizing a disease associated molecule in the
XX CC manufacture of a medicament for the prevention and treatment of a disease
XX CC condition. The ScFv antibody is useful in the manufacture of a
XX CC medicament, for affecting a disease in vivo, for preparing a
XX CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
XX CC treatment of a disease. The ScFv antibody is also useful for treating
XX CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
XX CC diseases, cancers, central nervous system disorders including Parkinson's
XX CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
XX CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
XX CC related diseases, and other immune disorders. The present sequence
XX CC represents an Ig-5T4 fusion protein
XX SQ Sequence 592 AA;

Query Match 30.4%; Score 1069; DB 4; Length 592;
Best Local Similarity 37.9%; Pred. No. 2.3e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;
1 EVOLQSGDPLVKGASVKISCKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
20 EVOLQSGDPLVKGASVKISCKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 79
61 NQKFKDKATLVKSSSTAYVELSLTSEDSAVVYCARSTMTNYVMDYWGQTSVTVS 120
80 NQKFKDKATLVKSSSTAYVELSLTSEDSAVVYCARSTMTNYVMDYWGQTSVTVS- 138
121 AKTTPSPVYPLAPGAAQNTSMVTLGCLVKGYFPEPVTVTWNSGSLSSGHTFPAVLQSD 180
139 ----- 138
181 LYTLSSSVTPSPSTWSPSETVTCNVAHPASTYKVDKKIVPRDSGSPSEKSEINEKURKK 240
139 -----SGG----- 141
241 SELQGTALGNLKIYYNKAITSSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
142 ----- 141
301 ATSEYEGSVDLGYAGYGYQCAGGTPNKTACWYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
142 -----GGSGGGGT----- 151
361 TVVPIDKVKTSKVEVVELDLQARHYLHGKFLGSLYNSDSFGKVGQVGLVPHSSEGSTVS 420
152 -----GG----- 153

QY 421 YDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTTSIWMQTPTSLLSVAGDRVTIT 480
DB 154 -----SSIVMTQTPTFLLSVAGDRVTIT 176
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRPSGSGYGTDTFTLTSSVQAE 540
DB 177 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRPSGSGYGTDTFTLTSSVQAE 236
QY 541 AAVFECQDYNPPTFGGTTKLEIKRADA-APTYSIPPSSEQLTSGGASVVCFLNNFYP 599
DB 237 LAVYFCQDYNPPTFGGTTKLEIKRADA-APTYSIPPSSEQLTSGGASVVCFLNNFYP 296
QY 600 KDINYKWK-----IDGSEKQNGVNSWTDQDSKSTYSMSSTLTITKDEYERHNSYTCAT 655
DB 297 EPTVTSWNSGALTSVHTFPAVLQS-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 348
QY 656 HKTSTSPVK 665
DB 349 HKPSNTRKVDK 358
RESULT 14
AAW86003
ID AAW86003 standard; protein; 595 AA.
XX AC AAW86003;
XX DT 15-MAR-1999 (first entry)
XX DE Anti-5T4 single chain antibody 5T4Sabl.
XX KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
XX KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX PN MO9855607-A2.
XX PD 10-DEC-1998.
XX PF 04-JUN-1998; 98WO-GB001627.
XX PR 04-JUN-1997; 97GB-00011579.
XX PR 20-JUN-1997; 97GB-00013150.
XX PR 04-JUL-1997; 97GB-00014230.
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX XX Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX DR N-PSDB; AAW80291.
XX PT New vector encoding a tumour interacting protein for treating cancer -
XX PT contains a desired nucleotide sequence and/or protein which recognises
XX PT tumours, and is used as a gene delivery system to treat cancer.
XX XX Example 1; Fig 1B; 82pp; English.
XX XX This is the amino acid sequence of a single chain antibody (Sabl), termed
XX CC 5T4Sabl, comprising an scfv derived from murine monoclonal antibody 5T4
XX CC (see AAW86002) and the human gi constant region. cDNA (see AAW80291),
XX CC encoding the Sabl has been inserted into vector pCineo to allow expression
XX CC in mammalian cells. The trophoblast cell surface antigen defined by 5T4
XX CC is expressed at high levels on the cells of a wide variety of human
XX CC tumours. The invention relates to a vector comprising a nucleotide
XX CC sequence coding for a tumour interacting protein (TIP) and optionally a
XX CC nucleotide sequence of interest (NOI) which encodes a protein of interest
XX CC (POI), the vector being capable of delivering the NOI and/or POI to the
XX CC tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The

CC vector is used to treat cancer, and may also used as a gene delivery
 CC system for introducing at least 1 gene encoding a rIP (preferably a
 CC tumour binding protein) into a haematopoietic cell lineage
 XX
 SQ Sequence 595 AA;

Query Match 30.4%; Score 1069; DB 2; Length 595;
 Best Local Similarity 37.9%; Pred. No. 2.3e-55;
 Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;

QY 1 EVLOQSGPDLVKGASVKISKASGYSTGYIMHWKQSPKGLWIGRINPNNGVTLY 60
 DB 23 EVLOQSGPDLVKGASVKISKASGYSTGYIMHWKQSHGKSLWIGRINPNNGVTLY 82
 QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTINYYMDYWGQTSVTYS 120
 DB 83 NQKFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTINYYMDYWGQTSVTYS- 141
 QY 121 AKTTPSVVPLAPGSAQAQNSMVTGLVKGYFPPEVTVTNWNSGSLSSGVHTFPAVLQSD 180
 DB 142 ----- 141
 QY 181 LYTLSSTVTPSTWSEVTCNVAHPASTTKVDKIVPRDSGGPSEKSEENEXDLRKK 240
 DB 142 -----SGG----- 144
 QY 241 SELQGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTGHPWYNLVDLGSPA 300
 DB 145 ----- 144
 QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360
 DB 145 -----GGSGGGGT-----GG----- 154
 QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDFGGKVGQVGLVIFHSSEGSTVS 420
 DB 155 -----GG----- 156
 QY 421 YDLFDAQQGYPDLLRIYRDNNTISSTLSISLYLTVTSIVMTQPTSLVLSAGDRVIT 480
 DB 157 -----SSIVMTQPTFLVLSAGDRVIT 179
 QY 481 CKASQSVNDVAVYQKPGQPKLLISYTSRYAGVPRDFSGSGYGTDTLTLSVQARD 540
 DB 180 CKASQSVNDVAVYQKPGQPKLLISYTSRYAGVPRDFSGSGYGTDTLTLSVQARD 239
 QY 541 AAVYFCQDYNPPTFGGKTKLEIKRADA-APTVSIFPPSPQLTSGGASVVCFLNNFYP 599
 DB 240 LAVYFCQDYNPPTFGGKTKLEIKRASKTGPVPLAPSSKSTSGGTAALGCLVKDYP 299
 QY 600 KQINVKK-----IDGERQGVNLNSWTDQDSKDSYMSSTLTTLTKDEYERHNSYTCEAT 655
 DB 300 EPTVSNWNSGALTSVHTFPAVLQS-----SGLYSLSSVTVTPSSSLGT-QTVICNVN 351
 QY 656 HKTSTSPIVK 665
 DB 352 HKPSNTKVDK 361

RESULT 15

AAR76088

ID AAR76088 standard; protein; 464 AA.

XX AAR76088;

AC AAR76088;

XX 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX MAB 55.1 heavy chain.

DE MAB 55.1 heavy chain.

XX MAB 55.1 heavy chain.

KW Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;

KW transgenic animal; transgenic plant; antibody engineering;
 KW humanized antibody; immunotoxin.
 XX Mus sp.
 XX Location/Qualifiers
 FH Key 1,19
 FT Peptide /label= Sig_peptide
 FT Protein 20..464
 FT /label= Mat_protein
 FT /note= "claim 3, page 97-98"
 XX W09515382-A1.
 PN 08-JUN-1995.
 PD 29-NOV-1994; 94WO-GB002610.
 XX 03-DEC-1993; 93GB-00024819.
 PR 03-JUN-1994; 94GB-00011089.
 XX (ZENE) ZENECA LTD.
 PA Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
 XX Blakey DC;
 PI WPI; 1995-215262/28.
 DR N-PSDB; AAQ94037.
 DR Antigen binding structures containing CDR's recognising the CA55.1
 FT antigen - produced by hybridomas and host cells, for use in the diagnosis
 PT and therapy of cancer.
 PS Disclosure; Fig 15; 121pp; English.
 XX MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)
 CC chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min
 CC humanized 55.1 constructs have been expressed in myeloma cells and E.
 CC coli. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 464 AA;

Query Match 30.1%; Score 1059.5; DB 2; Length 464;
 Best Local Similarity 37.5%; Pred. No. 6.3e-55;
 Matches 250; Conservative 61; Mismatches 107; Indels 249; Gaps 14;

QY 1 EVLOQSGPDLVKGASVKISKASGYSTGYIMHWKQSPKGLWIGRINPNNGVTLY 60
 DB 20 QVLOQSGPDLVKGASVKISKASGYSTGYIMHWKQSPKGLWIGRINPNNGVTLY 79
 QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMT-TNYVMDYWGQTSVTVS 119
 DB 80 NEKFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMT-TNYVMDYWGQTSVTVS 139
 QY 120 SAKTTPSVVPLAPGSAQAQNSMVTGLVKGYFPPEVTVTNWNSGSLSSGVHTFPAVLQS 179
 DB 140 SAKTTPSVVPLAPGSAQAQNSMVTGLVKGYFPPEVTVTNWNSGSLSSGVHTFPAVLQS 199
 QY 180 DLYTLSSSTVTPSTWSEVTCNVAHPASTTKVDKIVPRDSGGPSEKSEENEXDLR 239
 DB 200 DLYTLSSSTVTPSTWSEVTCNVAHPASTTKVDKIVPRDCG----- 243
 QY 240 KSELQGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTGHPWYNLVDLGST 299
 DB 244 -CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 272
 QY 300 AATSEYEGSSVDLYGAYGYQCAGTGNKACMYGGVTLHDNNRLTEKKVPIINLWDGK 359
 DB 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297
 QY 360 QTTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQVGLV 410
 DB 360 QTTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQVGLV 410

FT Misc-difference 121 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123 /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124 /note= "Given in the specification as U, no further
 FT details given"
 XX WO9324136-A1.
 XX 09-DEC-1993.
 XX 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 XX (TERM/) Terman D S.
 XX (STON/) STONE J L.
 XX Terman DS, Stone JL;
 XX WI; 1993-405418/50.
 XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 FT in a patient or for the treatment of auto-immune diseases.
 XX Disclosure; Fig 1; 90pp; English.
 XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 230 AA;
 PS Query Match 29.8%; Score 1048; DB 2; Length 230;
 CC Best Local Similarity 85.7%; Pred. No. 1.3e-54;
 CC Matches 197; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
 QY 229 SEINEKDLRKKELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTGHEW 288
 Db 1 SEINEKDLRKKELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTGHEW 60
 QY 289 YNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLETEK 348
 Db 61 YNDLLVDKGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLETEK 120
 QY 349 KVPINLWIDGKQTVPIDKVTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQRL 408
 Db 121 XVXXBKWIDGKQTVPIDKVTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQRL 180
 QY 409 IVFHSSEGSVSYDLDAQCYQPTLLIRYDNTTSSLSLSLYTT 458
 Db 181 IVFHSSEGSVSYDLDAQCYQPTLLIRYDNTTSSLSLSLYTT 230
 RESULT 18
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 XX AC ABB76235;
 XX AC ABB76235;
 DT 09-AUG-2002 (first entry)
 DE Staphylococcus aureus enterotoxin E.
 XX Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.

XX Staphylococcus aureus.
 XX Key Location/Qualifiers
 FT Misc-difference 120 /note= "given as 'J' in the specification"
 FT Misc-difference 121 /note= "given as 'J' in the specification"
 FT Misc-difference 123 /note= "given as 'O' in the specification"
 FT Misc-difference 124 /note= "given as 'U' in the specification"
 FT Misc-difference 125 /note= "given as 'V' in the specification"
 XX US2002051765-A1.
 XX 02-MAY-2002.
 XX 19-DEC-2000; 2000US-00741503.
 XX 03-OCT-1989; 89US-00416530.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1991; 91WO-US000342.
 XX 01-JUN-1992; 92US-00891718.
 XX 02-MAR-1993; 93US-00025144.
 XX 31-JAN-1994; 94US-00189424.
 XX 19-JUN-1995; 95US-00491746.
 XX (TERM/) Terman D S.
 XX Terman DS;
 XX WI; 2002-415198/44.
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.
 XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see AB376234-44). In the
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX Sequence 230 AA;
 PS Query Match 29.6%; Score 1044; DB 5; Length 230;
 CC Best Local Similarity 85.7%; Pred. No. 2.3e-54;
 CC Matches 197; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 QY 229 SEINEKDLRKKELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTGHEW 288
 Db 1 SEINEKDLRKKELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTGHEW 60
 QY 289 YNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLETEK 348
 Db 61 YNDLLVDKGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLETEK 120

QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQVGL 408
 Db 121 VXXKXKWDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQVGL 180
 QY 409 IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
 Db 181 IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTINSENHDIYLYTT 230

RESULT 19
 AAE18377
 ID AAE18377 standard; protein; 230 AA.
 AC AAE18377;
 DT 15-OCT-1991 (first entry)
 DE Staphylococcal enterotoxin E.
 KW SEE; cancer treatment; pyrogen; tumouricide.
 OS Staphylococcus aureus.
 XX WO9110680-A.
 PD 25-JUL-1991.
 PF 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1990; 90US-00466577.
 XX (TERM/) Terman D S.
 PA Terman DS;
 PI WPI; 1991-237984/32.
 DR Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 CC SEE was isolated and purified from S.aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX Sequence 230 AA;
 SQ Query Match 29.4%; Score 1035; DB 2; Length 230;
 Best Local Similarity 84.3%; Pred No. 7, 7e-54;
 Matches 194; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 229 SEINEKDLRKKSELOGTALGNLKOIYYNYSKATTSSEKSDQFLTNLLFKGFTGHPW 288
 Db 1 SEINEKDLRKKSELOGTALGNLKOIYYNYSKATTSSEKSDQFLTNLLFKGFTGHPW 60
 QY 289 YNDLIVDVGSTAAATSEYEGSSVDLYGVYQACAGTTPNKTACMYGGVTLHDNNRLTEEX 348
 Db 61 YNDLIVDVGSKDANKYKGGKVDLYGVYQACAGTTPNKTACMYGGVTLHDNNRLTEEX 120
 QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQVGL 408
 Db 121 VXXKXKWDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQVGL 180
 QY 409 IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 458

Db 181 IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTINSENHDIYLYTT 230

RESULT 20
 AAE18377
 ID AAE18377 standard; protein; 597 AA.
 AC AAE18377;
 DT 07-MAY-2002 (first entry)
 DE Human N-terminal DAV-1 heavy chain-mature TNF-alpha fusion protein.
 KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 KW cytostatic; vasotropic; ophthalmological; tumour necrosis factor-alpha;
 KW TNF-alpha; fusion protein.
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 FT Region 1..439
 FT /note= "N-terminal portion of DAV-1 heavy chain"
 FT Region 441..597
 FT /note= "Human mature TNF-alpha"
 XX WO200204522-A2.
 XX 17-JAN-2002.
 XX 09-JUL-2001; 2001WO-EP007878.
 XX 10-JUL-2000; 2000US-00613017.
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX (SCRI) SCRIPS RES INST.
 XX Nemerow GR, Li E;
 XX WPI; 2002-171707/22.
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 XX portion, and a targeting agent, useful for e.g. gene therapy, or for
 XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
 XX integrins.
 XX Claim 15; Page 98-99; 106pp; English.
 XX The present invention relates to a bifunctional molecule comprising an
 XX antibody or its antigen-binding portion, and a targeting agent where the
 XX antibody specifically binds to an antigen in a protein that binds to av
 XX integrin, and the targeting agent specifically binds to a cell surface
 XX protein that activates the phosphatidylinositol 3 (PI3K) signalling
 XX pathway. The bifunctional molecules are useful for gene therapy, for
 XX promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
 XX av integrins, for enhancing Ad binding and internalisation, and in gene
 XX delivery of by fibrous adenovirus particles. The bifunctional molecules
 XX permit targeting of viral and bacterial vectors to cells that express
 XX targeted receptors. Diseases that can be targeted include cancers,
 XX vascular disorders, diabetic retinopathies, restenosis, ophthalmic
 XX disorders, hyperproliferative disorders, and hormonal disorders. The
 XX present sequence is human N-terminal DAV-1 heavy chain-mature tumour
 XX necrosis factor-alpha (TNF-alpha) fusion protein which is used in the
 XX invention
 XX Sequence 597 AA;
 SQ Query Match 29.2%; Score 1028; DB 5; Length 597;
 Best Local Similarity 37.2%; Pred. No. 6, 4e-53;

Mus sp. Chimeric.	OS	253; Conservative	53; Mismatches	115; Indels	260; Gaps	15;
US2002164333-A1.	XX	1	EVQLQSGPELVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRINPNNGVTLY	60		
07-NOV-2002.	XX	20	EVQLQSGPELVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGIYIPYKGGTGY	79		
10-JUL-2001; 2001US-00903327.	XX	61	NQKFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMTITNYMDYWGOGTSVTYSS	120		
10-JUL-2000; 2000US-00613017.	XX	80	NQKFKSKATLTVDSSNTAYMELSLTSDSAVYVCARG-----IAYWGGTGLVTVA	132		
10-JUL-2000; 2000US-0325781P.	XX	121	AKTTPPSVYPLAPGSAATNSMTLGLVKGYPPPEVTVTNWNSGLSSGVHTFPVAVLQSD	180		
(Scri) Scripps Res Inst.	XX	133	AKTTPPSVYPLAPGSAATNSMTLGLVKGYPPPEVTVTNWNSGLSSGVHTFPVAVLQSD	192		
Nemerow GR, Li E;	XX	181	LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK	240		
WPI; 2002-171707/22.	XX	193	LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDCG-----KDDPEVQFSWFVD	235		
New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.	XX	241	SELQGTALGNLKIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLSTA	300		
Example 2; Page 38-39; 49pp; English.	XX	236	CRPCICTVPEVSSVFIIPPCK-----PKDVLITL-----	264		
The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents a fusion protein with mouse DAV-1 antibody heavy chain. (Updated on 23-OCT-2003 to standardise OS field)	XX	301	ATSEYEGSSVDLYGAYGYCAGGTGNTACTMGGVTLHDNNRLTEKKVPIINLWDGKQ	360		
Sequence 597 AA;	XX	265	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	289		
Query Match	XX	361	TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF	411		
Best Local Similarity	XX	290	-DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----	343		
Matches	XX	412	HSSEGSTVSYDLFDAGQYPTDLRLIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV	471		
29, 28; Score 1028; DB 5; Length 597;	XX	344	-----TISKT-----	348		
37.2%; Pred. No. 6.4e-53;	XX	472	SAGDRVTITCKASQSVNDVAVYQKPGKSLISYTSRAGVYDPRSGSGYGTDFTL	531		
53; Mismatches 115; Indels 260; Gaps 15;	XX	349	-----	348		
	XX	532	TISSVQAEAAVYFCQDYNSPTTGGGTLKLEIKRADAAPTVSIIPPSSEQTSGGASV	591		
	XX	349	-----KGRPKAPQVVTIPPPKQMAKDKVSLT	375		
	XX	592	CFLNNTYPKDINVKWIDQSERQNGVLNWTQDQSKDSTYSMSSTLTLTCKDYERHNSYT	651		
	XX	376	CMITDFPEDITVEWOMQPAEN-YKNTQPTMDT-DGSYFYVSKLVNQKSNWEAGNTFI	433		
	XX	652	CEATHKTSTSPIVKSFNRES	672		
	XX	434	CSVLHS-----FVRSSTRTPS	449		
	XX	RESULT 21				
	XX	ABG76352				
	XX	ID	ABG76352 standard; protein; 597 AA.			
	XX	AC				
	XX	XX				
	XX	23-OCT-2003 (revised)				
	XX	DT	10-MAY-2003 (first entry)			
	XX	DE	Mouse DAV-1 heavy chain-mature human TNF-alpha fusion protein.			
	XX	XX	Human; bifunctional molecule; antigen-binding portion; alpha integrin;			
	XX	XX	cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;			
	XX	XX	signalling pathway; targeted gene therapy; delivery vector;			
	XX	XX	adenoviral gene delivery particle; viral infection; cancer;			
	XX	XX	rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;			
	XX	XX	restenosis; ophthalmic disorder; hyperproliferative disorder;			
	XX	XX	hormonal disorder; varicicide; antiinflammatory; antirheumatic;			
	XX	XX	antiarthritic; ophthalmological; DAV-1 antibody heavy chain; TNF-alpha;			
	XX	XX	tumour necrosis factor-alpha; mouse.			
	XX	XX	Homo sapiens.			

Mus sp. Chimeric.	OS	253; Conservative	53; Mismatches	115; Indels	260; Gaps	15;
US2002164333-A1.	XX	1	EVQLQSGPELVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRINPNNGVTLY	60		
07-NOV-2002.	XX	20	EVQLQSGPELVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGIYIPYKGGTGY	79		
10-JUL-2001; 2001US-00903327.	XX	61	NQKFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMTITNYMDYWGOGTSVTYSS	120		
10-JUL-2000; 2000US-00613017.	XX	80	NQKFKSKATLTVDSSNTAYMELSLTSDSAVYVCARG-----IAYWGGTGLVTVA	132		
10-JUL-2000; 2000US-0325781P.	XX	121	AKTTPPSVYPLAPGSAATNSMTLGLVKGYPPPEVTVTNWNSGLSSGVHTFPVAVLQSD	180		
(Scri) Scripps Res Inst.	XX	133	AKTTPPSVYPLAPGSAATNSMTLGLVKGYPPPEVTVTNWNSGLSSGVHTFPVAVLQSD	192		
Nemerow GR, Li E;	XX	181	LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK	240		
WPI; 2002-171707/22.	XX	193	LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDCG-----KDDPEVQFSWFVD	235		
New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.	XX	241	SELQGTALGNLKIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLSTA	300		
Example 2; Page 38-39; 49pp; English.	XX	236	CRPCICTVPEVSSVFIIPPCK-----PKDVLITL-----	264		
The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents a fusion protein with mouse DAV-1 antibody heavy chain. (Updated on 23-OCT-2003 to standardise OS field)	XX	301	ATSEYEGSSVDLYGAYGYCAGGTGNTACTMGGVTLHDNNRLTEKKVPIINLWDGKQ	360		
Sequence 597 AA;	XX	265	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	289		
Query Match	XX	361	TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF	411		
Best Local Similarity	XX	290	-DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----	343		
Matches	XX	412	HSSEGSTVSYDLFDAGQYPTDLRLIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV	471		
29, 28; Score 1028; DB 5; Length 597;	XX	344	-----TISKT-----	348		
37.2%; Pred. No. 6.4e-53;	XX	472	SAGDRVTITCKASQSVNDVAVYQKPGKSLISYTSRAGVYDPRSGSGYGTDFTL	531		
53; Mismatches 115; Indels 260; Gaps 15;	XX	349	-----	348		
	XX	532	TISSVQAEAAVYFCQDYNSPTTGGGTLKLEIKRADAAPTVSIIPPSSEQTSGGASV	591		
	XX	349	-----KGRPKAPQVVTIPPPKQMAKDKVSLT	375		
	XX	592	CFLNNTYPKDINVKWIDQSERQNGVLNWTQDQSKDSTYSMSSTLTLTCKDYERHNSYT	651		
	XX	376	CMITDFPEDITVEWOMQPAEN-YKNTQPTMDT-DGSYFYVSKLVNQKSNWEAGNTFI	433		
	XX	652	CEATHKTSTSPIVKSFNRES	672		
	XX	434	CSVLHS-----FVRSSTRTPS	449		
	XX	RESULT 21				
	XX	ABG76352				
	XX	ID	ABG76352 standard; protein; 597 AA.			
	XX	AC				
	XX	XX				
	XX	23-OCT-2003 (revised)				
	XX	DT	10-MAY-2003 (first entry)			
	XX	DE	Mouse DAV-1 heavy chain-mature human TNF-alpha fusion protein.			
	XX	XX	Human; bifunctional molecule; antigen-binding portion; alpha integrin;			
	XX	XX	cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;			
	XX	XX	signalling pathway; targeted gene therapy; delivery vector;			
	XX	XX	adenoviral gene delivery particle; viral infection; cancer;			
	XX	XX	rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;			
	XX	XX	restenosis; ophthalmic disorder; hyperproliferative disorder;			
	XX	XX	hormonal disorder; varicicide; antiinflammatory; antirheumatic;			
	XX	XX	antiarthritic; ophthalmological; DAV-1 antibody heavy chain; TNF-alpha;			
	XX	XX	tumour necrosis factor-alpha; mouse.			
	XX	XX	Homo sapiens.			

QY 412 HSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSLSLYTTSIVMTQPTSLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVTITCKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVDRPFGSGVGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEAAVFCQDYNPPTFGGKLEIKRADAAPTTSIFPSSQLTSGGASVV 591
 Db 349 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 375
 QY 592 CFLNNFYKPDINVKWIDGSRQNGVLNSWTQDQSKDSTYSMSSTLTLTXDEVERHNSYT 651
 Db 376 CMITDFPFDITVWQNGQPAEN-YKNTQPIMDT-DGSFVYVSKLVNQKSNWEAGNTFI 433
 QY 652 CEATHKTSTPIVSNFRNES 672
 Db 434 CSVLHE-----FVRSSTRTPS 449
 RESULT 22
 AAW83041
 ID AAW83041 standard; protein; 464 AA.
 AC AAW83041;
 XX 25-MAR-2003 (revised)
 DT 15-MAR-1999 (first entry)
 XX Anti-Fas Mab HFE7A heavy chain.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;
 KW HFE7A; autoimmune disease; Hashimoto's disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma;
 KW Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis;
 KW autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis;
 KW Basedow's disease; thrombopenia purpura; insulin-dependent diabetes;
 KW allergy; atopy; arteriosclerosis; myocardiitis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region; CDR.
 XX Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide
 FT 20..464
 FT Region /label= Mat_protein
 FT 20..140
 FT Region /label= Variable
 FT 50..54
 FT Region /label= CDR H1
 FT /note= "claim 9"
 FT 69..84
 FT Region /label= CDR H2
 FT /note= "claim 9"
 FT 118..128
 FT Region /label= CDR H3
 FT /note= "claim 9"
 FT 141..464
 FT Region /label= Constant
 FT
 FN AU9859701-A.
 PN 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-00059701.
 XX
 PR 01-APR-1997; 97JP-00082953.
 PR 25-JUN-1997; 97JP-00169088.
 PR 08-OCT-1997; 97JP-00276064.

(SANY) SANKYO CO LTD.
 Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;
 Hiroko Y, Akio S, Shin Y;
 WPI: 1998-543440/01.
 N-PSDB; AAV71029.
 New antibodies and proteins bind conserved epitope of Fas antigen - used
 to evaluate drugs in animal models and to treat Fas-associated diseases
 e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
 hepatitis and AIDS.
 Example 4; Page 187-188; 292pp; English.
 This is the amino acid of the heavy chain of murine anti-human Fas
 monoclonal antibody HFE7A. CDNA (see AAV70129) encoding the heavy chain
 was obtained from HFE7A-secreting hybridoma (PERM BP-5828) RNA by RT-PCR
 (see AAV70125-26). The invention provides humanised HFE7A antibodies (see
 AAW83031-37) produced by CDR grafting. These antibodies are capable of
 inducing apoptosis in abnormal cells expressing Fas, and of inhibiting
 Fas-induced apoptosis in normal cells. They are used to evaluate, in
 animal models, treatments of diseases that involve Fas/Fas ligand
 interactions, and also to treat such diseases, including autoimmune
 disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft
 versus host disease, Sjogren syndrome, pernicious anaemia, Addison's
 disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-
 dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis,
 AIDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to
 correct DR field.)
 XX Sequence 464 AA;
 SQ
 Query Match 29.1%; Score 1025.5; DB 2; Length 464;
 Best Local Similarity 36.2%; Pred. No. 6.6e-53;
 Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;
 QY 1 EYVLOQSGPDLVKPGASVKISKASGYSFTGYVYHMKQSPKGLWIGRINNGVTLY 60
 Db 20 QVQLOQPGAEVLKPGASVKISKASGYFTSTYMWQWVKQRPQGLWIGEDPSDSYNY 79
 QY 61 NQKFKDKATLTVDKSTTAYMELRLTSEDSAVVYCARSTMTITNVMYDYGQGTSTVTS 119
 Db 80 NQKFKGKATLTVDTSSTAYMQLSLSLTSSEDSAVVYCARNDYNNWYFDVWGTGTVTS 139
 QY 120 SAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGLSSGVTTPAVLQS 179
 Db 140 SAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGLSSGVTTPAVLQS 199
 QY 180 DLYTLSSSVTPSPSTWPSGTTCNVHPASSTPKVDKIVPRDSGGPSESEINEKDLRK 239
 Db 200 DLYTLSSSVTPSPSTWPSGTTCNVHPASSTPKVDKIVPRDCG----- 243
 QY 240 KSELOGTALGNLKOIYYNNSKAITSEKSAQDFLNTLLFKGFFTHGHPWYNDLLVDLGS 299
 Db 244 -CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 272
 QY 300 AATSEYEGSSVDLYGAYGYQCAGGTGKNTACMYGVTLDHNNRLTEKKYPIINLWDGK 359
 Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV-- 297
 QY 360 QTTVPIDKVTSKKEV-----TQEELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIV 410
 Db 298 --DVEVHTAQTPREEQFNSTFRSVSELPIMHQNLNGKFKCRVNSAFAPIEK----- 351
 QY 411 FHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSLSLYTTSIVMTQPTSLV 470
 Db 352 -----TISKT----- 356

QY 531 LTSSVQAEADAAVFCQDYNPPTFGGTTKLEIKRADAAPTVSIIPPSSEQLTSGASV 590
 Db 357 -----KGRKAPQVVTTPPPKEQVAKDKVSL 382
 QY 591 VCLNFFPKDINVKWIDGSEON-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYE 645
 Db 383 TCMITDFPEDIITVEWQNGQPAENYKNTQPIWNT-----NGSYFVYSKLVNQKSNWE 435
 QY 646 RHNSYTCETHK 657
 Db 436 AGNTFTCSVLHE 447

RESULT 27
 AAE18380
 ID AAE18380 standard; protein; 613 AA.
 AC AAE18380;
 XX
 XX 07-MAY-2002 (first entry)
 DT
 DE Human N-terminal DAV-1 heavy chain-mature SCF fusion protein.
 KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 KW cytosolic; vasotropic; ophthalmological; stem cell factor; SCF;
 KW fusion protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.

Key Location/Qualifiers
 Region 1..438
 /note= "N-terminal portion of DAV-1 heavy chain"
 Region 439..449
 /note= "Linker peptide"
 Region 450..613
 /note= "Human mature SCF"
 XX WO200204522-A2.
 PN
 XX
 PD 17-JAN-2002.
 XX
 XX 09-JUL-2001; 2001WO-EP007878.
 XX
 XX 10-JUL-2000; 2000US-00613017.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 XX Nemerow GR, Li B;
 PI
 XX WPI; 2002-171707/22.
 DR
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX
 XX Claim 15; Page 102-103; 106pp; English.

The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent where the antibody specifically binds to an antigen in a protein that binds to av integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol 3 (PI3K) signalling pathway. The bifunctional molecules are useful for gene therapy, for promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking av integrins, for enhancing Ad binding and internalisation, and in gene delivery of by fibreless adenovirus particles. The bifunctional molecules

CC permit targeting of viral and bacterial vectors to cells that express
 CC targeted receptors. Diseases that can be targeted include cancers,
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic,
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence is human N-terminal DAV-1 heavy chain-mature stem cell
 CC factor (SCF) fusion protein which is used in the invention
 XX
 XX Sequence 613 AA;
 SQ
 Query Match 29.1%; Score 1024.5; DB 5; Length 613;
 Best Local Similarity 37.3%; Pred. No. 1.1e-52;
 Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;
 QY 1 EVLOQSGPDLVKPGASVKISKCKASGYFTGYVHWVKQSPKGLWIGRINPNNGVTLY 60
 Db 20 EVLOQSGPDLVKPGASVKISKCKASGYFTGYVHWVKQSPKGLWIGRINPNNGVTLY 79
 QY 61 NQKFKDKATLTVDKSSSTTAYMELRSLTSEDASVYCARSTWITNYMDYWGQGSVTYSS 120
 Db 80 NQKFKDKATLTVDKSSSTTAYMELRSLTSEDASVYCARSTWITNYMDYWGQGSVTYSS 132
 QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGVEPEPTVTWNSGSLSSGVHTFAVLQSD 180
 Db 133 AKTTPSVYPLAPGSAAGTNSMTLGLVKGVEPEPTVTWNSGSLSSGVHTFAVLQSD 192
 QY 181 LYTSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKVIYPRDSGGPSEKSEBINEKDLKK 240
 Db 193 LYTSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKVIYPRDSGGPSEKSEBINEKDLKK 235
 QY 241 SELQGTALGNLQIYYNSKAITSEKSAQDLNTLLFKGFTTCHPHYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIFPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 Db 265 -----TP-KVTCVVDIS-----KDDPEVQFSWEVD--- 289
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKGKVGRLIVF 411
 Db 290 -DVEVHTAQTPREQFNSFRSVELPMHQDLWNGKEFKRCVNSAAFPAPIEK----- 343
 QY 412 HSSEGSTVSYDLFDAQGYPDTLIRIYRDNTTISSTLSLSLYLVTTSIVMTQPTSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRAVITCKASQSVNDVAWYQQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAVFCQDYNPPTFGGTTKLEIKRADAAPTVSIIPPSSEQLTSGASV 591
 Db 349 -----KGRKAPQVVTTPPPKEQVAKDKVSLT 375
 QY 592 CFLNFFPKDINVKWIDGSEONGVLSNWTQDQSKDSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMTIDFPEDIITVEWQNGQPAEN-YKNTQPIWNT-DGSYFVYSKLVNQKSNWEAGNTFI 433
 QY 652 CEATHTSTSP 662
 Db 434 CSVLHEFCRYP 444

RESULT 28
 ABG76355
 ID ABG76355 standard; protein; 613 AA.
 XX
 XX ABG76355;
 XX
 XX 23-OCT-2003 (revised)
 DT 10-MAY-2003 (first entry)
 XX
 XX Mouse DAV-1 heavy chain-mature human SCF fusion protein.
 DS
 XX

KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antineumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; SCF;
 KW stem cell factor; mouse.
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX US2002164333-A1.
 PN 07-NOV-2002.
 XX 10-JUL-2001; 2001US-00903327.
 XX 10-JUL-2000; 2000US-00613017.
 PR 10-JUL-2000; 2000US-0325781P.
 XX (SCRI) SCRIPPS RES INST.
 PA Nemerow GR, Li E;
 PI WPI; 2002-171707/22.
 DR
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX
 PS Example 2; Page 42-44; 49pp; English.
 XX
 CC The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent. The
 CC antibody specifically binds to an antigen in a protein that binds to
 CC alpha integrin, and the targeting agent specifically binds to a cell
 CC surface protein that activates the phosphatidylinositol-3-OH kinase
 CC (PI3K) signalling pathway. The bifunctional molecules are useful for
 CC targeted gene therapy using targeting delivery vectors, such as
 CC adenoviral gene delivery particles. The bifunctional molecules are useful
 CC for treating viral infections, rheumatoid arthritis, cancers,
 CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence represents a fusion protein with mouse DAV-1 antibody
 CC heavy chain. (Updated on 23-Oct-2003 to standardise OS field)
 XX
 SQ Sequence 613 AA;

Query Match 29.1%; Score 1024.5; DB 5; Length 613;
 Best Local Similarity 37.3%; Pred. No. 1.1e-52;
 Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKSPGKLEWIGRINPNNGVTLY 60
 DB 20 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKSPGKLEWIGVYPIYKGGTY 79
 QY 61 NQXFKDKALITVDKSTTAYMELRSITSDSAVYYCARSTMTNYMDYWGQTSVTSS 120
 DB 80 NQXFKDKALITVDKSTTAYMELRSITSDSAVYYCARSTMTNYMDYWGQTSVTSS 132
 QY 121 AKTTPSVVPLAPGSAQAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
 DB 133 AKTTPSVVPLAPGSAQAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 192
 QY 181 LYTLLSSVTVPSSTWPSSTVTCNVAPASSTKVDDKIVPRDGGPSEKSEENEXDLRKK 240
 DB 193 LYTLLSSVTVPSSTWPSSTVTCNVAPASSTKVDDKIVPRDGGPSEKSEENEXDLRKK 235
 QY 241 SEIQGTALGNLKIYYYNKALITSSSEKSDAQFTNTLLFKGFTGHPWYNLLVDLGSTA 300

DB 236 CKPCICTVPESSVFIFPK-----PKDVLITL----- 264
 QY 301 ATSEVEGSSVDLYGAYGYOCAGGTENKACMGVTLHDNNRLTEKKVPINLWIDGKQ 360
 DB 265 -----TP-KVTCVVVDIS-----KDPPEVQFSWFD--- 289
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGKORGLIVF 411
 DB 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK----- 343
 QY 412 HSEGGSTVSVDLPDAQGYPTDLLRIYRDNNTISSTLSLSLYLYTTSIVMTQPTSLV 471
 DB 344 -----TISK----- 348
 QY 472 SAGDRVTITCKASQSVSNDAVWYQKQKPGPKLLISYTSRYAGVDPDRFSGSGYGTDTFL 531
 DB 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNSTPFTGGTGLEIKRADAAPTSTIFPSSSEQLTSGGASVV 591
 DB 349 -----KGRPKAPQVYTIPTPKSQMAKDKVSLT 375
 QY 592 CFLNNFYPKIDINVKWKIDGSRQGNVLSWTDQSKDSTYSMSSTLTLTDEYERHNSYT 651
 DB 376 CMITDFPEDITVENQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQKSNWEAGNTFI 433
 QY 652 CEATHKTSSTSP 662
 DB 434 CSVLHFCRYP 444

RESULT 29
 AAE18370
 ID AAE18370 standard; protein; 456 AA.
 XX
 AC AAE18370;
 DT 07-MAY-2002 (first entry)
 XX
 DE Human penton base monoclonal antibody, DAV-1 heavy chain.
 KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 KW cytostatic; vasotropic; ophthalmological.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 230..242
 FT /note= "Hinge region"
 FN WO200204522-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 09-JUL-2001; 2001WO-EP007878.
 XX
 PR 10-JUL-2000; 2000US-00613017.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Nemerow GR, Li E;
 XX
 DR WPI; 2002-171707/22.
 DR N-PSDS; AAD29308.
 XX
 PT New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av

PT integrins.
XX PS Claim 10; Page 91-92; 106pp; English.
XX The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent where the antibody specifically binds to an antigen in a protein that binds to an integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol 3 (PI3K) signalling pathway. The bifunctional molecules are useful for gene therapy, for promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking an integrin, for enhancing Ad binding and internalisation, and in gene delivery of by fibroless adenovirus particles. The bifunctional molecules permit targeting of viral and bacterial vectors to cells that express targeted receptors. Diseases that can be targeted include cancers, vascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence is human penton base monoclonal antibody, DAV-1 heavy chain

XX SQ Sequence 456 AA;
Query Match 29.1%; Score 1023.5; DB 5; Length 456;
Best Local Similarity 37.4%; Pred. No. 8.5e-53;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTL 60
DB 20 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWKQSPGKLEWIGIYIPKGGTGY 79

QY 61 NQKFKDKATLTVDKSSITAYMELSLTSDSAVYICARSTMTNVMYMDYWGQGTSTVVS 120
DB 80 NQKFKDKATLTVDKSSITAYMELSLTSDSAVYICARG-----IAYWGQGTLTVSA 132

QY 121 AKTTPSPVPLAPGSAAGTNSMTVLGCLVKGYPPEVTVTWNSGSLSSGVHTTFAVLQSD 180
DB 133 AKTTPSPVPLAPGSAAGTNSMTVLGCLVKGYPPEVTVTWNSGSLSSGVHTTFAVLQSD 192

QY 181 LYTSSSVTPSPSTPSTVTCNVAHPASSTKVDKXIVPRDSGSPSEKSEINEKDLRKK 240
DB 193 LYTSSSVTPSPSTPSTVTCNVAHPASSTKVDKXIVPRDCG----- 235

QY 241 SELQGTALGNLKQIYYNYSKAITSEKSAQDFLNTLLFKGFFTHGHPYNDLLVDLGSTA 300
DB 236 CKPCICTVPVSSVPIFPFK-----PKDVLITL----- 264

QY 301 ATSEYEGSSVDLYGAYGYQCAGTTPNKTACMGVGTLDHNNRLTEKKVPIINLWDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289

QY 361 TVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLIVF 411
DB 290 -DVEVHTAQTPREBEQFNSTFRSELSFIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343

QY 412 HSSEGSTVSYDLFDAQGGVPTLLRIYRDNTTISTSLISLYITTSIVMTQTPTSLV 471
DB 344 -----TISK----- 348

QY 472 SAGDRVITCKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDRFSGSGYGTDTFTL 531
DB 349 ----- 348

QY 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRAADAAPTSTVIFPPSSQLTSGGASV 591
DB 349 -----KGRKAPQVYTIPTPKQMAKDKVSLT 375

QY 592 CFLANNFYKIDNWKIDGSRQGNLSWTDQSDSTYSMSSTLTLTDKDEYERHNSYT 651
DB 376 CMTIDTFPPDITVEMQWNGQPAEN-YKNTQPIMDT-DGSFYVYSKLVNQKSNWEAGNTFI 433

QY 652 CEATHK 657
DB 434 CSQLHE 439

RESULT 30
ABG76345
ID ABG76345 standard; protein; 456 AA.
XX AC ABG76345;
XX DT 10-MAY-2003 (first entry)
XX DE Mouse DAV-1 heavy chain monoclonal antibody.
XX KW Mouse; bifunctional molecule; antigen-binding portion; alpha integrin; cell surface protein; phosphatidylinositol-3-OH kinase; PI3K; signalling pathway; targeted gene therapy; delivery vector; adenoviral gene delivery particle; viral infection; cancer; rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; virucide; antiinflammatory; antirheumatic; antiarthritic; ophthalmological; DAV-1 heavy chain;
XX KW penton base monoclonal antibody.
XX OS Mus sp.
XX US2002164333-A1.
XX PD 07-NOV-2002.
XX PF 10-JUL-2001; 2001US-00903327.
XX PR 10-JUL-2000; 2000US-00613017.
XX PR 10-JUL-2000; 2000US-0325781P.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX DR N-PSDB; ABX12744.
XX PT New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.
XX PS Claim 10; Page 30-31; 49pp; English.
XX The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents mouse DAV-1 heavy chain, penton base monoclonal antibody
XX SQ Sequence 456 AA;
Query Match 29.1%; Score 1023.5; DB 5; Length 456;
Best Local Similarity 37.4%; Pred. No. 8.5e-53;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTL 60
DB 20 EVQLQSGPDLVPGASVKISCKASGYSTGYMHWKQSPGKLEWIGIYIPKGGTGY 79
QY 61 NQKFKDKATLTVDKSSITAYMELSLTSDSAVYICARSTMTNVMYMDYWGQGTSTVVS 120

```

Db      80 NQKFKSKATLTTDSSSNTAYMELRSLTSDASAVYYCARG-----IAYWGQGLTAVTVA 132
QY      121 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPVPTVWNSGSLSSGVHTFPAVLQSD 180
Db      133 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPVPTVWNSGSLSSGVHTFPAVLQSD 192
QY      181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 240
Db      193 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 235
QY      241 SELQGTALGNLQIYYNNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db      236 CKPICITVPEVSVFIPPPK-----PKDVLTITL----- 264
QY      301 ATSEYEGSSVDLYGAYGYQCAGTPNKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db      265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
QY      361 TTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLIVF 411
Db      290 -DVEVHTAQTPREEQNFSTRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
QY      412 HSEGSTVSYDLFDACQGYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV 471
Db      344 -----TISKI----- 348
QY      472 SAGDRVTITCKASQSVNSDVANVQKPGQSKLLISYSSRVAGVDPDRFSGSGYCTDTL 531
Db      349 ----- 348
QY      532 TISSVQAEAAVVFQDYNPPTFGGPKLEIKRADAAPTYSIFPPSSEQLTSGGASV 591
Db      349 -----KGPAPQVYTIPTPPEKQWAKDKVSLT 375
QY      592 CFLNFPKIDINVKKIDGSEKQVNLNSWTQDSDKSTYSMSLTTLTKDEYERHNSYT 651
Db      376 CMITDFPEDITVWQWQNPQAEV-YKNTQPTMDT-DGSYFYVYSKLVNPKNSWEAGNTFI 433
QY      652 CEATHK 657
Db      434 CSVLHE 439

RESULT 31
AAE18379
ID AAE18379 standard; protein; 493 AA.
AC AAE18379;
DE
DT 07-MAY-2002 (first entry)
E
KW Human N-terminal DAV-1 heavy chain-mature EGF fusion protein.
KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytotatic; vasotropic; ophthalmological; epidermal growth factor; EGF;
KW fusion protein.
OS
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
FH
FT Region
FT 1..439
FT /note="N-terminal portion of DAV-1 heavy chain"
FT 441..493
FT /note="Human mature EGF"
PN WC0200204522-A2.
PD 17-JAN-2002.
XX

```

```

PF      09-JUL-2001; 2001WO-EP007878.
XX
XX      10-JUL-2000; 2000US-00613017.
XX
PA      (NOVS ) NOVARTIS AG.
PA      (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA      (SCRI ) SCRIPPS RES INST.
XX
XX      Nemerow GR, Li E;
XX
XX      WPI; 2002-171707/22.
XX
XX      New bifunctional molecules comprising an antibody or its antigen-binding
XX      portion, and a targeting agent, useful for e.g. gene therapy, or for
XX      promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX      integrins.
PS      Claim 15; Page 101-102; 106pp; English.
XX
XX      The present invention relates to a bifunctional molecule comprising an
XX      antibody or its antigen-binding portion, and a targeting agent where the
XX      antibody specifically binds to an antigen in a protein that binds to av
XX      integrin, and the targeting agent specifically binds to a cell surface
XX      protein that activates the phosphatidylinositol 3 (PI3K) signalling
XX      pathway. The bifunctional molecules are useful for gene therapy, for
XX      promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
XX      av integrins, for enhancing Ad binding and internalisation, and in gene
XX      delivery of by fibroless adenovirus particles. The bifunctional molecules
XX      permit targeting of viral and bacterial vectors to cells that express
XX      targeted receptors. Diseases that can be targeted include cancers,
XX      vascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX      disorders, hyperproliferative disorders, and hormonal disorders. The
XX      present sequence is human N-terminal DAV-1 heavy chain-mature epidermal
XX      growth factor (EGF) fusion protein which is used in the invention
XX
XX      Sequence 493 AA;
XX
XX      Query Match          29.1%; Score 1023.5; DB 5; Length 493;
XX      Best Local Similarity 37.4%; Pred. No. 9.3e-53;
XX      Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
XX
QY      1 EVQLQQSGDPLVRFPGASVKISCKASGYSTFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db      20 EVQLQQSGDPLVRFPGASVKISCKASGYSTFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 79
QY      61 NQKFKSKATLITDSSSNTAYMELRSLTSDASAVYYCARG-----IAYWGQGLTAVTVA 120
Db      80 NQKFKSKATLITDSSSNTAYMELRSLTSDASAVYYCARG-----IAYWGQGLTAVTVA 132
QY      121 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPVPTVWNSGSLSSGVHTFPAVLQSD 180
Db      133 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPPVPTVWNSGSLSSGVHTFPAVLQSD 192
QY      181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 240
Db      193 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 235
QY      241 SELQGTALGNLQIYYNNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db      236 CKPICITVPEVSVFIPPPK-----PKDVLTITL----- 264
QY      301 ATSEYEGSSVDLYGAYGYQCAGTPNKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db      265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
QY      361 TTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLIVF 411
Db      290 -DVEVHTAQTPREEQNFSTRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
QY      412 HSEGSTVSYDLFDACQGYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV 471
Db      344 -----TISKI----- 348

```

QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSPQLTSGASV 591
 Db 349 -----KGRPKAPQVVTIPPPKQMAKDKVSLT 375
 QY 592 CFLNFPKIDINVKWKIDGSRQNGVNSWTDQSDKSTYSMSSTLTITKDEYERHNSYT 651
 Db 376 CMITDFPEDITVQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNOKSNWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439
 RESULT 32
 ABG76354
 ID ABG76354 standard; protein; 493 AA.
 AC ABG76354;
 XX
 XX 23-OCT-2003 (revised)
 DT 10-MAY-2003 (first entry)
 DE
 DE Mouse DAV-1 heavy chain-mature human EGF fusion protein.
 XX
 KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; EGF;
 KW epidermal growth factor; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX US2002164333-A1.
 PD 07-NOV-2002.
 XX
 PF 10-JUL-2001; 2001US-00903327.
 XX
 PR 10-JUL-2000; 2000US-00613017.
 PR 10-JUL-2000; 2000US-0325781P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Nemerow GR, Li B;
 PI
 XX WPI; 2002-171707/22.
 DR
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX
 PS Example 2; Page 41-42; 49pp; English.
 XX
 CC The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent. The
 CC antibody specifically binds to an antigen in a protein that binds to
 CC alpha integrin, and the targeting agent specifically binds to a cell
 CC surface protein that activates the phosphatidylinositol-3-OH kinase
 CC (PI3K) signalling pathway. The bifunctional molecules are useful for
 CC targeted gene therapy using targeting delivery vectors, such as
 CC adenoviral gene delivery particles. The bifunctional molecules are useful
 CC for treating viral infections, rheumatoid arthritis, cancers,

CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence represents a fusion protein with mouse DAV-1 antibody
 CC heavy chain. (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 493 AA;
 Query Match 29.1%; Score 1023.5; DB 5; Length 493;
 Best Local Similarity 37.4%; Pred. No. 9.3e-53;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVQLQQSGPDLVKGASVKISKASGYFTGYMHVWKQSPKGLWIGRINPNNGVTLY 60
 Db 20 EVQLQQSGPELVKPCASVKISKASGYFTFDYNNHVKQSHGKSLWIGYIYPKGTGY 79
 QY 61 NQKPKDKATLTVDKSTTAYNELSLTSEDASVYVCARSTMTITNVMDYMQCGTSVTSS 120
 Db 80 NQKFKSKATLTDDSSNTAYNELSLTSDASAVYVCARG-----TAYWQGGTLVTVA 132
 QY 121 AKTTPPSVYPLAPGSAQAQNSMTVLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
 Db 133 AKTTPPSVYPLAPGSAQAQNSMTVLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 192
 QY 181 LYTLSSTVTPSSSTWPSSTVTCNVAPASSTKVDDKIVPRDSGGPSEKSEINEKDLRKK 240
 Db 193 LYTLSSTVTPSSSTWPSSTVTCNVAPASSTKVDDKIVPRDCG----- 235
 QY 241 SELQGTALGNLKIYYNSKAITSEKSAQOFLNTLLFKGFTTGHFWNDLLVLDLSTA 300
 Db 236 CKPCICTVPESSSVFIFPK-----PKDVLNLT----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQACAGTPNTACMGVTLHDNRLTEKKVPINLWIDCKQ 360
 Db 265 -----TP-KVTCVWVDIS-----KDDPEVQFSWFDV--- 289
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHVLHGK-FGL-YNSDSFGGKVQGRGLIVF 411
 Db 290 -DVEVHTAQTPREQPNSTFRSVELFIMHQDLNKGKFCRVNSAFAPIEK----- 343
 QY 412 HSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQPTSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSPQLTSGASV 591
 Db 349 -----KGRPKAPQVVTIPPPKQMAKDKVSLT 375
 QY 592 CFLNFPKIDINVKWKIDGSRQNGVNSWTDQSDKSTYSMSSTLTITKDEYERHNSYT 651
 Db 376 CMITDFPEDITVQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNOKSNWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439
 RESULT 33
 AAE18378
 ID AAE18378 standard; protein; 510 AA.
 XX
 XX AAE18378;
 AC
 XX 07-MAY-2002 (first entry)
 DT
 XX Human N-terminal DAV-1 heavy chain-mature IGF-1 fusion protein.
 DE
 XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;

KW cytotostatic; vasotropic; ophthalmological; insulin growth factor-1; IGF-1;
 KW fusion protein.
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX Key Location/Qualifiers
 XX 1.439
 FT Region /note= "N-terminal portion of DAV-1 heavy chain"
 FT Region 441..510
 FT Region /note= "Human mature IGF-1"
 PN WO200204522-A2.
 XX 17-JAN-2002.
 XX 09-JUL-2001; 2001WO-EPC07878.
 XX 10-JUL-2000; 2000US-00613017.
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX Nemerow GR, Li E;
 XX WPI; 2002-171707/22.
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX Claim 15; Page 100; 106pp; English.
 XX The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent where the
 CC antibody specifically binds to an antigen in a protein that binds to av
 CC integrin, and the targeting agent specifically binds to a cell surface
 CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
 CC pathway. The bifunctional molecules are useful for gene therapy, for
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
 CC av integrins, for enhancing Ad binding and internalisation, and in gene
 CC delivery of by fibreless adenovirus particles. The bifunctional molecules
 CC permit targeting of viral and bacterial vectors to cells that express
 CC targeted receptors. Diseases that can be targeted include cancers,
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence is human N-terminal DAV-1 heavy chain-mature insulin
 CC growth factor-1 (IGF-1) fusion protein which is used in the invention
 XX Sequence 510 AA;
 SQ
 Query Match 29.1%; Score 1023.5; DB 5; Length 510;
 Best Local Similarity 37.4%; Pred.No.9.7e-53;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTILY 60
 Db 20 EVQLQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTILY 79
 QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYVCARSTMTNVMYWGQGTSTVYS 120
 Db 80 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYVCARSTMTNVMYWGQGTSTVYS 132
 QY 121 AKTTPSPVYPLAPGSAQNSMTVGLCLVKGFPEPTVWNSSGLSSGVHFFPAVLQSD 180
 Db 133 AKTTPSPVYPLAPGSAQNSMTVGLCLVKGFPEPTVWNSSGLSSGVHFFPAVLQSD 192
 QY 181 LYTSSSVTPGSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSENEKDLRKK 240
 Db 193 LYTSSSVTPGSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSENEKDLRKK 235

QY 241 SELOQTALGNLKLQIYYNYSKAITSEKSAQDQFLINTLLFKGFTTGHFWYNDLLVLDGSA 300
 Db 236 CKPCICTVPEVSSVFPPPK-----PKDVLATL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTAQMGVTLHDNNRLTEEEKVPIINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFD----- 289
 QY 361 TTVPIDKVKTSKEY-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
 Db 290 -DVEVHTAQTQPRBEQFNSTFRSVELPMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
 QY 412 HSSGSGTVSYDLFDAQGYQPTLLRIYRDNTIISTSLISLYLYTTSIVMTQTPSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVITITKASQSVNDVAVYQKQKPGQSPKLLIYSYTSRYAGVDPDRFSGSGYGTFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAVFCQDYNSPPTFGGTGKLEIKRADAAPTVSPSSSEQLTSGGASVV 591
 Db 349 -----KGRPKAPQVYTPPPKQMAKDKVSLT 375
 QY 592 CFLNNEYPKDNVKKIDGSRONGVLSNWDQSDKSTYSMSSTLTTLTKDVEYERHSY 651
 Db 376 CMITDFFPEDITVWQWNGQPAEN-YKNTQPIMDT-DGSIYFVSKLVQKSNWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439
 RESULT 34
 ABG76353
 ID ABG76353 standard; protein; 510 AA.
 XX AC ABG76353;
 XX DT 23-OCT-2003 (revised)
 XX DT 10-MAY-2003 (first entry)
 XX DE Mouse DAV-1 heavy chain-mature human IGF-1 fusion protein.
 KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; IGF-1;
 KW insulin-like growth factor-1; mouse.
 XX Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX US2002164333-A1.
 XX PD 07-NOV-2002.
 XX PF 10-JUL-2001; 2001US-00903327.
 XX PR 10-JUL-2000; 2000US-00613017.
 XX PR 10-JUL-2000; 2000US-0325781P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Nemerow GR, Li E;
 XX WPI; 2002-171707/22.

XX New bifunctional molecules comprising an antibody or its antigen-binding
PT portion, and a targeting agent, useful for e.g. gene therapy, or for
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
PT integrins.
XX
XX
XX Example 2; Page 39-41; 49pp; English.
XX
XX The present invention relates to a bifunctional molecule comprising an
CC antibody or its antigen-binding portion, and a targeting agent. The
CC antibody specifically binds to an antigen in a protein that binds to
CC alpha integrin, and the targeting agent specifically binds to a cell
CC surface protein that activates the phosphatidylinositol-3-OH kinase
CC (PI3K) signalling pathway. The bifunctional molecules are useful for
CC targeted gene therapy using targeting delivery vectors, such as
CC adenoviral gene delivery particles. The bifunctional molecules are useful
CC for treating viral infections, rheumatoid arthritis, cancers,
CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence represents a fusion protein with mouse DAV-1 antibody
CC heavy chain. (Updated on 23-OCT-2003 to standardise OS field)
XX
XX Sequence 510 AA;
XX
XX Query Match 29.1%; Score 1023.5; DB 5; Length 510;
XX Best Local Similarity 37.4%; Pred. No. 9.7e-53;
XX Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
XX
XX 1 EVOLQSQGDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGINPNNGVTLY 60
XX 20 EVOLQSQGPELVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGIYIPYKGTGY 79
XX
XX 61 NQFKDKATLTVDKSSFTAYMELSLTSEDSAVVYCARSTMTITNYMDYWGQSTVTVSS 120
XX 80 NQFKSKATLTVDSSNTAYMELSLTSDASAVYICARG-----TAYMGQGLTVTVSA 132
XX
XX 121 AKTTPSVYPLAPGSAATNSMTVLGCLVKGYPPEVTVTWNSGLSSGVHTFPVAVLQSD 180
XX 133 AKTTPSVYPLAPGSAATNSMTVLGCLVKGYPPEVTVTWNSGLSSGVHTFPVAVLQSD 192
XX
XX 161 LYTLSSSTVPSSTWPSSTVTCNVAHPASSTKVKIVPRDSGCPSEKSEINEKDLKK 240
XX 193 LYTLSSSTVPSSTWPSSTVTCNVAHPASSTKVKIVPRDCG----- 235
XX
XX 241 SELQGTALGNLKQIYYNKAITSSEKSAQDFLNTLLFKGFFTCHPWINDLLVDLGSTA 300
XX 236 CKPCICTVPSVSVFIPPK-----PKDVLITL----- 264
XX
XX 301 ATSEYEGSVDLYGAYGYQACAGTNPNTACMGVGVTLHDNNRTEKKVPINLWIDGKQ 360
XX 265 -----TP-KVTCVWVDIS-----KDDPEVQFSWFVD--- 289
XX
XX 361 TVVPIDKVKTSKEV-----TVQELDLQARHVLHGK-FGL-YNSDSFGKVGKORGLIVF 411
XX 290 -DVEVHTTAQTQPREQFNSTRSVSELPIMHQDWLNGKEFKCRVNSAFAPIEK----- 343
XX
XX 412 HSSEGSTVSYDLFDAQGGYPTDLLRIYRDNTTISTSLISLYLYTTSIVMTQPTSLV 471
XX 344 -----TISKT----- 348
XX
XX 472 SAGDRVITICKASQSVSNDAVYQQKPGQSKLLISYTSRYAGVDPDRFSGSGYCTDFTL 531
XX 349 ----- 348
XX
XX 532 TISSVQAEADAAYVFCQDYNSPPTFGGTKLEIKRADAAPTYSIFPSPSEQLTSGGASV 591
XX 349 -----KGRPKAPQVYTIPTPEKQMAXDKVSLT 375
XX
XX 592 CFLNPFYKPDINVKKIDGSEKQNGVNSWTDQSDKSTYSMSSTLTITKDEYERHNSYT 651
XX 376 CMITDFFEDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFYVSKLVNOKNWEAGNTFI 433
XX
XX 652 CEATHK 657

Db 434 CSVLHE 439
RESULT 35
AAE18372
ID AAE18372 standard; protein; 438 AA.
XX
XX AAE18372;
AC
XX
XX 07-MAY-2002 (first entry)
DT
XX
XX Human penton base monoclonal antibody, DAV-1 heavy chain fragment.
DE
XX
XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytostatic; vasotropic; ophthalmological.
XX
XX Homo. sapiens.
OS
XX
XX WO200204522-A2.
PN
XX
XX 17-JAN-2002.
PD
XX
XX 09-JUL-2001; 2001WO-EP007878.
PF
XX
XX 10-JUL-2000; 2000US-00613017.
PR
XX
XX (NOVS) NOVARIS AG.
PA
XX
XX (NOVS) NOVARIS-ERFINDUNGEN VERW GES MBH.
PA
XX
XX (SCRI) SCRIPPS RES INST.
XX
XX Nemerow GR, Li E;
PI
XX
XX WPI; 2002-171707/22.
DR
XX
XX N-PSDB; AAE18372.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding
PT portion, and a targeting agent, useful for e.g. gene therapy, or for
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
PT integrins.
XX
XX Claim 10; Page 96; 106pp; English.
XX
XX The present invention relates to a bifunctional molecule comprising an
CC antibody or its antigen-binding portion, and a targeting agent where the
CC antibody specifically binds to an antigen in a protein that binds to av
CC integrin, and the targeting agent specifically binds to a cell surface
CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
CC pathway. The bifunctional molecules are useful for gene therapy, for
CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
CC av integrins, for enhancing Ad binding and internalisation, and in gene
CC delivery of by fibreless adenovirus particles. The bifunctional molecules
CC permit targeting of viral and bacterial vectors to cells that express
CC targeted receptors. Diseases that can be targeted include cancers,
CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence is human penton base monoclonal antibody, DAV-1 heavy
CC chain fragment
XX
XX Sequence 438 AA;
XX
XX Query Match 29.0%; Score 1022.5; DB 5; Length 438;
XX Best Local Similarity 37.4%; Pred. No. 9.3e-53;
XX Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;
XX
XX 1 EVOLQSQGDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGINPNNGVTLY 60
XX 20 EVOLQSQGPELVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGIYIPYKGTGY 79
XX
XX 61 NQFKDKATLTVDKSSFTAYMELSLTSEDSAVVYCARSTMTITNYMDYWGQSTVTVSS 120

Db 80 NQFKSKATLTSSNTAYMELRLTSDASAVVYCARG-----IAYWQGTLLVTSVA 132
 Qy 121 AKTTTPSVYPLAPGSAAGTNSMTLGLVKGYFPEPVTWNSGSLSSGVHTFPVAVLQSD 180
 Db 133 AKTTTPSVYPLAPGSAAGTNSMTLGLVKGYFPEPVTWNSGSLSSGVHTFPVAVLQSD 192
 Qy 181 LYTLSSSVTPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSENEKDLRKK 240
 Db 193 LYTLSSSVTPSTWSPSETVTCNVAHPASSTKVDKIVPRDCG----- 235
 Qy 241 SELQGTALGNLKIYVYNSKAITSSSEKSAQFLNTLLPKGPTGHPWYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 264
 Qy 301 ATSEYEGSSVDLYGAYYGOCAGGTNKTACMGVGTLLHNNRLTEKKVPINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
 Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIVF 411
 Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAFPAPIEK----- 343
 Qy 412 HSSEGSTVSYDLFDAQOQYPTDLLRIYRDNNTTISLSISLYLYTTSIWMQTPTSLV 471
 Db 344 -----TISK----- 348
 Qy 472 SAGDRVTITCKASQSVNSNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 Qy 532 TISSVQAEADAAYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSEQLTSGGASVV 591
 Db 434 CSVLH 438
 Qy 652 CEATH 656
 Db 434 CSVLH 438
 RESULT 36
 ID ABG76347
 AC ABG76347 standard; protein; 438 AA.
 XX ABG76347;
 XX 10-MAY-2003 (first entry)
 XX Portion of mouse DAV-1 heavy chain monoclonal antibody.
 XX Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;
 XX cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 XX signalling pathway; targeted gene therapy; delivery vector;
 XX adenoviral gene delivery particle; viral infection; cancer;
 XX rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 XX restenosis; ophthalmic disorder; hyperproliferative disorder;
 XX hormonal disorder; varicella; antiinflammatory; antirheumatic;
 XX antiarthritic; ophthalmological; DAV-1 heavy chain;
 XX penton base monoclonal antibody.
 XX Mus sp.
 XX US2002164333-A1.
 XX 07-NOV-2002.
 XX 10-JUL-2001; 2001US-00903327.
 XX 10-JUL-2000; 2000US-00613017.
 XX 10-JUL-2000; 2000US-0325781P.

(SCRI) SCRIPPS RES INST.
 Nemerow GR, Li E;
 WPI; 2002-171707/22.
 N-PSDB; ABX12746.
 New bifunctional molecules comprising an antibody or its antigen-binding
 portion, and a targeting agent, useful for e.g. gene therapy, or for
 promoting Adenoviral vector-mediated gene delivery to cells lacking av
 integrins.
 Claim 10; Page 35-36; 49pp; English.
 The present invention relates to a bifunctional molecule comprising an
 antibody or its antigen-binding portion, and a targeting agent. The
 antibody specifically binds to an antigen in a protein that binds to
 alpha integrin, and the targeting agent specifically binds to a cell
 surface protein that activates the phosphatidylinositol-3-OH kinase
 (PI3K) signalling pathway. The bifunctional molecules are useful for
 targeted gene therapy using targeting delivery vectors, such as
 adenoviral gene delivery particles. The bifunctional molecules are useful
 for treating viral infections, rheumatoid arthritis, cancers, ophthalmic
 cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
 disorders, hyperproliferative disorders, and hormonal disorders. The
 present sequence represents a portion of the mouse DAV-1 heavy chain that
 is used for a fusion protein bifunctional antibody
 Sequence 438 AA;
 Query Match 29.0%; Score 1022.5; DB 5; Length 438;
 Best Local Similarity 37.4%; Pred. No. 9.3e-53;
 Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;
 Qy 1 EVLQQSGPDLVAPGSAVKISCKASGYFTGYMHWKQSPGKLEIGRNPNGVTLY 60
 Db 20 EVLQQSGPDLVAPGSAVKISCKASGYFTGYMHWKQSPGKLEIGRNPNGVTLY 79
 Qy 61 NQFKSKATLTVDKSSNTAYMELRLTSDASAVVYCARSTMTNVMYDQGGTSTVSS 120
 Db 80 NQFKSKATLTVDKSSNTAYMELRLTSDASAVVYCARSTMTNVMYDQGGTSTVSS 132
 Qy 121 AKTTTPSVYPLAPGSAAGTNSMTLGLVKGYFPEPVTWNSGSLSSGVHTFPVAVLQSD 180
 Db 133 AKTTTPSVYPLAPGSAAGTNSMTLGLVKGYFPEPVTWNSGSLSSGVHTFPVAVLQSD 192
 Qy 181 LYTLSSSVTPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSENEKDLRKK 240
 Db 193 LYTLSSSVTPSTWSPSETVTCNVAHPASSTKVDKIVPRDCG----- 235
 Qy 241 SELQGTALGNLKIYVYNSKAITSSSEKSAQFLNTLLPKGPTGHPWYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 264
 Qy 301 ATSEYEGSSVDLYGAYYGOCAGGTNKTACMGVGTLLHNNRLTEKKVPINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
 Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIVF 411
 Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAFPAPIEK----- 343
 Qy 412 HSSEGSTVSYDLFDAQOQYPTDLLRIYRDNNTTISLSISLYLYTTSIWMQTPTSLV 471
 Db 344 -----TISK----- 348
 Qy 472 SAGDRVTITCKASQSVNSNDVAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 Qy 532 TISSVQAEADAAYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSEQLTSGGASVV 591

Db 349 -----KGRPKAQVYTIPTPPKEQMAKDKVSLT 375

QY 592 CFLNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHNSYT 651

Db 376 CMTIDFFPEDITVQWNGOFAEN-YKNTQPIMDT-DGSYFVYSKLVQKSNWEAGNTFI 433

QY 652 CEATH 656

Db 434 CSVLH 438

RESULT 37

AAV39452

ID AAV39452 standard; protein; 206 AA.

XX AAV39452;

XX 19-NOV-1999 (first entry)

XX Antibody ABX-CBL light chain sequence.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Disclosure; Page 58; 245pp; English.

XX This sequence represents the light chain of the antibody ABX-CXL. The

CC invention relates to a monoclonal antibody (Mab) with an isotype that

CC fixes complement and a variable region that binds to the epitope on CD147

CC bound by the IgM Mab ABX-CBL, providing that the antibody is not CBL1.

CC The Mab can selectively kill activated T-cells, activated B-cells or

CC resting or activated monocytes. The products and methods can be used for

CC treating diseases involving activated T-cells or B-cells or monocytes,

CC e.g. graft versus host disease (GVHD), organ transplant rejection

CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.

CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),

CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.

CC arthritis)

XX Sequence 206 AA;

SQ

Query Match 28.9%; Score 1018; DB 2; Length 206;

Best Local Similarity 95.1%; Pred. No. 7e-53;

Matches 193; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 469 LLVSGADRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFGSGYGTD 528

Db 3 LLVSGADRVTITCKASQSVNDVAVYQKPGQSPKLLIYASNYTGVDPDRFTGSGYGTD 62

QY 529 FTLTISVQAEADAVYFCQDYSSPYTFGGGTGKLEIKRADAAPTIVSIPPPSSEQLTSGGA 589

Db 63 FTFITISTVQAEADAVYFCQDYSSPYTFGGGTGKLEIKRADAAPTIVSIPPPSSEQLTSGGA 122

QY 589 SVVCFNNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHN 648

Db 123 SVVCFNNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHN 182

QY 649 SYTCEATHKTSTSPIVKSFNENE 671

Db 183 SYTCEATHKTSTSPIVKSFNENE 205

RESULT 38

AA66758

ID AAR66758 standard; protein; 465 AA.

XX AAR66758;

XX 01-SEP-1995 (first entry)

XX Anti-tobacco mosaic virus monoclonal Ab heavy chain.

DE Tobacco mosaic virus; TMV; monoclonal antibody; heavy chain;

XX Tobacco-resistant plants; biofarming.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= leader

FT Peptide 20..465

FT /label= mat_peptide

FT Domain 20..128

FT /note= "variable heavy domain"

FT Domain 129..141

FT /note= "J heavy 4 domain"

FT Domain 142..465

FT /note= "constant heavy domain"

XX JP06319396-A.

XX 22-NOV-1994.

XX 07-MAY-1993; 93JP-00131208.

XX 07-MAY-1993; 93JP-00131208.

XX (NISE) JAPAN TOBACCO INC.

PA (KURS) KURARAY CO LTD.

XX WPI; 1995-040220/06.

XX N-PSDB; AAQ79930.

XX Transformed plant producing animal-derived anti-virus antibody - esp.

PT tobacco plants producing anti-tobacco mosaic virus monoclonal antibody.

XX Example 2; Page 14-15; 26pp; Japanese.

XX AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy

CC chains of an animal derived anti-tobacco mosaic virus (TMV) monoclonal

CC antibody. The cDNAs were incorporated into a TI plasmid vector, which was

CC incorporated into A. tumefaciens. The resultant plant expression vector

CC was used to transform tobacco plants, making them TMV resistant, the

CC plants could also be biofarmed for the prodn. of anti-virus antibodies

XX Sequence 465 AA;

SQ

Query Match 28.9%; Score 1018; DB 2; Length 465;

Best Local Similarity 36.3%; Pred. No. 1.9e-52;

Matches 244; Conservative 60; Mismatches 109; Indels 260; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEIGRINPNNGVTLY 60

Db 20 QVQLQSGAEELARPGASVKLSCKASGYTFTSYVMQWVKORPGQLEWIGAIYPSGNGDTRY 79
QY 61 NQKFKDKATLTVDKSSATTAYMELRSITSDSAVYYCAR--STMITNYVMYDYGQGTSTVT 118
Db 80 TQKFKGKATLTADKSSASTAYMQLSALSDSAVYYCAREGGYSWSDYANDYWGQGTSTVT 139
QY 119 SSAKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQ 178
Db 140 SSAKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQ 199
QY 179 SDLYTLSSSVTPSSVPSETVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLR 238
Db 200 SDLYTLSSSVTPSSVPSETVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLR 244
QY 239 KXSELOGTALGNLKIYIYNSKAITSSKASDAQFLNTLLFKGFFTGHPWYNDLLVDLGS 298
Db 245 --CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 273
QY 299 TAATSEYSGSDLYGAIYGYOCAGCTPNKTCMGVGLHDNNRLTEKKYPINLWIDG 358
Db 274 -----TP-KVTCVVVDIS-----KDDPEVQFQSFVD- 298
QY 359 KQTVPIDVKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVRQGLI 409
Db 299 ---DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKFKCRVNSAAFPAIEK-- 352
QY 410 VFHSSEGSVVDLFDPAQGYDPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSL 469
Db 353 -----TISKT----- 357
QY 470 LVSAGDRVITTCASQSNVDVAWYQKPKGPKLLISYTSRYAGVPDRFSGSGVGTDF 529
Db 358 ----- 357
QY 530 TLTISVQAEADAAYFCQDYNSPPTFGGKLEIKRADAAPTVSIFPSSBQLSGGAS 589
Db 358 -----KGRPKAPQVYTIPTPKQMAKDKVS 382
QY 590 VVCFLLNFKDINVKWKIDGSEKON-----GVLSNWTQDSDKSTYSMSSTLTITKDEY 644
Db 383 LTCMITDFPFDITVQWNGQPAENYKNTQPIMNT-----NGSIFYSKLNKVNKSNW 435
QY 645 ERHNSYTCRATHK 657
Db 436 EAGNTFTCSVLHE 448

RESULT 39
AAW85692
ID AAW85692 standard; protein; 711 AA.
AC AAW85692;
XX
XX
DT 12-AUG-1999 (first entry)
XX
DE
XX
XX
KW Antibody; humanised; variable region; heavy chain; light chain;
KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW multivalent; ruminant.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Domain /label= Mouse_D9D10_light_chain_signal_peptide
FT 21..137
FT /note= "Humanised heavy chain variable domain of D9D10"
FT 138..467
FT /note= "human IgG1 heavy chain constant domain"
FT Misc-difference 468

FT Region /note= "Leu added by cloning strategy"
FT 469..472
FT /label= Gly(3)ser_linker
FT 473..711
FT /label= Humanised_D9D10_ScFv
XX
PN WO9909055-A2.
XX
PD 25-FEB-1999.
XX
XX 14-AUG-1998; 98WO-EP005165.
XX
XX 18-AUG-1997; 97EP-00870122.
XX 18-JUN-1998; 98EP-00870139.
XX (INNO-) INNOGENETICS NV.
XX
XX Buyse M, Sablon E;
XX WPI; 1999-180969/15.
XX N-P8DB; AAW85692.
XX
PT New engineered antibodies which bind and neutralise interferon-gamma -
PT useful for prevention and treatment of septic shock, cachexia, immune
PT diseases and skin disorders.
XX
PS Disclosure; Fig 20; 134pp; English.
XX
XX New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
CC be used as a medicant, for preventing or treating septic shock, cachexia,
CC immune diseases including multiple sclerosis and Crohn's disease and skin
CC disorders including bullous, inflammatory and neoplastic dermatoses. The
CC antibody is selected from a single chain antibody (scFv), a chimeric
CC monoclonal mouse anti-IFN gamma antibody p9D10; a multivalent antibody;
CC or a ruminant antibody. The antibodies are also useful for determining
XX IFN gamma levels in a sample
SQ Sequence 711 AA;

Query Match 27.8%; Score 980.5; DB 2; Length 711;
Best Local Similarity 35.3%; Pred. No. 5.2e-50;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;

QY 1 EVQLQSGSDPLVKGASVKISCKASGYFTGYVMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKKEGASVKISCKASGYFTDYGVMWVKQAPGQGLKRWGINTYTGESTY 80
QY 61 NQKFKDKATLTVDKSSATTAYMELRSITSDSAVYYCARSTMITNYVMYDYGQGTSTVTSS 120
Db 81 VDDEKGRFVPSLDTSVSAAYLQISLKAEDTATYFCARRGF---YAMDYNGQGTSTVTSS 137
QY 121 AKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQSD 180
Db 138 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYPEPVTVSWNSGALTSPVHTTFAVLQSS 197
QY 181 -LYTLSSSVTPSSVPSETVTCNVAHPASSTKVDKIVPRDS-----GG 224
Db 198 GLYSLSSTVTPSSSLGTQYICNVNHPKNTKVDKEPKSCDKTHTCPCPAPELGG 257
QY 225 PS-----EKSEBI-----NKDLRKKSELOGTALGNLK---QIYYN 258
Db 258 PSVFLFPFKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPISEKTISKAKGQPREPOVYITLPPREE 377
QY 272 FLTN-----TLFKGFTTCHPWFYNDLLVDLQSTA-ATSEYEGSS--VDLYGAIYGYOCAGG 324
Db 378 MTKNQVSLTCLVKGYF-----SDIAVEWESNGPENNYKTTPEVLDSGDSFFLYSKL-- 430
QY 325 TPNTKATCMYGGV----TLHD--NNRLETEK-----KVINLWIDGKQTVTPIDK 368

Db 431 TVDKSRWQGNVFCVSNVHEALHNHYTKSLSLSPGKLGGSQVQLVQSGSELKPKGASV 490
 Qy 369 KTSKKEVTVQELDLQARHLYHGKGLNNSDFGKVORGLIVHSSSGSTVSDLPDAQ 428
 Db 491 KISK-----ASGYTPTDGMVWVKQAPQGGLKMGWINTVGTSTYVD--DFKG 538
 Qy 429 QYPTDLLRIYDNTTISTSLIS-----LVLVT----- 457
 Db 539 RF-----VFLDTSVAAYLQISLKAEDTATFCARRGFYADYWGQGTTVTVSSGG 592
 Qy 458 -----TSIVMTQPTSLNLSAGDRVTITCKASQSVNSDVAWYQKPGQSPKLLI 506
 Db 593 GSGGGSGGGSDIVLTQSPATMSAPGERVTLTCSASSISY-MFWYHQRPGQSPRELI 651
 Qy 507 SYTSRVAGVPDRSGSGYGHDFLTITSSVQAEAAVYFCQDDVNSPPTFGGKLEIKR 566
 Db 652 YDTNLSAGVPAFSGSGSGTSLTISRMEPEDFATYFCHQSSSYPTFTGQGTLEIKR 711

RESULT 40
 ADE06766
 ID ADE06766 standard; protein; 223 AA.

XX ADE06766;

XX 29-JAN-2004 (first entry)

DE D18 heavy chain protein SEQ ID NO:36.

XX hybrid polypeptide; protein aggregation; prion polypeptide;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; cyostatic; nephrotropic; cardiant;
 KW antiinflammatory; antiarteriosclerotic; gene therapy;
 KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
 KW Alzheimer's disease; Type II diabetes; Huntington's disease;
 KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
 KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
 KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
 KW familial amyloidotic polyneuropathy; medullary carcinoma;
 KW chronic renal failure; congestive heart failure; chronic inflammation;
 KW atherosclerosis.

OS Synthetic.

XX WO2003085086-A2.

PD 16-OCT-2003.

XX 08-APR-2003; 2003WO-US010856.

XX 09-APR-2002; 2002US-0371610P.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Williamson RA, Moroncini G;

XX WPI, 2003-877028/81.

DR N-PSDB; ADE06765.

XX New motif-grafted hybrid polypeptides binding to the infectious form of a
 PT prion, useful for diagnosing or treating diseases of protein aggregation
 PT or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
 PT diabetes.

XX Disclosure; SEQ ID NO 36; 115pp; English.

XX The present invention describes a hybrid polypeptide (I) comprising: (a)
 CC a polypeptide motif containing a sufficient number of contiguous amino
 CC acid residues from a polypeptide associated with a disease of protein
 CC aggregation or conformation to bind an aggregating form of the
 CC polypeptide or to a disease-associate conformer of the polypeptide; and
 CC (b) an additional amino acids from a polypeptide other than the

CC polypeptide from which the motif is derived, where the resulting hybrid
 CC polypeptide binds with greater affinity to a disease causing or
 CC infectious conformer of the polypeptide that is the source of the
 CC polypeptide motif compared to a benign form of the polypeptide. Also
 CC described: (1) a nucleic acid molecule encoding (1); (2) a vector
 CC comprising the nucleic acid molecule; (3) a cell comprising the vector;
 CC (4) detecting an isoform or a PRSC form of a prion polypeptide or a
 CC polypeptide associated with a disease of protein aggregation, in a sample
 CC; (5) a solid support comprising a plurality of polypeptides described
 CC above; (6) detecting cells that contain a protein conformer associated
 CC with a disease of protein aggregation; (7) preparing a hybrid molecule
 CC that specifically interacts with one conformer of a protein involved in
 CC the disease mentioned above; and (8) an anti-idiotype antibody that
 CC specifically binds to an infectious form of a prion protein. (1) has
 CC neuroprotective, nontropic, antidiabetic, anticonvulsant,
 CC cerebroprotective, antiparkinsonian, cyostatic, nephrotropic, cardiant,
 CC antiinflammatory and antiarteriosclerotic activities, and can be used in
 CC gene therapy. The composition and methods of the present invention can be
 CC used in diagnosing or treating diseases of protein aggregation or
 CC conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine
 CC spongiform encephalopathy, Alzheimer's disease, Type II diabetes,
 CC Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis
 CC associated with chronic inflammatory disease, hereditary systemic
 CC amyloidosis associated with autosomal dominant inheritance of variant
 CC transthyretin gene, amyotrophic lateral sclerosis, Pick's disease,
 CC Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma
 CC cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma
 CC of thyroid, chronic renal failure, congestive heart failure, senile
 CC cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis
 CC or familial amyloidosis. The present sequence is used in the
 CC exemplification of the present invention.

XX Sequence 223 AA;

XX Query Match 27.8%; Score 979.5; DB 7; Length 223;

XX Best Local Similarity 87.4%; Pred. NO. 1.5e-50;

XX Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;

Qy 1 EVQ-LQSGPDLVKPGASVKISKASGYSTFYGMHWKQSPGKLEWIGRINPNNGVTL 59

Db 3 EVCLLEQSGPELVKPGSSVKISKASRYTFDINDMWKQHGKRLWIGRIYPTNTGVIG 62

Qy 60 YNQKFKRATLTVDKSSTTAYMELRSLTSEDSAVYICARSTMITNYMVDYWGQGTSTVTS 119

Db 63 YNQRFKRATLTVDKSSSTAYMELRSLTSEDSAVYICAG---FYGMVDYWGQGTSTVTS 118

Qy 120 SAKTTPPSVYPLAPGSAQTNSMTLGLVKGYFPPEPTVTWNSSLSGGVHTFPVAVLQS 179

Db 119 SAKTTPPSVYPLAPGSAQTNSMTLGLVKGYFPPEPTVTWNSSLSGGVHTFPVAVLQY 178

Qy 180 DLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 221

Db 179 DLYTWSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 220

RESULT 41

XX AAY55081

XX ID AAY55081 standard; protein; 626 AA.

XX AC AAY55081;

XX DT 25-FEB-2000 (first entry)

XX DE Single chain Fv protein sequence sHPM1-kappa-BvGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; scfv.

OS Synthetic.

XX WO9960113-A1.

CC treat cancer, and may also used as a gene delivery system for introducing
CC at least 1 gene encoding a rTP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage

XX	SQ	Sequence 243 AA;	
		Query Match	27.6%; Score 972.5; DB 2; Length 243;
		Best Local Similarity	40.1%; Pred. No. 4.3e-50;
		Matches 227; Conservative	3; Mismatches 13; Indels 323; Gaps 5;
QY	1	EVQLQQSGPDLVKGASVKISKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTL	60
DB	1	EVQLQQSGPDLVKGASVKISKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTL	60
QY	61	NOKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQTSVTSS	120
DB	61	NOKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQTSVTSS	119
QY	121	AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFP	180
DB	120	-----	119
QY	181	LYTLSSSVTPSSWPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK	240
DB	120	-----	122
QY	241	SELOQTALGNLKOIYYNNSKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVGLSTA	300
DB	123	-----	122
QY	301	ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINLWDGKQ	360
DB	123	-----	132
QY	361	TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS	420
DB	133	-----	134
QY	421	YDLFDAQQYPTLLRIYRDNNTTISLSLSLYLTTSIVMTQPTSLSLVSAGDRVTIT	480
DB	135	-----	157
QY	481	CKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDRSGSGYGTDTLTITSSVQAE	540
DB	158	CKASQSVNDVAVYQKQPGSKLLISYTSRYAGVDPDRFGSGYGTDTLTITSSVQAE	217
QY	541	AAVYFCQDYNSPPTFGGKTKLEIKR	566
DB	218	LAVYFCQDYNSPPTFGGKTKLEIKR	243
		RESULT 43	
ID	AA42294		
XX	AA42294	standard; protein; 243 AA.	
AC	AA42294;		
XX	AA42294;		
DT	06-DEC-1999	(first entry)	
DE	Anti-5T4 secreted single chain antibody Fv fragment.		
KW	Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;		
KW	nucleus.		
OS	Homo sapiens.		
OS	Synthetic.		
PN	WO9945127-A2.		
XX	10-SEP-1999.		
PD	05-MAR-1999;	99WO-GB000674.	
PF			
XX			

PR 06-MAR-1998; 99GB-00004841.
PR 19-AUG-1998; 99GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous X;
XX
XX WPI; 1999-551046/46.
DR N-PSDB; AAZ19786.
XX
XX New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors.
PT
PS Example 9; Fig 3; 187pp; English.
XX

CC This sequence represents an example of a secreted single chain antibody
CC Fv fragment (in this case, directed against the 5T4 antigen), which is
CC involved in transcellular localisation. A secreted single chain antibody
CC Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives
CC such as anchorless P450R (AA42287) or Fv fragment (AA42288). This
CC enables the fusion protein to be delivered to other cells where it is
CC then transported to the nucleus. Many drugs' sites of action are in the
CC nucleus, rather than the cytoplasm, where P450R normally functions. P450R
CC or its derivatives can be used to activate prodrugs to their active form
CC via reduction. Administration of a prodrug is useful where the active
CC drug may be metabolised before it reaches its site of action or where the
CC active drug is cytotoxic, e.g., anticancer drugs. Targeted delivery of
CC such prodrug activators allows a reduction in dose of the prodrug, and
CC thus of systemic side-effects. P450R derivative fusion proteins, or
CC vectors that express them, are specifically used to treat tumours,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g., cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, ischaemia or
CC hypoglycemia, or to deliver antibiotics, antiviral agents, anaesthetics,
CC anaesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents

XX	SQ	Sequence 243 AA;	
		Query Match	27.6%; Score 972.5; DB 2; Length 243;
		Best Local Similarity	40.1%; Pred. No. 4.3e-50;
		Matches 227; Conservative	3; Mismatches 13; Indels 323; Gaps 5;
QY	1	EVQLQQSGPDLVKGASVKISKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTL	60
DB	1	EVQLQQSGPDLVKGASVKISKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTL	60
QY	61	NOKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQTSVTSS	120
DB	61	NOKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQTSVTSS	119
QY	121	AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFP	180
DB	120	-----	119
QY	181	LYTLSSSVTPSSWPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK	240
DB	120	-----	122
QY	241	SELOQTALGNLKOIYYNNSKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVGLSTA	300
DB	123	-----	122
QY	301	ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINLWDGKQ	360
DB	123	-----	132
QY	361	TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS	420
DB	133	-----	134

QY 421 YDLFDAQQGYPTLLRIYRDNTTISTSLISLYYTSIVMTQTPTLLVSAGDRVTIT 480
 Db 135 -----SSIVMTQTPTLLVSAGDRVTIT 157
 QY 481 CKASQSVSNDAVYQKQPGSKLLISYTSRYAGVDPDFSGGYGTPTLTISVQAE 540
 Db 158 CKASQSVSNDAVYQKQPGSKLLISYTSRYAGVDPDFSGGYGTPTLTISVQAE 217
 QY 541 AAVYFCQDYNPPTFGGKTLEIKR 566
 Db 218 LAVYFCQDYNPPTFGGKTLEIKR 243

RESULT 44

AAI27407
 ID AAY27407 standard; protein; 243 AA.

AC AAY27407;

DT 23-NOV-1999 (first entry)

DE 5T4 scFv antibody signal peptide.

QY Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
 Db Prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
 QY inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
 Db rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
 QY 5T4 scFv.

OS Unidentified.

PN WO9945126-A2.

PD 10-SEP-1999.

PF 05-MAR-1999; 99WO-GB000672.

PR 06-MAR-1998; 98GB-00004841.

PR 19-AUG-1998; 98GB-00018103.

PR 29-JAN-1999; 99GB-00002081.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;

PI Mitrophanous K;

PI WPI; 1999-540852/45.

PI N-PSDB; AA207810.

PS New prodrug activating agent targeted to selected cells or tissues,

PS particularly hypoxic cells, for treating e.g. tumors or inflammation.

PS Example 9; Fig 3F; 149pp; English.

CC The invention provides a new prodrug activating agent that comprises: (i)
 CC a localization domain (LD; other than a tumor-selective antibody) and a
 CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
 CC a cytochrome P450 and under control of at least one constitutive or
 CC inducible expression control sequence or (iii) a modified hematopoietic
 CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
 CC under control of elements as in (ii). The prodrug activating agent or
 CC vectors that express them, are specifically used to treat tumors,
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be
 CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
 CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
 CC locations or by delivering it to neighboring cells (bystander effect),
 CC and allow a reduction in dose of prodrug, and thus of systemic side-
 CC effects. Nucleic acids encoding the agent may be expressed selectively in
 CC hypoxic cells. The present sequence represents the single chain variable
 CC antibody fragment against the tumor antigen 5T4 (5T4 scFv). 5T4 scFv is

CC used in the construction of a fusion protein comprising 5T4 scFv and a
 CC human P450 reductase derivative alp450R

SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 2; Length 243;
 Best Local Similarity 40.1%; Pred. No. 4.3e-50;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60

QY 61 NQKFKDKATLTVDKSTTAYMELRLTSEDSAVYICARSTMITNYVMDYVGQGTSTVSS 120

Db 61 NQKFKDKATLTVDKSTTAYMELRLTSEDSAVYICARSTMITNYVMDYVGQGTSTVSS- 119

QY 121 AKTTPPSVYPLAPGSAAGTNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180

Db 120 ----- 119

QY 181 LYTLSSTVTPSPWPSETVTQNVAPASSTKVDKKIIVPRDSGPPSEKSEINEKDLRKK 240

Db 120 -----SGG----- 122

QY 241 SELQGTALGNLKOIYYVNSKAITSSSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300

Db 123 ----- 122

QY 301 ATSEYEGSSVDLYGAYYGYCAGGTPTNKTACMYGGVTLHDNNRLTBKKVPINLWIDGKQ 360

Db 123 -----GGSGGGGT-----GG----- 132

QY 361 TTVPIDKVKTSKEVTQVELDLOARHYLHGKFLGYNLSDFGKQVQRGLIIVHSEGSTVS 420

Db 133 -----GG----- 134

QY 421 YDLFDAQQGYPTLLRIYRDNTTISTSLISLYYTSIVMTQTPTLLVSAGDRVTIT 480

Db 135 -----SSIVMTQTPTLLVSAGDRVTIT 157

QY 481 CKASQSVSNDAVYQKQPGSKLLISYTSRYAGVDPDFSGGYGTPTLTISVQAE 540

Db 158 CKASQSVSNDAVYQKQPGSKLLISYTSRYAGVDPDFSGGYGTPTLTISVQAE 217

QY 541 AAVYFCQDYNPPTFGGKTLEIKR 566

Db 218 LAVYFCQDYNPPTFGGKTLEIKR 243

RESULT 45

AAB83835

ID AAB83835 standard; protein; 243 AA.

AC AAB83835;

DT 23-JUL-2001 (first entry)

DE Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.

QY Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 Db hypersensitivity; autoimmune disease; central nervous system disorder;
 QY Parkinson's disease; periodontal disease; cardiopulmonary disease;
 Db cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 QY Helicobacter-related disease; immune disorder.

OS Synthetic.

OS Mus sp.

PH Key Location/Qualifiers

FT Misc-difference 169

FT /note= "Ala encoded by GDT"

PN W0200136486-A2.
 XX 25-MAY-2001.
 PD 13-NOV-2000; 2000WO-GB004317.
 XX 18-NOV-1999; 99WO-GB003859.
 PR 15-FEB-2000; 2000GB-00003527.
 PR 02-MAR-2000; 2000GB-00005071.
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 PI Myers KA;
 XX WPI: 2001-343805/36.
 DR N-PSDB; AAF89729.
 XX Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.
 XX
 PS Claim 3; Fig 1; 118pp; English.
 XX The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, pericardial diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC represents a 574 ScFv of the invention. The antibody comprises the VH and
 CC VL regions from murine 574 monoclonal antibody, joined by a linker
 CC sequence
 XX
 SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 4; Length 243;
 Best Local Similarity 40.1%; Pred. No. 4.3e-50;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
 QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTL 60
 DB 1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTL 60
 QY 61 NQKPKDKATLVDSSTAYMELSLTSEDSAVYVCARSTMTNYMDYWGQTSVTSS 120
 DB 61 NQKPKDKATLVDSSTAYMELSLTSEDSAVYVCARSTMTNYMDYWGQTSVTSS- 119
 QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYPPEPTVTWNSGSLSGGVHTFPVLQSD 180
 DB 120 ----- 119
 QY 181 LYTSSSVTPSPSTWSPSTVTCNVNAPASSTKVDKIVPRDSGDPSEKSEINEKLRKK 240
 DB 120 -----SGG----- 122
 QY 241 SELQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 DB 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 DB 123 -----GGSGGGGT----- 132
 QY 361 TTVPIDKVKTSKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQRGVLIVFHSSEGSTVS 420
 DB 133 -----GG----- 134

QY 421 YDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLTTSIVMTOTPTPTLLVSAGDRVIT 480
 DB 135 -----SSIVMTOTPTPTLLVSAGDRVIT 157
 QY 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPFRFGSGYGTDTFTTISVQAE 540
 DB 158 CKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPFRFGSGYGTDTFTTISVQAE 217
 QY 541 AAVYFCQDYNPPTFGGTTKLEIKR 566
 DB 218 LAVYFCQDYNPPTFGGTTKLEIKR 243
 RESULT 46
 AAY44176
 ID AAY44176 standard; protein; 214 AA.
 XX
 AC AAY44176;
 XX DT 01-FEB-2000 (first entry)
 XX MAb Fab13B5 heavy chain protein sequence.
 DE
 XX Peptide ligand; affinity; p24; human immune deficiency virus-1; HIV-1;
 KW light chain; heavy chain; Fab; monoclonal antibody; hypervariable region;
 KW infection.
 XX Mus sp.
 XX FR2777285-A1.
 XX 15-OCT-1999.
 PD
 XX 10-APR-1998; 98FR-00004876.
 PF
 XX 10-APR-1998; 98FR-00004876.
 PR
 XX (INMR) BIO MERIEUX.
 PA
 XX Novelli RA, Monaco S, Piga N, Berthet C, Mallet F, Cusack S;
 PI Chassaing V;
 PI WPI: 1999-593428/51.
 DR N-PSDB; AA228805.
 DR
 XX New peptide ligand specific for p24 of human immune deficiency virus
 PT contains hypervariable regions of antibody 13B5, used for diagnosing HIV
 PT infection.
 PT
 XX Claim 2; Page 20-21; 27pp; French.
 PS
 XX The invention relates to a peptide ligand with specific affinity for the
 CC p24 protein of human immune deficiency virus-1 (HIV-1) comprising at
 CC least one peptide strand corresponding to the N-terminal region of the
 CC light and/or heavy chain of the Fab fragment of monoclonal antibody 13B5
 CC in which: (i) the light chain includes three hypervariable regions (HVR)
 CC at amino acid (aa) positions 24-33, 49-55 and 88-95 of AAY44175; and (ii)
 CC the heavy chain includes three HVR at aa positions 26-35, 49-65 and 99-
 CC 109 of this sequence. The peptide ligands are reagents for detecting p24
 CC (by standard immunoassays) in biological samples, specifically for
 CC diagnosis of HIV-1 infection or can be used to treat HIV-1 infections
 XX
 SQ Sequence 214 AA;

Query Match 27.5%; Score 970; DB 2; Length 214;
 Best Local Similarity 85.0%; Pred. No. 5.2e-50;
 Matches 182; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTL 60
 DB 1 EVQLQQSGAELARPASVKMSCKASGYSFTGYMHVWVQSPGKLEWIGRINPSSGSYNY 60

Qy	61	NQKFKDKATLLTVDKSTTAYWELASLISEDAAVYICARSTMIINYYMDYWGQGTSTVWS	120
Db	61	NQKFKDKATLLTVDKSSSTAYWQLSSLTSEDAAVYICSRPVRLGYNFDYWGQGTSTVWS	120
Qy	121	AKTTPSVVPLAPGSAAQNTSMVTLGCLVKGYPPEPVTVTWNGSSLSGGVHTFPAPVQLSD	180
Db	121	AKTTPSVVPLAPGSAAQNTSMVTLGCLVKGYPPEPVTVTWNGSSLSGGVHTFPAPVQLSD	180
Qy	181	LYTLSSSVTPSPSTPSPSTVTCNVAHPASSSTKVD	214
Db	181	LYTLSSSVTPSPSTPSPSTVTCNVAHPASSSTKVD	214

RESULT	47
AAW86004	
ID	AAW86004 standard; protein; 488 AA.
XX	
XX	
AAW86004;	
XX	
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Human B7-1.5T4.1 protein fusion, specific for human 5T4.
XX	
XX	
KW	Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW	monoclonal antibody; single chain antibody; mouse; human; B7-1;
KW	co-stimulatory molecule.

DE Human B7-1.5T4.1 protein fusion, specific for human 5T4.

Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
KW
monoclonal antibody; single chain antibody; mouse; human; B7-1;
KW
co-stimulatory molecule.
KW

OS	Mus sp.
OS	Homo sapiens.
OS	Synthetic.

XX PN WO9855607-A2.

PD 10-DEC-1998.

PF 04-JUN-1998;

PR 04-JUN-1997; 97GB-00011579.

PR 04-JUL-1997; 97GB-00014230.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.

PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;

DR WPI; 1999-059910/05.

XX

PT contains a desired nucleotide sequence and/or protein which recognises PT tumours, and is used as a gene delivery system to treat cancer.

PS Example 5; Fig 2; 82pp; English.

CC This is the amino acid sequence of B7-1.574.1, a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human co-
CC stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 574 monoclonal antibody. B7-1.574.1
CC (cDNA (see AAW80292) can be inserted into vector pCI to allow expression
CC of the fusion protein in mammalian cells. The trophoblast cell surface
CC antigen defined by 574 is expressed at high levels on the cells of a wide
CC variety of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP) and
CC optionally a nucleotide sequence of interest (NOI) which encodes a
CC protein of interest (POI), the vector being capable of delivering the NOI
CC and/or POI to the tumour recognised by the TIP. Delivery can be in vivo
CC or ex vivo. The vector is used to treat cancer, and may also used as a
CC gene delivery system for introducing at least 1 gene encoding a TIP
CC (preferably a tumour binding protein) into a haematopoietic cell lineage.
CC B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells

CC
T-cells

Query Match	27.5%	Score 967.5	DB 2	Length 488
Best local Similarity	40.0%	Pred. No. 2e-49		
Matches 226	Conservative	3	Mismatches 13	Indels 323
				Gaps 5
Qy	1	EVQLQSGGPDLVKPGASVKISCKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY	60	
Db	247	EVQLQSGGPDLVKPGASVKISCKASGYSFTGYMHVWKQSHGKLEWIGRINPNNGVTLY	306	
Qy	61	NQPKDKAIIITVDKSTTAYMELRSLTSEDASVYICARSTMITNYMDYMGQGTSTVVS	120	
Db	307	NQPKDKAIIITVDKSTTAYMELRSLTSEDASVYICARSTMITNYMDYMGQGTSTVVS	365	
Qy	121	AKITPPSVIPLAFGSAQAQTSMVTLGCLVKGYIPEPVTVTWNSGSLSSGVHPTPAVLQSD	180	
Db	366	-----	365	
Qy	181	LYTLSSVTVFSPSTWPSSETVTCNVHPASSTKVDKIIVRDSGSPSEKSEINEKD.RKK	240	
Db	366	-----SGG-----	368	
Qy	241	SELQGTALGNLKQIYYNYSKAITSSSEKSAQDFLTNTLLFKGFFTGCHWYNDLLVDLGSTA	300	
Db	369	-----	368	
Qy	301	ATSEYEGSSVDLYGAVYGYQACGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWDGKQ	360	
Db	369	-----GGSGGGGT-----GG-----	378	
Qy	361	TTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKQVQGLIVFHSSEGSTVS	420	
Db	379	-----GG-----	380	
Qy	421	YDLFDAQGGYDPTLLRIYRDNNTITSSLSLSLYLTTSIVMTQPTSLIVSAGDRVIT	480	
Db	381	-----SSIVMTQPTFLIVSAGDRVIT	403	
Qy	481	CKASQSVSNDVAMYQKPGGSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISVQAE	540	
Db	404	CKASQSVSNDVAMYQKPGGSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISVQAE	463	
Qy	541	AAVYFCQDYNSPPTFGGTTKLEIK	565	
Db	464	LAIVYFCQDYNSPPTFGGTTKLEIK	488	

RESULT 48

AAB83836
ID AAB83836 standard; protein; 488 AA.

AC AAB83836;

DT 23-JUL-2001 (first entry)

DE Amino acid sequence of a B7-1.5T4.1 fusion protein.

KW Single chain antibody; SCFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder.

OS Synthetic.

Homo sapiens.

PN WO200136486-A2.

PD 25-MAY-2001.

PF 13-NOV-2000; 2000WO-GB004317.

1

PR 18-NOV-1999; 99WO-GB003859.
 PR 15-FEB-2000; 2000GB-00003527.
 PR 02-MAR-2000; 2000GB-00005071.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 XX Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 PI Myers KA;
 XX
 XX WPI; 2001-343805/36.
 DR N-PSDB; AAF89730.
 XX
 PT Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.
 XX
 PS Claim 3; Fig 2; 118pp; English.
 XX
 CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC represents a B7-1.574.1 fusion protein. This comprises the N-terminus of
 CC the 574 ScFv is fused after amino acid 215 of human B7-1
 XX
 SQ Sequence 488 AA;
 Query Match 27.5%; Score 967.5; DB 4; Length 488;
 Best Local Similarity 40.0%; Pred. No. 2e-49;
 Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
 QY 1 EVOIQSGPDLVKPGASVKISCKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 247 EVOIQSGPDLVKPGASVKISCKASGYSFTGYNHWKQSPGKLEWIGRINPNNGVTLY 306
 QY 61 NQKFKDKATLVDSSTTAYMELSLTSEDSAVYICARSTMTINVMYDYGQSTVTVS 120
 DB 307 NQKFKDKATLVDSSTTAYMELSLTSEDSAVYICARSTMTINVMYDYGQSTVTVS 365
 QY 121 AKTTPSPVYPLAPGSAAGTNSMTVLGCLVKGYFPPEVTVTNWNSGSLSSGVTTPAVLQSD 180
 DB 366 ----- 365
 QY 181 LYTLSSTVTPSTWSPSETVTCNVAHPASTKVDKIVPRDSGGPSEKSEINEKDLRX 240
 DB 366 -----SGG----- 368
 QY 241 SELQGTALGNLKQIYYNSKAITSSSEKADQFLNTLLFKGFFTCGHPWYNDLLDLGSTA 300
 DB 369 ----- 368
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTCMGYGVTLHDNNRLTEBKVFINLWIDGKQ 360
 DB 369 -----GGSGGGT----- 378
 QY 361 TTVPLDKVTSKKEVTVOELDQARHYLHGKFLGYNLSDSGGKVGQRLIVHSSSEGTVS 420
 DB 379 ----- 380
 QY 421 YDLFDAQGYPDLLRIYRDNVTISSTLSLSLYLTTSIVMTOTPTSLVLSAGDRVTIT 480
 DB 381 -----SSIVMTOTPTSLVLSAGDRVTIT 403
 QY 481 CKASQSVNDVAVYQKPGQSPFTLLISYTSRYAGVPRFICSGYGTDTFTTISTLQAD 540
 DB 481 CKASQSVNDVAVYQKPGQSPFTLLISYTSRYAGVPRFICSGYGTDTFTTISTLQAD 540

DB 404 CKASQSVNDVAVYQKPGQSPFTLLISYTSRYAGVPRFICSGYGTDTFTTISTLQAD 463
 QY 541 AAVYFCQQDYNPPTFGGKLEIK 565
 DB 464 LAVYFCQQDYNPPTFGGKLEIK 488
 RESULT 49
 ABU07262
 ID ABU07262 standard; protein; 488 AA.
 XX
 XX AC ABU07262;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1963.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 OS Homo sapiens.
 XX
 XX WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1963; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 488 AA;
 Query Match 27.5%; Score 967.5; DB 6; Length 488;
 Best Local Similarity 40.0%; Pred. No. 2e-49;

QY 541 AAVYFCQDYNPPTFGGTTKLEIK 565
 DB 464 LAVYFCQDYNPPTFGGTTKLEIK 488

RESULT 51
 ABP96772
 ID ABP96772 standard; protein; 209 AA.

AC ABP96772;

DT 05-JUN-2003 (first entry)

DE TSH receptor antibody 3C7 heavy chain amino acid sequence.

KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.

OS Synthetic.

XX WO2003018632-A2.

XX PD 06-MAR-2003.

XX PF 21-AUG-2002; 2002WO-GB003831.

XX PR 23-AUG-2001; 2001GB-00020649.

XX PR 01-JUL-2002; 2002GB-00015212.

XX PA (RSRR-) RSR LTD.

XX PI Smith BR, Furmaniak J, Sanders JF;

XX DR WPI; 2003-290051/28.

XX DR N-PSDB; ACC44927.

XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.

XX Claim 67; Fig 46; 196pp; English.

XX The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid tissue
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention

SQ Sequence 209 AA;

Query Match 27.4%; Score 966.5; DB 6; Length 209;
 Best Local Similarity 87.4%; Pred. No. 8.2e-50;
 Matches 187; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVQLQSGDPLVPGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLY 60
 DB 1 DVQLXSGDELVKPGASMKISKASGYSTGYTMNWKQSHGKNDLWIGLINPNYGGTSY 60

QY 61 NQKFYDKATLTVDKSTTAYMELRSITSEDSAVVYCARSTMTITNVMYMDYWGQGTSTVVS 120
 DB 61 DQKFKGATLTVDKSSSTAYMELLSITSEDSAVVYCARDGL-----MDYWGQGTSTVVS 115

QY 121 AKTTPPSVYPLAPGSAQAQTNSMTVLGCLVKGYFPEPTVTWNSGLSSGVHTFPAVLQSD 180
 DB 116 AKTTPPSVYPLAPGSAQAQTNSMTVLGCLVKGYFPEPTVTWNSGLSSGVHTFPAVLQSD 175

QY 181 LYTLLSSVTPSPSTWPSSETVTCNVAHPASSIKVD 214
 DB 176 LYTLLSSVTPSPSTWPSSETVTCNVAHPASKTKVD 209

RESULT 52

ABP96771

ID ABP96771 standard; protein; 209 AA.

AC ABP96771;

DT 05-JUN-2003 (first entry)

DE TSH receptor antibody 3C7 heavy chain amino acid sequence.

XX Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.

OS Synthetic.

XX WO2003018632-A2.

XX PD 06-MAR-2003.

XX PF 21-AUG-2002; 2002WO-GB003831.

XX PR 23-AUG-2001; 2001GB-00020649.

XX PR 01-JUL-2002; 2002GB-00015212.

XX PA (RSRR-) RSR LTD.

XX Smith BR, Furmaniak J, Sanders JF;

XX WPI; 2003-290051/28.

XX N-PSDB; ACC44926.

XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.

XX Claim 71; Fig 45; 196pp; English.

XX The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; (3) a binding partner for a TSH receptor, which is capable of

ID AAR40385 standard; protein, 225 AA.
 AC AAR40385;
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 08-FEB-1994 (first entry)
 XX Monoclonal antibody M(alpha)2-3 light-chain.
 XX anti-snake small neurotoxin antibody; kappa; light chain; immunoglobulin;
 KW bispecific bivalent antibody; cell-targeting; cytotoxic agent.
 XX Unidentified.
 XX Key Location/Qualifiers
 FH 1. 12
 FT Peptide /label= signal_peptide
 FT Region 13. 118
 FT /label= variable
 FT Region 119. 225
 FT /label= constant
 XX EP556111-AL.
 PN 18-AUG-1993.
 PD 09-FEB-1993; 93EP-00400323.
 XX 11-FEB-1992; 92EP-00001505.
 PR (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA Boulain J, Ducancel F, Gillet D, Menez A;
 PI WPI; 1993-260351/33.
 DR N-PSDB; AAQ48038.
 XX New immunoglobulin hybrid proteins - with immunoglobulin fragments linked
 FT to dimeric protein, for diagnostic or therapeutic use.
 XX Example 1; Fig 3B; 37pp; French.
 XX A fragment of the heavy chain (VH + CH1) from the anti-snake small
 CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from
 CC hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain
 CC fragment (VL + CL) was amplified from the same source using primers
 CC AAQ48041 and AAQ48042. The two amplified fragments were inserted into the
 CC same vector; the H-chain fragment was inserted (in-frame) between codons
 CC 6-7 of the phoA coding sequence and the L-chain fragment was inserted
 CC into a cassette which contained a phoA S-D sequence, a signal peptide and
 CC the first 6 codons of phoA. The cassette was positioned between the
 CC termination codon and the transcription termination sequence of phoA. The
 CC fusion construct is expected to encode a hybrid protein comprising two
 CC identical Ab-derived units. The invention also covers hybrid proteins
 CC containing two different Ab-derived units (i.e. to produce bispecific
 CC antibodies). When a toxic protein is used in place of phoA, the hybrid
 CC molecules can be used as cell-targeting therapeutic agents. (Updated on
 CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence-225 AA;
 SQ Query Match 27.3%; Score 961.5; DB 2; Length 225;
 Best Local Similarity 88.6%; Pred. No. 1.8e-49;
 Matches 194; Conservative 4; Mismatches 8; Indels 13; Gaps 5;
 QY 459 SIVMTQTPTSLVSGDRVTTCRASQSVNDVAVYKQPGQSKLLIS--YTSRYAGV 516
 DB 13 SIVMTQTPTKFLLSAGDRVTTCRASQSVNDVAVY--KPGQSPKLLIQYASRYTGV 70
 QY 517 PDRFSGSGVGTFTLTISVVAEDAAVYFCQDYSS-YTFGGGKLEIKRADAAPTVSIF 576

DB 71 PDRFTSGYGTFTTISTVQAEADLAVYFCQDYSS-YTFGGGKLEIKRADAAPTVSIF 129
 QY 577 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKDYSSMSST 636
 DB 130 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKDYSSMSST 189
 QY 637 LTLTKDEYERH-----NSVTCETHKTSPIVKSFNRE 671
 DB 190 LTL-----YERHTKDENSYTCETHKTSPIVKSFNRE 224
 RESULT 55
 AAW15932
 ID AAW15932 standard; protein, 212 AA.
 XX AAW15932;
 XX 09-DEC-1997 (first entry)
 DT Antibody 7G12 heavy chain variable region.
 DE catalytic antibody; enantioselective hydrolysis; hybridoma; ZAA7G12;
 XX ZAA3G2; ds.
 XX Mus.
 XX WO9629426-A1.
 PN 26-SEP-1996.
 PD 17-MAR-1995; 95WO-JP0000462.
 XX 17-MAR-1995; 95WO-JP0000462.
 XX (PROT-) PROTEIN ENG RES INST.
 PA Fujii I, Tanaka F, Kinoshita K;
 PI WPI; 1996-443199/44.
 DR N-PSDB; AAT67815.
 XX Catalytic antibody for enantioselective hydrolysis of amino acid ester(s)
 FT - also new hybridoma secreting the antibody.
 XX Disclosure; Page 31-32; 49pp; Japanese.
 XX The patent discloses new catalytic antibodies which hydrolyse amino acid
 CC esters enantioselectively. Preferably the esters are 4-nitro- benzyl
 CC esters and the esterified amino acids are amino-protected. Also disclosed
 CC are new hybridomas expressing the catalytic antibodies, especially
 CC ZAA7G12 (FERM BP-4947) and ZAA3G2 (FERM BP-4946). The antibodies are
 CC raised in mice using the compound p-nitrobenzyl [4-carboxy-1-
 CC (benzyloxy-carbonylamino)-butyl]phosphonate as haptens. They are used for
 CC efficient resolution of racemic amino acids with high optical
 CC selectivity, giving optically active amino acids useful for the
 CC production of optically active drugs and chiral separation agents. The
 CC present sequence represents the variable region of the heavy chain of
 CC antibody 7G12, produced by the hybridoma ZAA7G12
 XX Sequence 212 AA;
 SQ Query Match 27.3%; Score 950; DB 2; Length 212;
 Best Local Similarity 84.7%; Pred. No. 2e-49;
 Matches 183; Conservative 11; Mismatches 14; Indels 8; Gaps 1;
 QY 6 QSGPDLVKGASVKISCKASGYSFTGYMHWVKQSPGKLEWIGRINPNNGVTLYNQKFK 65
 DB 2 ESGTELAKEGASVKQSCASGYFTSYWIHWKQRPQGLEWIGYINFTDYTEVIQKFK 61
 QY 66 DKATLTVDKSSYATYWEIRLSLTSEDASVYICARSTMIINYVDWYGQSTSVTSVSAKTFP 125
 DB 62 DKATLTADKSSYATYWEIRLSLTSEDASVYICV-----MKDYWGQSTSVTSVSAKTFP 113

QY 126 PSVYPLAPGSAQTNSMTLGLVKGYPFPPVTVTNWSSGLSSGVHTFFAVLQSDLYTLS 185
 DB 114 PSVYPLAPGSAQTNSMTLGLVKGYPFPPVTVTNWSSGLSSGVHTFFAVLQSDLYTLS 173
 QY 186 SSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 221
 DB 174 SSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 209

RESULT 56
 AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX AAR13203;
 XX AC AAR13203;
 XX DT 15-OCT-1991 (first entry)
 XX DE Staphylococcal enterotoxin A.
 XX SE; cancer treatment; pyrogen; tumouricide.
 XX OS Staphylococcus aureus.
 XX PN WO9110680-A.
 XX PD 25-JUL-1991.
 XX PF 17-JAN-1990; 90US-00466577.
 XX PR 17-JAN-1990; 90US-00466577.
 XX PA (TERM/) Terman D S.
 XX PI Terman DS;
 XX DR WPI; 1991-237984/32.
 XX PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX PS Disclosure; Fig 1; 74pp; English.
 XX SE

Query Match 27.3%; Score 960; DB 2; Length 233;
 Best Local Similarity 77.3%; Pred. No. 2.3e-49;
 Matches 180; Conservative 21; Mismatches 32; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDRKKSELOGTALGNLKOIYYNSKAITSEKSAOFLNTLLFGFTG 285
 DB 1 SEKSEINEKDRKKSELOGTALGNLKOIYYNEKAKTENKESHQFLQHTLFLKGFPG 60
 QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 345
 DB 61 HSWYNDLLVDKSGKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
 QY 346 EEKVPINLWIDKQTVTDIKVTSKKEVTVOELDLQARHYLHGKFGYNSDSFGKQV 405
 DB 121 EEKVPINLWIDKQTVTDIKVTSKKEVTVOELDLQARHYLHGKFGYNSDSFGKQV 180
 QY 406 RGLIVPHSSEGSTVSVDLFDACQVPTLLIRYRDNNTTISSTLSLVLVTT 458
 DB 181 RGLIVPHSTEPSVNDLFDACQVNTLLIRYRDNNTTISSTLSLVLVTT 233

RESULT 57
 AAR75456
 ID AAR75456 standard; protein; 223 AA.
 XX AC AAR75456;
 XX DT 07-FEB-1996 (first entry)
 XX DE Mouse antibody FB3-2 heavy chain variable region protein sequence.
 XX KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
 KW antibody; immunotolerance; animal; variegated display library;
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
 KW familial hypercholesterolaemia; binding affinity.
 XX OS Mus musculus.
 XX PN WO9515982-A2.
 XX PD 15-JUN-1995.
 XX PF 08-DEC-1994; 94WO-US014106.
 XX PR 08-DEC-1993; 93US-00164022.
 XX PR 06-DEC-1994; 94US-00350400.
 XX PA (GENZ) GENZYME CORP.
 XX PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
 XX DR WPI; 1995-224291/29.
 XX DR N-PSDB; AAQ92500.
 XX PT Generating new antibodies specific for immunorecessive epitopes - by
 PT selection from variegated V gene library cloned from immunotolerance
 PT derived antibody repertoire, useful in diagnosis, purificn. and therapy,
 PT e.g. of cancer.
 XX PS Disclosure; Page 74-75; 109pp; English.
 XX SE

The sequence of the heavy chain variable region from the mouse antibody
 FB3-2. This sequence was isolated from a variegated display library (VDL)
 of variable regions derived from a repertoire of antibodies from an
 immunotolerised animal. The VDL is generated by PCR amplifying the
 variable regions from the antibody coding sequences using the primers
 AAQ74153-74. The variable regions, esp the complementarity determining
 regions (CDR; see AAR75462-93 for examples of CDRs) from the
 immunotolerant animals' antibodies are used to construct an antibody
 against a immunorecessive antigen e.g. a cell surface marker on a foetal,
 cancer or stem cell, which can differentiate between variant or related
 forms of the antigen. The antibodies generated can be used in the
 diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
 e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
 The method of production of the antibody allows rapid and sensitive
 isolation of antibodies that would be difficult to isolate by standard
 methods. The antibodies produced have greater binding affinity than those
 produced by combinatorial/hybridoma methods

Query Match 27.1%; Score 953.5; DB 2; Length 223;
 Best Local Similarity 83.0%; Pred. No. 5.3e-49;
 Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;
 QY 1 EVQLQQSGPDLVKGPGASVKISCKASGYSTGYNHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVQLQQSGPELMPGASVKISCKATGYTLSSYWLWVKQSPGHCLEWIGILFGSGSAHY 60
 QY 61 NQKFKDKATLTVDKSSATNWLRLSTSDSANTYCARSTMTNY--VMDYWGQGTSTVTV 118

PR 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PT WPT; 2003-201467/19.
 DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
 XX receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 XX Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX Sequence 233 AA;
 SQ
 Query Match 26.9%; Score 948; DB 6; Length 233;
 Best Local Similarity 76.4%; Pred. No. 1.2e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLQHILFKGFTD 60
 QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 345
 DB 61 HSWYNDLLVDFSDKIDVYKGGKVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 120
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 405
 DB 121 BEKKVPINLWIDGKQTTVPLETVTKTKNKNVTVOELDLQARRYLOEKYLNYSNDFDGVQ 180
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQYDPDILLRIYRDNNTTISSTLSISLYLTT 458
 DB 181 RGLIVFHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKNTINSENMHDIYLYTS 233
 RESULT 62
 AAU14104
 ID AAU14104 standard; peptide; 257 AA.
 XX AAU14104;
 XX
 XX 21-NOV-2001 (first entry)
 DE Peptide sequence from Staphylococcus aureus enterotoxin A.
 XX Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
 XX antiviral; HIV transmission.
 XX Staphylococcus aureus.
 XX WC200151673-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 05-JUL-2000; 2000WO-US035727.
 XX
 PR 09-JUL-1999; 99US-00350841.
 XX

PA (TRIM-) TRIMERIS INC.
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 XX WPI; 2001-442157/47.
 XX
 XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 XX Disclosure; Fig 42; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from Staphylococcus aureus enterotoxin A
 XX Sequence 257 AA;
 SQ
 Query Match 26.9%; Score 948; DB 4; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 285
 DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLQHILFKGFTD 84
 QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDFSDKIDVYKGGKVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 144
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 405
 DB 145 BEKKVPINLWIDGKQTTVPLETVTKTKNKNVTVOELDLQARRYLOEKYLNYSNDFDGVQ 204
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQYDPDILLRIYRDNNTTISSTLSISLYLTT 458
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKNTINSENMHDIYLYTS 257
 RESULT 63
 ABO10269
 ID ABO10269 standard; protein; 257 AA.
 XX ABO10269;
 XX
 XX 19-AUG-2003 (first entry)
 DT S. aureus enterotoxin A.
 DE HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 XX Spstein-Barr virus infection; heptad repeat motif.
 XX Staphylococcus aureus.
 XX US6518013-B1.
 XX
 PD 11-FEB-2003.
 XX
 PF 07-JUN-1995; 95US-00485546.
 XX

XX 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX (TRIM-) TRIMERIS INC.
 XX Barney SO, Lambert DM, Petteway SR;
 XX WPI; 2003-465599/44.
 XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 XX Example; Fig 42; 716pp; English.
 XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 18-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLMOT15,
 CC 107x178x4 or PIZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX Sequence 257 AA;

Query Match 26.9%; Score 948; DB 6; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLQIYYNKAITSSEKSADQFLNTLLKGFPG 285
 DB 25 SEKSEINEKDLRKXSELOGTALGNLQIYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
 QY 286 HPWYNDLLVDLGSTAAITSYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDLDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDVFQGVQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 64
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX ADD44368;
 XX 15-JAN-2004 (first entry)
 DT Staphylococcus aureus enterotoxin A protein.
 XX enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 XX ice cream.

XX Staphylococcus aureus.
 OS WC2003080865-A1.
 XX 02-OCT-2003.
 XX 26-MAR-2002; 2002WO-IB001150.
 XX 26-MAR-2002; 2002WO-IB001150.
 XX (COUL) COUNCIL SCI & IND RES.
 PA Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
 PI WPI; 2003-779273/73.
 DR N-PSDB; ADD44369.
 DR Novel oligonucleotide primers directed against enterotoxin A gene of
 XX Staphylococcus aureus and heat stable enterotoxin gene of *Yersinia*
 PT enterocolitica, useful for detecting food poisoning causing bacteria.
 XX Example 2; Page 14-15; 34pp; English.
 XX The invention relates to novel oligonucleotide primers directed against
 CC enterotoxin A gene (ent A) of *Staphylococcus aureus* and heat stable
 CC enterotoxin gene (yest) of *Yersinia enterocolitica*. The novel
 CC oligonucleotide primers are useful for simultaneously detecting food
 CC poisoning bacterial species *Staphylococcus aureus* and/or *Yersinia*
 CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
 CC without prior enrichment for preventing food poisoning outbreak. The PCR
 CC detection method is useful for detecting the bacteria strains in quantity
 CC as low as one cell. The method can be directly used for detecting
 CC bacterial strains. The oligonucleotide primers allow quick and highly
 CC sensitive detection of the food poisoning bacterial species. This
 CC sequence represents the protein derived from the enterotoxin A gene from
 CC *Staphylococcus aureus* of the invention.
 XX Sequence 257 AA;

Query Match 26.9%; Score 948; DB 7; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLQIYYNKAITSSEKSADQFLNTLLKGFPG 285
 DB 25 SEKSEINEKDLRKXSELOGTALGNLQIYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
 QY 286 HPWYNDLLVDLGSTAAITSYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDLDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDVFQGVQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 65
 AAO29870
 ID AAO29870 standard; protein; 234 AA.
 XX AAO29870;
 XX 27-AUG-2003 (first entry)
 DT Mouse anti-human DR5 antibody (TRA-8) light chain.
 XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
 XX inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
 KW

KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW Crohn's disease; diabetes mellitus; antibody; mouse.
XX
OS Mus sp.
XX WO2003037913-A2.
XX PD 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035333.
XX PR 01-NOV-2001; 2001US-0346402P.
XX PA (UABR-) UAB RES FOUND.
XX PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX WPI; 2003-441350/41.
XX DR N-PSDB; AAL60478.
XX
XX New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer, or
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
XX Example 16; Page 225-226; 251pp; English.
PS
CC The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is mouse anti-human DR5
CC antibody (TRA-8) light chain
XX
SQ Sequence 234 AA;

Query Match 26.8%; Score 945; DB 6; Length 234;
Best Local Similarity 83.3%; Pred. No. 1.8e-48;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

QY 453 LLYLT---TSIVMTQPTSLIVSAGDRVTITCKASQSVSNDAVYQQKQSPKLLISYT 509
DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQDVGTAVAWYQQKQSPKLLIYA 72

QY 510 SRYAGVDRSGSGYGTDFLTITSSVQAEADAVYFCQDYNSPPTFGGKLEIKRADA 569
DB 73 STRHTGVDPDRFTSGSGGDFLTITSNVQSEDLADYFCQQ-YSSYRTFGGKLEIKRADA 131

QY 570 APTVSIFFPSSSOLTSFGASVVCFLNNFPKIDINVKWIDGSRQNGVLSNWTQDQSKDS 629
DB 132 APTVSIFFPSSSEQLTSFGASVVCFLNNFPKIDINVKWIDGSRQNGVLSNWTQDQSKDS 191

QY 630 TVSMSTLTLDKDEYERHNSYTCATHTKTSTSPIVKSFNRNE 671
DB 192 TVSMSTLTLDKDEYERHNSYTCATHTKTSTSPIVKSFNRNE 233

RESULT 66
ABP96752
ID ABP96752 standard; protein; 209 AA.
XX
AC ABP96752;
XX
DT 05-JUN-2003 (first entry)
XX
DE TSH receptor antibody 4D7 heavy chain amino acid sequence.

XX Thytotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
XX
OS Synthetic.
XX WO2003018632-A2.
XX PD 06-MAR-2003.
XX PF 21-AUG-2002; 2002WO-CB003831.
XX PR 23-AUG-2001; 2001GB-00020649.
XX PR 01-JUL-2002; 2002GB-00015212.
XX PA (RSRR-) RSR LTD.
XX PI Smith BR, Furmaniak J, Sanders JF;
XX WPI; 2003-290051/28.
XX DR N-PSDB; ACC44907.
XX
XX New polypeptide sequence having part or all of the primary structural
PT conformation of one or more TSH receptor epitopes, useful for treating an
PT autoimmune disease associated with an immune reaction to a TSH receptor,
PT e.g. thyroid cancer.
XX
PS Claim 67; Fig 10; 196pp; English.
XX
XX The present invention describes a polypeptide sequence comprising part or
CC all of the primary structural conformation of one or more thyrotropin
CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC produced in response to a TSH receptor interact. Also described: (1) one
CC or more receptor TSH epitopes with which the autoantibodies and/or
CC lymphocytes interact, as with the polypeptide sequence described above;
CC (2) a method of screening for autoantibodies or lymphocytes produced in
CC response to a TSH receptor in a sample of body fluid obtained from a
CC subject suspected of suffering from, susceptible to, having or recovering
CC from autoimmune disease associated with an immune reaction to a TSH
CC receptor; (3) a binding partner for a TSH receptor, which is capable of
CC binding to a TSH receptor to stimulate the TSH receptor, where the
CC binding partner does not comprise TSH or naturally produced antibodies to
CC the TSH receptor; and (4) a combination comprising the binding partner
CC and one or more further agents capable of stimulating thyroid tissue,
CC and/or tissue containing a TSH receptor, for simultaneous, separate or
CC sequential use in stimulating thyroid tissue, and/or tissue containing a
CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC gene therapy. The polypeptide, compositions and methods from the present
CC invention can be used for treating an autoimmune disease associated with
CC an immune reaction to a TSH receptor. The specific binding partner is
CC useful for the manufacture of a medicament for stimulating thyroid tissue
CC or tissue containing a TSH receptor, and for treating thyroid cancer.
CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC and VL domains given in ABP96751 to ABP96778, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 209 AA;

Query Match 26.8%; Score 944.5; DB 6; Length 209;
Best Local Similarity 85.5%; Pred. No. 1.7e-48;
Matches 183; Conservative 10; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSTGYTHHWKQSPGKLEWIGINPNNGVTLY 60
DB 1 DVQLKHSGLPELVKPGASVKISCKASGYSTGYTHHWKQSHGKLEWIGLINPYTGTTY 60

QY 61 NQKFKKALITVDKSTTAYMELRLSTSDSAVYVCASSTMTITNYMDYMGQSTSVTVSS 120
DB 61 NQKFKGKALITVDKSSSTAFMELLSTSDSAVYVCARDGN-----LDWGGQGTILTVSS 115

QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPVAVLQSD 180

DB 116 AKTTPSVPLAPGSAQAQNSWVTGCLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 175

QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVD 214

DB 176 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVD 209

RESULT 67

ABP96751

ID ABP96751 standard; protein; 209 AA.

XX

AC ABP96751;

XX

DT 05-JUN-2003 (first entry)

XX

DE TSH receptor antibody 4D7 heavy chain amino acid sequence.

XX

KW Thyrotropin receptor; TSH receptor; epitope region; antibody;

KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;

KW gene therapy; immune reaction; thyroid cancer.

OS Synthetic.

XX

PN WO2003018632-A2.

XX

PD 06-MAR-2003.

XX

PF 21-AUG-2002; 2002WO-GB003831.

XX

PR 23-AUG-2001; 2001GB-00020649.

PR 01-JUL-2002; 2002GB-00015212.

XX

PA (RSRR-) RSR LTD.

XX

PI Smith BR, Furmaniak J, Sanders JF;

XX

DR WPI; 2003-290051/28.

DR N-PSDB; ACC44906.

XX

PT New polypeptide sequence having part or all of the primary structural

PT conformation of one or more TSH receptor epitopes, useful for treating an

PT autoimmune disease associated with an immune reaction to a TSH receptor,

PT e.g. thyroid cancer.

XX

PS Claim 71; Fig 9; 196pp; English.

XX

CC The present invention describes a polypeptide sequence comprising part or

CC all of the primary structural conformation of one or more thyrotropin

CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes

CC produced in response to a TSH receptor interact. Also described: (1) one

CC or more receptor TSH epitopes with which the autoantibodies and/or

CC lymphocytes interact, as with the polypeptide sequence described above;

CC (2) a method of screening for autoantibodies or lymphocytes produced in

CC response to a TSH receptor in a sample of body fluid obtained from a

CC subject suspected of suffering from, susceptible to, having or recovering

CC from autoimmune disease associated with an immune reaction to a TSH

CC receptor; (3) a binding partner for a TSH receptor, which is capable of

CC binding to a TSH receptor to stimulate the TSH receptor, where the

CC binding partner does not comprise TSH or naturally produced antibodies to

CC the TSH receptor; and (4) a combination comprising the binding partner

CC and one or more further agents capable of stimulating thyroid tissue,

CC and/or tissue containing a TSH receptor, for simultaneous, separate or

CC sequential use in stimulating thyroid tissue, and/or tissue containing a

CC receptor. A TSH receptor has cytostatic activity and can be used in

CC gene therapy. The polypeptide, compositions and methods from the present

CC invention can be used for treating an autoimmune disease associated with

CC an immune reaction to a TSH receptor. The specific binding partner is

CC useful for the manufacture of a medicament for stimulating thyroid tissue

CC or tissue containing a TSH receptor, and for treating thyroid cancer.

CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor

CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH

CC and VL domains given in ABP96751 to ABP96778, which are used in the

CC exemplification of the present invention

XX

SQ Sequence 209 AA;

Query Match 26.8%; Score 944.5; DB 6; Length 209;

Best Local Similarity 85.5%; Pred. No. 1.7e-48;

Matches 183; Conservative 10; Mismatches 16; Indels 5; Gaps 1;

QY 1 EVQLQQSGPDLVKGASVKISCKASGYSGFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60

DB 1 DVQLKHSGPELVKPGASMKISCKASGYSGFTGYTMNVYKQSHGKNLEWIGINPYTGCTNY 60

QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYMDYWGQSTSVTVSS 120

DB 61 NQKFKGKAKLTVDKSSSTAFMELLSLTSEDSAVYYCARDGN-----LDYWGQGTTLTVSS 115

QY 121 AKTTPSVYPLAPGSAQAQNSWVTGCLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180

DB 116 AKTTPSVYPLAPGSAQAQNSWVTGCLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 175

QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVD 214

DB 176 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVD 209

RESULT 68

AAR76087

ID AAR76087 standard; protein; 239 AA.

XX

AC AAR76087;

XX

DT 25-MAR-2003 (revised)

DT 21-NOV-1995 (first entry)

XX

DE MAB 55.1 light chain.

XX

KW Antigen binding structure; complementarity determining region; CDR;

KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;

KW transgenic animal; transgenic plant; antibody engineering;

KW humanized antibody; immunotoxin.

OS Mus sp.

XX

FH Key Location/Qualifiers

FT Peptide 1..20 /label= Sig_peptide

FT Protein 21..239 /label= Mat_protein

FT /note= "claim 3, page 98"

XX

WO9515382-A1.

XX

PD 08-JUN-1995.

XX

PP 29-NOV-1994; 94WO-GB0002610.

XX

PR 03-DEC-1993; 93GB-00024819.

PR 03-JUN-1994; 94GB-00011089.

XX

PA (ZENE) ZENECA LTD.

XX

PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;

PI Blakey DC;

XX

DR WPI; 1995-215262/28.

DR N-PSDB; AAQ94036.

XX

PT Antigen binding structures containing CDR's recognising the CA55.1

PT antigen - produced by hybridomas and host cells, for use in the diagnosis

PT and therapy of cancer.

XX

PS Disclosure; Fig 16; 121pp; English.

CC MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)
 CC chains of 55.1 were isolated, and F(ab')₂, Fab, Fv, scFv or V-min
 CC humanized 55.1 constructs have been expressed in myeloma cells and E.
 CC coli. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 239 AA;

Query Match 26.8%; Score 944.5; DB 2; Length 239;
 Best Local Similarity 78.1%; Pred. No. 2e-48;
 Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTSLTSLVLYIT-...SIVMTPTPSLAVSAGDRVTITCKASQSVND-...VAVY 494
 DB 3 SQAQVLLILLVWVSGTCGDIWMSQPSLAVSAGERTVMSCKSSQLNSTRKNLAWY 62

QY 495 QOKPGQPKLLISYTSRYAGVDPFRFGSGYGTDTLTITSSVQAEADAAYVFCQDYNPP 554
 DB 63 QORFGQPKLLIYASTRTSGVDPFRFGSGYGTDTLTITSSVQAEADLAIYCKQSY-TLR 121

QY 555 TFGGKTLEIKRADAAPTIVSIFPPSSQLTSGASVVCFLNNYPKDIYVKKIDGSEKQ 614
 DB 122 TFGGKTLEIKRADAAPTIVSIFPPSSQLTSGASVVCFLNNYPKDIYVKKIDGSEKQ 181

QY 615 NGVLNMTDQDSKSTYSMSSTLTLTKDEYRHNSTYCEATHKTSPIVKSFNRYE 671
 DB 182 NGVLNMTDQDSKSTYSMSSTLTLTKDEYRHNSTYCEATHKTSPIVKSFNRYE 238

RESULT 69
 AAW06738
 ID AAW06738 standard; protein; 233 AA.
 XX
 AC AAW06738;
 XX
 DT 08-MAR-1997 (first entry)
 XX
 DE Staphylococcus enterotoxin A.
 XX
 KW Enterotoxin A; superantigen; antigen; cytokine; Chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; Gene therapy; cancer; vaccine;
 KW adjuvant.
 XX
 OS Staphylococcus sp.
 XX
 PN WO9636366-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 20-MAY-1996; 96WO-US007432.
 XX
 PR 18-MAY-1995; 95US-00446918.
 PR 29-DEC-1995; 95US-00580806.
 XX
 PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 PI Dow SW, Elmalie RE, Potter TA;
 XX
 DR WPI; 1997-011857/01.
 DR N-PSDB; AAT45699.
 XX
 PT Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer.
 XX
 PS Example 1; Page 98-99; 131pp; English.
 XX
 CC A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
 CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
 CC AAW06739), esp. truncated forms of the superantigen lacking the leader
 CC peptide, can be used in the gene therapy of cancer, infectious diseases
 CC and immunological disorders. The nucleic acid, optionally in combination

CC with cytokine or chemokine nucleic acids, is delivered to an animal using
 CC e.g. liposomes. It acts by controlling the activity of effector cells,
 CC such as T-cells, macrophages, monocytes and/or natural killer cells.
 CC Localised prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal
 XX
 SQ Sequence 233 AA;

Query Match 26.8%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 2e-48;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDKRKSELOGTALGNLKOIYYNSKAITSSKSAQDFTNTLLFKGFTGH 286
 DB 2 EKSEINEKDKRKSELOGTALGNLKOIYYNEKAKTENKESHDFLQHTILFKGFTDH 61

QY 287 PWYNDLLVDLSTATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNELTE 346
 DB 62 SWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNELTE 121

QY 347 EKKVPINLWIDGKOTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGVQV 406
 DB 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRVLOEKYLYNSDVEDGVQV 181

QY 407 GLIVFHSSEGSTSVYDLPDAQGYPDTLRIYRNTTISLSISLYLTT 458
 DB 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 70
 AAR45011
 ID AAR45011 standard; protein; 233 AA.
 XX
 AC AAR45011;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX
 DE Staphylococcal enterotoxin SEA.
 XX
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 49
 FT /note= "Given in the specification as O, no further
 FT details given"
 XX
 PN WO9324136-A1.
 XX
 PD 09-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US005213.
 XX
 PR 01-JUN-1992; 92US-00891718.
 XX
 PA (TERM/) TERMAN D S.
 PA (STON/) STONE J L.
 XX
 PI Terman DS, Stone JL;
 XX
 DR WPI; 1993-405418/50.
 XX
 PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX
 PS Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal

CC agents for treating cancers and autoimmune disease. They exhibit
CC tumorigenic activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;

Query Match 26.7%; Score 942; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 2.7e-48;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGLTALGNLKOIYYNSKAITSEKSAOFLNNTLLKXGFFTG 285
DB 1 SEKSEINEKDLRKSELOGLTALGNLKOIYYNEKAKTENKESHOFLLHILFKGFFD 60
QY 286 HPWYNDLLVDLSTAAATSEYSSVDLYGAYYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
DB 61 HSWYNDLLVDFSDKIDVYKGGKDLVYGYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQNTVVDIKVTKSKSVTVQELDLQARHVLHGKFGLYNSDSFGKQV 405
DB 121 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDPQARRYLQEKYINLYNSDVFGRVQ 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTTSSTSLSLSLYLYTT 458
DB 181 RGLIVFHTSTEPSVYDLFCAQOQYNTLLRIYRDNTTINSENHIDIYLYTS 233

RESULT 71
ID AAR76086
AC AAR76086 standard; peptide; 219 AA.
XX
AC AAR76086;
XX
DT 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
DE MAb 55.1 light chain.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
XX
OS Mus sp.
XX
PN WO9515382-A1.
XX
PD 08-JUN-1995.
XX
PF 29-NOV-1994; 94WO-GB002610.
XX
PR 03-DEC-1993; 93GB-00024819.
PR 03-JUN-1994; 94GB-00011089.
XX
PA (ZENE) ZENECA LTD.
XX
PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
PI Blakey DC;
XX
DR WPI; 1995-215262/28.
XX
PT Antigen binding structures containing CDR's recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the diagnosis
PT and therapy of cancer.
XX
PS Claim 3; Page 98; 121pp; English.
XX
CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)
CC of the heavy (AAR76085) and light (AAR76086) chains of MAb 55.1 (EACAC
CC 93081901), which recognises the colorectal tumor-associated antigen
CC CA55.1. It is optionally humanized and in the form F(ab')2, F(ab)', Fab,

CC Fv, scFv or V-min, and is produced in transgenic animals or plants.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 219 AA;

Query Match 26.7%; Score 941.5; DB 2; Length 219;
Best Local Similarity 83.0%; Pred. No. 2.7e-48;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;

QY 460 IVMTQTPTSLIVSAGDRVTITCKASQSVND-----VAMVQQKPGQSPKLLISYTSRY 513
DB 2 IVMSQSPSSLAVSAGEKVTMSCKSQSLNSTRKKNVLAWYQRPQSPKLLIYWASTRT 61
QY 514 AGVDRPFGSGYGTDFLTITSSVOAEAAVYFCQDYNPSPTFGGTYKLSIKRADAAPT 573
DB 62 SGVDFRFTGSGSGTDFLTITSSVOAEALAIYCKQSY-TLRTFGGTYKLSIKRADAAPT 120
QY 574 SIFPPSEQLTSGASVVCFLNFPKDIIVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 633
DB 121 SIFPPSEQLTSGASVVCFLNFPKDIIVKWKIDGSRQNGVLNSWTQDQSKDSTYSM 180
QY 634 SSTLTATKDEYERNHNSYTCBATHKTSTSPIVKSFNRNE 671
DB 181 SSTLTATKDEYERNHNSYTCBATHKTSTSPIVKSFNRNE 218

RESULT 72
ID AAW35373
AC AAW35373 standard; peptide; 233 AA.
XX
AC AAW35373;
XX
DT 20-APR-1998 (first entry)
XX
DE Staphylococcus enterotoxin SEA wild-type superantigen.
XX
KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
KW cancer; infection; autoimmune disease; antibody.
XX
OS Staphylococcus sp.
XX
PN WO9736932-A1.
XX
PD 09-OCT-1997.
XX
PF 26-MAR-1997; 97WO-SE000537.
XX
PR 29-MAR-1996; 96SE-00001245.
PR 12-AUG-1996; 96US-00695692.
XX
PA (PHAA) PHARMACIA & UPJOHN AB.
XX
PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
PI Abrahamson L, Forsberg G;
XX
DR WPI; 1997-503052/46.
XX
PT Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX
PS Claim 8; Page 36-37; 58pp; English.
XX
CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
CC SEA superantigen can be modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. The modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be

CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in vitro specific
CC manner) in which cysteines providing for interchain cysteine linkages in
CC the native antibody have been replaced (preferably by serine residues) to
CC prohibit cysteine formation. The modified wild-type superantigen is used
CC for treating cancer, viral infections, parasitic infestations and
CC autoimmune disease. The modified wild type superantigen has a lower
CC immunogenicity and reactivity with neutralising antibodies and has fewer
CC side-effects when used as a drug, compared to wild type superantigen
XX
SQ Sequence 233 AA;

Query Match 26.7%; Score 941; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 3.1e-48;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSDQFLTWLTFKGFPTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSDQFLTWLTFKGFPTG 60
QY 286 HPWNDDLLVLDGSAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HSWNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
DB 121 BEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 458
DB 181 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENMHDIYLYTS 233

RESULT 73
AAB67338
ID AAB67338 standard; peptide; 233 AA.

XX AC AAB67338;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin A protein.
XX DR Tumour; cancer; immune; enterotoxin.
XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-004931746.
XX (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX

CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 233 AA;

Query Match 26.7%; Score 941; DB 4; Length 233;
Best Local Similarity 76.0%; Pred. No. 3.1e-48;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSDQFLTWLTFKGFPTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSDQFLTWLTFKGFPTG 60
QY 286 HPWNDDLLVLDGSAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HSWNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
DB 121 BEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 458
DB 181 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENMHDIYLYTS 233

RESULT 74
AAU72802
ID AAU72802 standard; protein; 234 AA.

XX AC AAU72802;
XX DT 26-FEB-2002 (first entry)
XX DE TRA-8 light chain.
XX OS Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
XX TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
XX autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
XX rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
XX Addison disease; scleroderma; Goodpasture's syndrome; sterility;
XX myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
XX allergy; arteriosclerosis; myocarditis; cardiomyopathy;
XX glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX MS musculus.
XX WO2000183560-A1.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014151.
XX 02-MAY-2000; 2000US-0201344P.
XX (UABR-) UAB RES FOUND.
XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX WPI; 2002-049338/06.
XX N-PSDB; AAS97063.

XX Novel antibody specific for tumor necrosis factor-related apoptosis-
XX inducing ligand, useful for inhibiting cell proliferation in cancer.
XX Claim 30; Page 200; 229pp; English.
XX The invention describes a novel antibody which recognizes a tumour
XX

CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
 CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
 CC activity to a cell expressing DR5 in vivo. It is also useful for
 CC preparing a therapeutic for selective apoptosis of abnormal or
 CC dysregulated cells, and for inhibiting cell proliferation in a cell,
 CC preferably a human breast, ovary, colon, haematopoietic, prostate,
 CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
 CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
 CC antibody is used to treat an autoimmune disease, systemic lupus
 CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
 CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
 CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
 CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
 CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
 CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
 CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
 CC breast tissue. Peptides used to design primers for isolating heavy and
 CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
 CC shown in AAU72799 and AAU72800
 CC
 CC Sequence 234 AA;
 CC

Query Match 26.5%; Score 938; DB 5; Length 234;
 Best Local Similarity 82.5%; Pred. No. 4.7e-48;
 Matches 184; Conservative 12; Mismatches 22; Indels 4; Gaps 2;
 QY 453 LYLVT---TSIVMTQPTSLLSAGDRVITTCASQSVNDVAVYQKQPGKLLISVT 509
 DB 13 LFLFAGVEGDIYVQSHKFWISVGDVSVITCKASODVGTAVYQKQPGKLLIYWA 72
 QY 510 SRYAGVDPDRFGSGYGTDFTLTISVQAEADAVYFCQDDYNSPPTFGGTYKLEIKRADA 569
 DB 73 STRHTGVDPDRFTGSGSGTDTLTISNVQSEDLADYFCQY-SYSYRTFGGTYKLEIKRADA 131
 QY 570 APTVSIFFPSSSEOLTSGGASVVCFLNNVPKDNVKKWIDGGERONGVLSNWTDDQSDS 629
 DB 132 APTVSIFFPSSSEOLTSGGASVVCFLNNVPKDNVKKWIDGGERONGVLSNWTDDQSDS 191
 QY 630 TYSMSSTLTITKDEYHRHNSYTCETHKSTSTSPIVKSFNRNE 671
 DB 192 TYSMSSTLTITLDEYHRHNSYTCETHKSTSTSPIVKSFNRNE 233

RESULT 75
 ABU79068
 ID ABU79068 standard; protein; 257 AA.
 AC ABU79068;
 XX
 XX 18-JUN-2003 (first entry)
 XX
 XX S. aureus SEA (staphylococcus enterotoxin A) protein.
 XX
 XX Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 KW APC; antitumour.
 XX
 XX Staphylococcus aureus.
 CS
 XX
 XX US2002177551-A1.
 PN
 XX
 XX 28-NOV-2002.
 PD
 XX
 XX 30-MAY-2001; 2001US-00870759.
 PF
 XX
 XX 31-MAY-2000; 2000US-0208128P.
 PR
 XX
 XX (TERM/) TERMAN D S.
 PA
 XX
 XX Terman DS;
 PT
 XX

WPI; 2003-361759/34.
 N-PSDB; ACA64694.
 A mammalian cell receptor, useful in the treatment of cancer by binding
 to tumour associated lipids where the binding induces energy or apoptosis
 in T cells and antigen presenting cells.
 Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the
 treatment of cancer, which binds to tumour associated lipids and induces
 energy or apoptosis in the T cells and antigen presenting cells (APCs).
 Also included are a mammalian cell useful in the treatment of cancer
 where the receptor which binds tumour associated lipids and induces
 cellular inactivation or death is deleted or functionally deactivated,
 producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 (by allowing tumour associated lipids to contact immunocytes in which
 receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 sphingolipids, glycosphingolipids, phospholipids, gangliosides,
 sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 deleted), a construct useful in the treatment of cancer comprising a
 superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 useful in the treatment of cancer (where an adaptor protein which
 inhibits T cell activation by tumour associated antigens is deleted or
 functionally deactivated), a composition useful in the treatment of
 cancer (comprising a lipid raft conjugated to a superantigen), producing
 (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 allowing tumour associated lipids to contact immunocytes, in which
 receptors for the lipids are inactivated or deleted to produce a
 tumouricidal immunocyte population, and administering the tumouricidal APC
 activated immunocytes to the host), producing (M3) a tumouricidal APC
 population ex vivo in a mammal (by allowing a tumour associated lipid to
 contact APCs, in which receptors for the tumour associated lipids are
 inactivated or deleted to produce a tumouricidally activated population,
 and administering APCs to the host), producing a tumouricidal T cell
 population ex vivo in a mammal (by allowing a tumour associated lipid to
 contact T cells, in which adaptor proteins, which inhibit T cell
 activation by tumour associated antigens, are deleted or functionally
 deactivated to produce a tumouricidal population of T cells, and
 administering the tumouricidally activated T cells to the host, or
 allowing a superantigen-lipid raft to contact T cells ex vivo, and
 administering the tumouricidally activated T cells to the host), treating
 (M5) cancer in a mammal (by administering a lipid binding molecule which
 binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 a tumouricidal T cell population in vivo in a mammal (by allowing a
 tumour associated antigen to contact immunocytes in which adaptor
 proteins which inhibit T cell activation by tumour associated antigens
 are deleted or functionally deactivated) and producing (M7) a
 tumouricidal T cell population ex vivo in a mammal comprising allowing a
 superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 receptors, methods and compositions are useful for treating cancers and
 tumours. Bacterial superantigens are co-administered or administered as
 fusion constructs with anti-tumour proteins or motifs. The present
 sequence represents a bacterial superantigen protein (e.g. a
 staphylococcal enterotoxin). Note: The sequence data for this patent did
 not form part of the printed specification, but was obtained in
 electronic format from the US patent office website at
 "seqdata.uspto.gov/sequence.html?DocID=20020177551"

Sequence 257 AA;
 Query Match 26.5%; Score 935; DB 6; Length 257;
 Best Local Similarity 75.5%; Pred. No. 7.9e-48;
 Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
 QY 226 SEKSEENKDLRKSELOQTALGNLKIYYNKAITSSEKSDAQTLTWLLEKGGPTG 285
 DB 25 SEKSEENKDLRKSELOQTALGNLKIYYNKAITSSEKSDAQTLTWLLEKGGPTG 84
 QY 286 HPWYNDLLVLDGTAATSEYGGSSVDLYGAYVQCACGGTPNKIACMYGGVTLHNNRLT 345
 DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYVQCACGGTPNKIACMYGGVTLHNNRLT 144

QY	346	BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVQ	405
Db	145	BEKKVPINLWLDGKQNTVPLETVKTKKNVTQELDLQARRYLQEKYNLYNSDVFDGKQVQ	204
QY	406	RGLIVHSSEGSTVSYDLFDAGGQYPPDTLLRIYRDNTTISSTLSLSLSLYTT	458
Db	205	RGLIVFHTSTBSVNYDLFGAQGQNSNTLLRIYRDNKTINSENNHIDIYLYTS	257

Search completed: August 12, 2004, 13:29:58
Job time : 97.4429 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:32:36 ; Search time 71.4517 Seconds
(without alignments)
2952.472 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSGFDLVKPGASVKI.....EATHXTSTPIVKSFRNRS 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/2/pubpaa/FCR_NEW_PUB.pcp.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/ptodata/2/pubpaa/FCRUS_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3522	100.0	672	10	US-09-900-766-1
2	1832.5	52.0	478	16	US-10-679-620-72
3	1832.5	52.0	509	16	US-10-679-620-90
4	1653	46.9	552	16	US-10-679-620-86
5	1257	35.7	669	9	US-09-807-721-2
6	1218	34.6	233	10	US-09-900-766-2
7	1130	32.1	233	10	US-09-900-766-3
8	1107	31.4	233	10	US-09-900-766-7
9	1107	31.4	233	14	US-10-283-838-8
10	1107	31.4	257	12	US-10-267-682-112
11	1107	31.4	257	12	US-10-267-748-112
12	1072	30.4	248	9	US-09-870-759-16
13	1072	30.4	248	10	US-09-751-708A-16
14	1069	30.4	600	16	US-10-334-235-38
15	1028	29.2	597	9	US-09-903-327A-11

16	1025.5	29.1	464	14	US-10-216-484-9	Sequence 9, Appli
17	1025.5	29.1	464	14	US-10-384-933-9	Sequence 9, Appli
18	1024.5	29.1	613	9	US-09-903-327A-14	Sequence 14, Appli
19	1023.5	29.1	456	9	US-09-903-327A-2	Sequence 2, Appli
20	1023.5	29.1	493	9	US-09-903-327A-13	Sequence 13, Appli
21	1023.5	29.1	510	9	US-09-903-327A-12	Sequence 12, Appli
22	1022.5	29.0	438	9	US-09-903-327A-6	Sequence 6, Appli
23	1000	28.4	700	16	US-10-679-620-94	Sequence 94, Appli
24	980.5	27.8	711	14	US-10-071-485-90	Sequence 90, Appli
25	979.5	27.8	223	15	US-10-410-907A-36	Sequence 36, Appli
26	972.5	27.6	243	16	US-10-334-235-37	Sequence 37, Appli
27	967.5	27.5	488	16	US-10-334-235-39	Sequence 39, Appli
28	965.5	27.4	510	16	US-10-679-620-74	Sequence 74, Appli
29	965.5	27.4	510	16	US-10-679-620-92	Sequence 92, Appli
30	958	27.2	214	16	US-10-679-620-84	Sequence 84, Appli
31	957	27.2	468	10	US-09-795-515-7	Sequence 7, Appli
32	957	27.2	468	12	US-10-704-352-7	Sequence 7, Appli
33	957	27.2	468	16	US-10-704-071-7	Sequence 7, Appli
34	952	27.0	222	16	US-10-679-620-82	Sequence 82, Appli
35	948	26.9	233	10	US-09-900-766-4	Sequence 4, Appli
36	948	26.9	233	14	US-10-283-838-7	Sequence 7, Appli
37	948	26.9	257	12	US-10-267-682-113	Sequence 113, App
38	948	26.9	257	12	US-10-267-748-113	Sequence 113, App
39	945	26.8	234	14	US-10-281-479A-24	Sequence 24, Appli
40	945	26.8	234	14	US-10-275-180A-24	Sequence 24, Appli
41	945	26.8	234	14	US-10-286-132A-24	Sequence 24, Appli
42	944	26.8	233	12	US-10-354-948-4	Sequence 4, Appli
43	935	26.5	257	9	US-09-870-759-8	Sequence 8, Appli
44	935	26.5	257	10	US-09-751-708A-8	Sequence 8, Appli
45	926	26.3	451	16	US-10-679-620-118	Sequence 118, App
46	925	26.3	257	14	US-10-002-784A-2	Sequence 2, Appli
47	921	26.1	233	14	US-10-002-784A-4	Sequence 4, Appli
48	915	26.0	238	14	US-10-216-484-11	Sequence 11, Appli
49	915	26.0	238	14	US-10-384-933-11	Sequence 11, Appli
50	912	25.9	238	9	US-09-903-327A-4	Sequence 4, Appli
51	908	25.8	257	8	US-08-882-431-2	Sequence 2, Appli
52	903	25.6	233	8	US-08-882-431-4	Sequence 4, Appli
53	900.5	25.6	462	14	US-10-281-479A-23	Sequence 23, Appli
54	900.5	25.6	462	14	US-10-286-132A-23	Sequence 23, Appli
55	900.5	25.6	464	14	US-10-275-180A-23	Sequence 23, Appli
56	894	25.4	218	16	US-10-679-620-80	Sequence 80, Appli
57	894	25.4	712	16	US-10-679-620-116	Sequence 116, App
58	890.5	25.3	215	16	US-10-679-620-120	Sequence 120, App
59	890.5	25.3	483	16	US-10-679-620-122	Sequence 122, App
60	885	25.1	363	15	US-10-291-265-335	Sequence 335, App
61	884.5	25.1	451	16	US-10-679-620-78	Sequence 78, Appli
62	872	24.8	453	14	US-10-159-006-18	Sequence 18, Appli
63	866.5	24.6	215	15	US-10-410-907A-34	Sequence 34, Appli
64	863.5	24.5	472	14	US-10-159-006-30	Sequence 30, Appli
65	859.5	24.3	473	9	US-09-910-059-131	Sequence 131, App
66	857.5	24.2	235	10	US-09-795-515-5	Sequence 5, Appli
67	852.5	24.2	235	12	US-10-704-352-5	Sequence 5, Appli
68	852.5	24.2	235	16	US-10-704-071-5	Sequence 5, Appli
69	852	24.2	448	16	US-10-467-546-4	Sequence 4, Appli
70	849	24.1	448	15	US-10-378-567-2	Sequence 2, Appli
71	841.5	23.9	384	15	US-10-291-265-804	Sequence 804, App
72	841.5	23.9	384	15	US-10-291-265-805	Sequence 805, App
73	841.5	23.9	384	15	US-10-291-265-806	Sequence 806, App
74	841.5	23.9	384	15	US-10-291-265-807	Sequence 807, App
75	827.5	23.5	470	14	US-10-216-484-143	Sequence 143, App
76	827.5	23.5	470	14	US-10-384-933-143	Sequence 143, App
77	825.5	23.4	470	14	US-10-216-484-145	Sequence 145, App
78	825.5	23.4	470	14	US-10-384-933-145	Sequence 145, App
79	824.5	23.4	470	14	US-10-216-484-117	Sequence 117, App
80	824.5	23.4	470	14	US-10-216-484-147	Sequence 147, App
81	824.5	23.4	470	14	US-10-384-933-117	Sequence 117, App
82	824.5	23.4	470	14	US-10-384-933-147	Sequence 147, App
83	821	23.3	367	15	US-10-291-265-899	Sequence 899, App
84	818.5	23.2	472	14	US-10-159-006-43	Sequence 43, Appli
85	816.5	23.2	470	14	US-10-216-484-89	Sequence 89, Appli
86	816.5	23.2	470	14	US-10-384-933-89	Sequence 89, Appli
87	809.5	23.0	449	16	US-10-318-397-22	Sequence 22, Appli
88	809.5	23.0	449	16	US-10-317-747-22	Sequence 22, Appli

Sequence 6, Appli
Sequence 4, Appli
Sequence 157, App
Sequence 157, App
Sequence 71, Appl
Sequence 208511,
Sequence 46, Appl
Sequence 2, Appli
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl

89 807 22.9 448 9 US-09-917-410-6
90 805.5 22.9 451 15 US-10-423-299-4
91 805.5 22.9 470 14 US-10-216-484-157
92 805.5 22.9 470 14 US-10-384-933-157
93 802 22.8 452 10 US-09-726-258-71
94 797 22.6 471 12 US-10-424-599-208511
95 797 22.6 471 12 US-10-292-088-46
96 796 22.6 614 12 US-10-389-223A-2
97 794.5 22.6 448 12 US-10-411-037-56
98 794.5 22.6 448 12 US-10-411-026-56
99 794.5 22.6 448 16 US-10-410-962-56
100 794.5 22.6 448 16 US-10-411-049-56

ALIGNMENTS

RESULT 1
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALUSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPRANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 100.0%; Score 3522; DB 10; Length 672;
Best Local Similarity 100.0%; Pred. No. 3e-184;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60

QY 61 NOKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTITNYMDYWGQGTSTVTVSS 120
Db 61 NOKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTITNYMDYWGQGTSTVTVSS 120

QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTITWNSGSLSSGVHTFPVQLQSD 180
Db 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTITWNSGSLSSGVHTFPVQLQSD 180

QY 181 LYTLSSTVTPSSWPSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
Db 181 LYTLSSTVTPSSWPSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240

QY 241 SELQGTALGNLKQIYYNSKAITSSSEKSDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
Db 241 SELQGTALGNLKQIYYNSKAITSSSEKSDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300

QY 301 ATSEYEGSSVDLYGAYGYGACAGTTPNKTAQWGGVTLHNNRLTEBKVPINLWDGKQ 360
Db 301 ATSEYEGSSVDLYGAYGYGACAGTTPNKTAQWGGVTLHNNRLTEBKVPINLWDGKQ 360

QY 361 TTVPIDKVKTSKKEVTYQELDLQARHYLHGKFLYNSDSFGKVQORGLIVFHSSEGSTVS 420
Db 361 TTVPIDKVKTSKKEVTYQELDLQARHYLHGKFLYNSDSFGKVQORGLIVFHSSEGSTVS 420

QY 421 YDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTTYSIVMTQTPTSLVSAGDRVIT 480
Db 421 YDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTTYSIVMTQTPTSLVSAGDRVIT 480

QY 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTFTLTISVQAE 540
Db 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTFTLTISVQAE 540

QY 541 AAVYFCQDDYNSPPTFGGSKLEIKRAADAPTSTFFPPSSQLTSGGASVVCFLNNFPK 600
Db 541 AAVYFCQDDYNSPPTFGGSKLEIKRAADAPTSTFFPPSSQLTSGGASVVCFLNNFPK 600

QY 601 DINVKWKIDGSRQNGVLNSWTDDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKTST 660
Db 601 DINVKWKIDGSRQNGVLNSWTDDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKTST 660

QY 661 SPIVKSFNRES 672
Db 661 SPIVKSFNRES 672

RESULT 2

US-10-679-620-72
; Sequence 72, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL740 , see Example 12
US-10-679-620-72

Query Match 52.0%; Score 1832.5; DB 16; Length 478;
Best Local Similarity 56.5%; Pred. No. 3.1e-92;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 2 QQLQQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 61

QY 61 NOKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTITNYMDYWGQGTSTVTVSS 120
Db 62 DPKFDKATITADTSNTAYLQVSRSLTSEDYSAVYCSRGGDGFYANDYWGQASVTVSS 121

QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTITWNSGSLSSGVHTFPVQLQSD 180
Db 122 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTITWNSGSLSSGVHTFPVQLQSD 181

QY 181 LYTLSSTVTPSSWPSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
Db 182 LYTLSSTVTPSSWPSETVTCNVAHPASSTKVDKKIIVPRDCGG-----GK 227

QY 241 SELQGTALGNLKQIYYNSKAITSSSEKSDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
Db 228 RTIQDSDA-----TDT-----VDLGAE 244

QY 301 ATSEYEGSSVDLYGAYGYGACAGTTPNKTAQWGGVTLHNNRLTEBKVPINLWDGKQ 360
Db 245 HRDDPPPTASDI----- 256

```

QY 361 TTVPIDKVKTSKKEVTYQELDLQARHLYHGKFLYNSDFGKVGQGLIVFHSSEGSTVS 420
Db 257 -----GKRGKRGD----- 265
QY 421 YDLFDAQGOYPTDLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLILVSAGDRVIT 480
Db 266 -----IVMTQSHKFMSTSVGDRVSIT 286
QY 481 CKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
Db 287 CKASQSVNTAVAVYQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
QY 541 AAVYFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVWCFNNFYK 600
Db 347 LAVYICQOYHTPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVWCFNNFYK 600
QY 601 DINVKWIDGSRONGVLNSWTDQSDKSTYSMSSTLTITKDEYERHNSYTCATHKTST 660
Db 407 DINVKWIDGSRONGVLNSWTDQSDKSTYSMSSTLTITKDEYERHNSYTCATHKTST 660
QY 661 SPIVKSFRNE 671
Db 467 SPIVKSFRNE 477

RESULT 3
US-10-679-620-90
; Sequence 90, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1766, see Example 12
US-10-679-620-90

Query Match 52.0%; Score 1832.5; DB 16; Length 509;
Best Local Similarity 56.5%; Pred. No. 3.3e-92;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

```

```

QY 1 EVLQOQSGDPLVKPGASVKISKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 33 QVQLQSGDPLVKPGASVKISKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
QY 61 NQKPKDQKATLVDSKSTTAYMELRLTSDSAVYICARSTMTITNYVMDYWGQSTSVTVSS 120
Db 93 DPKFQDKATITADTSNTAYLVQSRITSDTAVYICARSTMTITNYVMDYWGQSTSVTVSS 120
QY 121 AKTTPSVVPLAGSAQNTNSMTLGLVKGYPEPTVTVNSGSLSSGVHTFPVQLQSD 180
Db 153 AKTTPSVVPLAGSAQNTNSMTLGLVKGYPEPTVTVNSGSLSSGVHTFPVQLQSD 180
QY 181 LYTLSSTVTPSSWTSPSETVTCNVAHPASSTKVDKIKIVPRDSDGPGSEKEINEKDLRKK 240
Db 213 LYTLSSTVTPSSWTSPSETVTCNVAHPASSTKVDKIKIVPRDSDGPGSEKEINEKDLRKK 240
QY 241 SEIQGTALGNLKOIYYNSKAITSEKSDAQDLTNTLLFKGFTTGHPTWNTDLLDLGSTA 300
Db 259 RTIQDSA-----TDT-----VDLGAE 275

```

```

QY 301 ATSEVEGSSVDLYGAYYQACAGTPNKTACTMYGGVTLHDNNRLTEEKVPIINLWIDGK 360
Db 276 HRDPPPTASDI----- 287
QY 361 TTVPIDKVKTSKKEVTYQELDLQARHLYHGKFLYNSDFGKVGQGLIVFHSSEGSTVS 420
Db 288 -----GKRGKRGD----- 296
QY 421 YDLFDAQGOYPTDLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLILVSAGDRVIT 480
Db 297 -----IVMTQSHKFMSTSVGDRVSIT 317
QY 481 CKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
Db 318 CKASQSVNTAVAVYQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
QY 541 AAVYFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVWCFNNFYK 600
Db 378 LAVYICQOYHTPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVWCFNNFYK 600
QY 601 DINVKWIDGSRONGVLNSWTDQSDKSTYSMSSTLTITKDEYERHNSYTCATHKTST 660
Db 438 DINVKWIDGSRONGVLNSWTDQSDKSTYSMSSTLTITKDEYERHNSYTCATHKTST 660
QY 661 SPIVKSFRNE 671
Db 498 SPIVKSFRNE 508

RESULT 4
US-10-679-620-86
; Sequence 86, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1736, see Example 15
US-10-679-620-86

Query Match 46.9%; Score 1653; DB 16; Length 552;
Best Local Similarity 51.5%; Pred. No. 2.3e-82;
Matches 351; Conservative 40; Mismatches 85; Indels 206; Gaps 7;

```

```

QY 1 EVLQOQSGDPLVKPGASVKISKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 65 EVDLVESGGDILVKPGGSLKLSCAASGFTFSGHYGMSWVRQTPDKRLEWVATIGSRGTTHY 124
QY 61 NQKPKDQKATLVDSKSTTAYMELRLTSDSAVYICARSTMTITNYVMDYWGQ 113
Db 125 PDSVKGRFTTISRDNKALYQMSLSKSDTAMVYCARSEFFYGYGNTYYYSANDYWGQ 184
QY 114 TSVTVSSAKTTPSVVPLAGSAQNTNSMTLGLVKGYPEPTVTVNSGSLSSGVHTF 173
Db 185 ASVTVSSAKTTPSVVPLAGSAQNTNSMTLGLVKGYPEPTVTVNSGSLSSGVHTF 244
QY 174 PAVLQSDLYTLSSSVTPSSWTSPSETVTCNVAHPASSTKVDKIKIVPRDSDGPGSEKSEIN 233
Db 245 PAVLQSDLYTLSSSVTPSSWTSPSETVTCNVAHPASSTKVDKIKIVPRDSDGPGSEKSEIN 295

```


Db 61 HPWYNDLLVDSGTAATSEYEGSSVDLYGAYGYQCAGTTPNKTAQMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 7
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 32.1%; Score 1130; DB 10; Length 233;
Best Local Similarity 91.4%; Pred. No. 3e-54;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAOFNTLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAOFNTLLFKGFTG 60
QY 286 HPWYNDLLVDSGTAATSEYEGSSVDLYGAYGYQCAGTTPNKTAQMYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVDSGKDATNKYKGGKVDLYGAYGYQCAGTTPNKTAQMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 8
US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7
Query Match 31.4%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.4e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAOFNTLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAOFNTLLFKGFTG 60
QY 286 HPWYNDLLVDSGTAATSEYEGSSVDLYGAYGYQCAGTTPNKTAQMYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVDSGKDATNKYKGGKVDLYGAYGYQCAGTTPNKTAQMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 9
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US2003002894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
; Johan Hansson, Terje Kalland, Lars
; Abrahamsen and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-267-682-8

Query Match 31.4%; Score 1107; DB 14; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.4e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDADQELTNTLLPKGFTG 285
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDADQELTNTLLPKGFTG 60
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 120
QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 405
DB 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 10

US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US2004003235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-267-682-112

Query Match 31.4%; Score 1107; DB 12; Length 257;
Best Local Similarity 89.7%; Pred. No. 6e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDADQELTNTLLPKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDADQELTNTLLPKGFTG 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 11

US-10-267-748-112

; Sequence 112, Application US/10267748

; Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

```
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-748-112

Query Match      31.4%; Score 1107; DB 12; Length 257;
Best Local Similarity 89.7%; Pred. No. 6e-53; Indels 0; Gaps 0;
Matches 209; Conservative 9; Mismatches 15;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNLLVDLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTINSENHLDLYLTT 257

RESULT 12
US-09-870-759-16
/ Sequence 16, Application US/09870759
/ Patent No. US20020177552A1
/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
/ FILE REFERENCE: 870759
/ CURRENT APPLICATION NUMBER: US/09/870,759
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/208,128
/ PRIOR FILING DATE: 2000-05-30
/ NUMBER OF SEQ ID NOS: 166
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match      30.4%; Score 1072; DB 9; Length 248;
Best Local Similarity 90.2%; Pred. No. 4.7e-51; Indels 0; Gaps 0;
Matches 202; Conservative 9; Mismatches 13;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNLLVDLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLS 449
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTINSEN 248

RESULT 13
US-09-751-708A-16
/ Sequence 16, Application US/09751708A
/ Publication No. US2003057113A1
/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
```

```
/ FILE REFERENCE: 751708
/ CURRENT APPLICATION NUMBER: US/09/751.708A
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: US 60/173,371
/ PRIOR FILING DATE: 1999-12-28
/ NUMBER OF SEQ ID NOS: 166
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match      30.4%; Score 1072; DB 10; Length 248;
Best Local Similarity 90.2%; Pred. No. 4.7e-51; Indels 0; Gaps 0;
Matches 202; Conservative 9; Mismatches 13;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNLLVDLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLS 449
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTINSEN 248

RESULT 14
US-10-334-235-38
/ Sequence 38, Application US/10334235
/ Publication No. US20040131591A1
/ GENERAL INFORMATION:
/ APPLICANT: Oxford Biomedica (UK) Ltd.
/ APPLICANT: Kingsman, Alan
/ APPLICANT: Bebbington, Christopher
/ APPLICANT: Carroil, Miles
/ APPLICANT: Ellard, Fiona
/ APPLICANT: Kingsman, Susan
/ APPLICANT: Myers, Kevin
/ APPLICANT: Lamikandra, Abigail
/ TITLE OF INVENTION: VECTOR SYSTEM
/ FILE REFERENCE: 532682000920
/ CURRENT APPLICATION NUMBER: US/10/334,235
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 10/060,585
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/GB00/04317
/ PRIOR FILING DATE: 2000-11-13
/ PRIOR APPLICATION NUMBER: US 09/445,375
/ PRIOR FILING DATE: 1998-06-04
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows version 4.0
/ SEQ ID NO 38
/ LENGTH: 600
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide of 574SAb1
US-10-334-235-38

Query Match      30.4%; Score 1069; DB 16; Length 600;
Best Local Similarity 37.9%; Pred. No. 1.8e-50; Indels 336; Gaps 9;
Matches 254; Conservative 20; Mismatches 60;

QY 1 EVOLOQSQPDLVKPGASVKISKASGYFTGYMHWKQSPGKLEIGRINPNNGVTLY 60
```

Db 23 EVLQOQSPDLVKPGASVKISKASGYSTGYNHWKQSHGKSLWGRINPNNGVTLY 82
 QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYCARSTMTINYNVDYGGQSTVTYSS 120
 Db 83 NQKFKDKAILTVDKSSSTAYMELSLTSDSAVYCARSTMTINYNVDYGGQSTVTYSS 141
 QY 121 AKTTTPSVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 180
 Db 142 ----- 141
 QY 181 LYTSSSVTPSPSTWPTSETVTCNVAHPASSTKYDKIIVPRDSGGPSEKSEINEKDLRKK 240
 Db 142 ----- 144
 QY 241 SELOGTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 145 ----- 144
 QY 301 ATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 360
 Db 145 ----- 154
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQRGKLIIVFHSSEGSTVS 420
 Db 155 ----- 156
 QY 421 YDLFDAQQQYPTLLRIYRDNTTSSSTSLISLYLTTISVMTQTPTSLVSSAGDRVTIT 480
 Db 157 ----- 179
 QY 481 CKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDPDRSGSGYGTDFTLTSSVQAE 540
 Db 180 CKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDPDRSGSGYGTDFTLTSSVQAE 239
 QY 541 AAVTFCQDYNSPTFGGGTGLEIKRADA-APTYSIIPPSEQLTSGASVWCFNNFY 599
 Db 240 LAVTFCQDYNSPTFGGGTGLEIKRASKTGPSPVFLAPSKSTSGTAAIGCLVKDYFP 299
 QY 600 KDINVKWK-----IDGSRQNGVLNSWTDQSKDSTYSMSSTLTLDKDEYERHNSYTCAT 655
 Db 300 EPVTVSMNSGALTSGVHTTFAVLQSD-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 351
 QY 656 HKTSTSPIVK 665
 Db 352 HKPSNTKVDK 361

RESULT 15
 US-09-903-327A-11
 ; Sequence 11, Application US/09903327A
 ; Patent No. US20020164333A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nemerow, Glen R.
 ; APPLICANT: Li, Erquan
 ; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
 ; TITLE OF INVENTION: GENE
 ; TITLE OF INVENTION: DELIVERY
 ; FILE REFERENCE: 22908-1228
 ; CURRENT APPLICATION NUMBER: US/09/903,327A
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 09/613,017
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 597
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
 ; OTHER INFORMATION: and TNF alpha mature peptide
 US-09-903-327A-11

Query Match 29.2%; Score 1028; DB 9; Length 597;
 Best Local Similarity 37.2%; Pred No. 3.1e-48;
 Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;
 QY 1 EVLQOQSPDLVKPGASVKISKASGYSTGYNHWKQSHGKSLWGRINPNNGVTLY 60
 Db 20 EVLQOQSPDLVKPGASVKISKASGYSTGYNHWKQSHGKSLWGRINPNNGVTLY 79
 QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYCARSTMTINYNVDYGGQSTVTYSS 120
 Db 80 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYCARSTMTINYNVDYGGQSTVTYSS 132
 QY 121 AKTTTPSVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 180
 Db 133 AKTTTPSVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 192
 QY 181 LYTSSSVTPSPSTWPTSETVTCNVAHPASSTKYDKIIVPRDSGGPSEKSEINEKDLRKK 240
 Db 193 LYTSSSVTPSPSTWPTSETVTCNVAHPASSTKYDKIIVPRDCG----- 235
 QY 241 SELOGTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIFPPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSMFVD--- 289
 QY 361 TTVPIDKVKTSKEY-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVQRGKLIIVF 411
 Db 290 -DVEVHTAQTPREQFNSTFRSSELPIMHQDWLNGKEFKCRVNSAFAPIEK----- 343
 QY 412 HSSEGSTVSVDLFDAGQYPTLLRIYRDNTTSSSTSLISLYLTTISVMTQTPTSLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVTITCKASQSVNDVAVTQKPGQPKLLISYTSRYAGVDPDRSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNSPTFGGGTGLEIKRADAAPTYSIIPPSEQLTSGGASV 591
 Db 349 -----XGRKAPQVYTIPTPPKQMAKDKVSLT 375
 QY 592 CFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLDKDEYERHNSY 651
 Db 376 CMITDFFPDITVEQWNGQPAEN-YKNTQIPMDT-DGSYFYVSKLVQKSNWEAGNTFI 433
 QY 652 CEATHKTSPIVKSFRNENES 672
 Db 434 CSVLHE-----FVRSSTRTPS 449

RESULT 16
 US-10-216-484-9
 ; Sequence 9, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Pas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/216,484
 ; CURRENT FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 9


```

; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-9

Query Match      29.1%; Score 1025.5; DB 14; Length 464;
Best Local Similarity 36.2%; Pred. No. 3.2e-48;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYIMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEVLKPGASVKLSKASGYTFTSYMQWVKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NQKPKKATLTVDKSSSTAYMELRSLTSEDSAVYICARS-TMITNYMDYWGQTSVTVS 119
Db 80 NQKPKKATLTVDTSSTAYMQLSSLTSEDSAVYICARNRDYSNNWYFDVWGTGTTVTVS 139
QY 120 SAKTTPPSVYPLAPGSAATNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 179
Db 140 SAKTTPPSVYPLAPGSAATNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 199
QY 180 DLYTLSSVTPSPSTWPSQVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSVTPSPSTWPSQVTCNVAHPASSTKVDKKIIVPRDCG----- 243
QY 240 KSELQGTALGNLKIYYNSKAITSEKSDAQFLNTLLFKGFFTHGHPWYNDLLVDLGST 299
Db 244 -CKFCICVPEVSSVFIPEPK-----PKDVLITL----- 272
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPIINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297
QY 360 QTTVPIDVKVTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIV 410
Db 298 --DVEVHTAQTPQREOFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK--- 351
QY 411 FHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNITTSISLSISLYLYTTSIVMTQPTSL 470
Db 352 -----TISK----- 356
QY 471 VSAGDRVITTCASQSVNSDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDT 530
Db 357 ----- 356
QY 531 LTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASV 590
Db 357 -----KGRPKAPQVYTIPTPPKEQMAKDKVSL 382
QY 591 VCLNNFYPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSSMSSTLTLTDEYE 645
Db 383 TCMITDFPEDITVEWQWQPAENYKNTQPIMNT-----NGSYFVYKLVNQSKE 435
QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447

RESULT 17
US-10-384-933-9
; Sequence 9, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
```

```

; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-9

Query Match      29.1%; Score 1025.5; DB 14; Length 464;
Best Local Similarity 36.2%; Pred. No. 3.2e-48;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYIMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEVLKPGASVKLSKASGYTFTSYMQWVKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NQKPKKATLTVDKSSSTAYMELRSLTSEDSAVYICARS-TMITNYMDYWGQTSVTVS 119
Db 80 NQKPKKATLTVDTSSTAYMQLSSLTSEDSAVYICARNRDYSNNWYFDVWGTGTTVTVS 139
QY 120 SAKTTPPSVYPLAPGSAATNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 179
Db 140 SAKTTPPSVYPLAPGSAATNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS 199
QY 180 DLYTLSSVTPSPSTWPSQVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSVTPSPSTWPSQVTCNVAHPASSTKVDKKIIVPRDCG----- 243
QY 240 KSELQGTALGNLKIYYNSKAITSEKSDAQFLNTLLFKGFFTHGHPWYNDLLVDLGST 299
Db 244 -CKFCICVPEVSSVFIPEPK-----PKDVLITL----- 272
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPIINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297
QY 360 QTTVPIDVKVTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIV 410
Db 298 --DVEVHTAQTPQREOFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK--- 351
QY 411 FHSSEGSTVSYDLFDAQQGVPDTLLRIYRDNITTSISLSISLYLYTTSIVMTQPTSL 470
Db 352 -----TISK----- 356
QY 471 VSAGDRVITTCASQSVNSDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDT 530
Db 357 ----- 356
QY 531 LTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASV 590
Db 357 -----KGRPKAPQVYTIPTPPKEQMAKDKVSL 382
QY 591 VCLNNFYPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSSMSSTLTLTDEYE 645
Db 383 TCMITDFPEDITVEWQWQPAENYKNTQPIMNT-----NGSYFVYKLVNQSKE 435
QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447

RESULT 18
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erqiang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETED
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
```

FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 613
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14

Query Match 29.1%; Score 1024.5; DB 9; Length 613;
Best Local Similarity 37.3%; Pred. No. 5e-48;
Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;

QY 1 EVQLQDSGPDLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQDSGPELVKPGASVKISCKASGYFTDYNNHWVKQSHGKSLWIGYIYPKGGTGY 79
QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDASAVYCARSTMTINVMYDYGQGTSTVSS 132
QY 121 AKTTPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 180
DB 133 AKTTPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 192
QY 181 LYTSSSVTPSPSTWPTSTVTCNVAHPASSTKVDKXIVPRDSGGSPSEKSEINEKDLRKK 240
DB 193 LYTSSSVTPSPSTWPTSTVTCNVAHPASSTKVDKXIVPRDCG-----PKDVLITL 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTCAGYGVTHDNNRLTEKVKYPIINLWDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY 361 TTPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-VNSDSFGKVGQGLIVF 411
DB 290 -DVEHTAQTPREBQFNSTFRSVSELPIMHQDWLNGKEFKRVNSAAPPAPIEK----- 343
QY 412 HSEGSTVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSISLYLTTTSIVMTQTPTSLV 471
DB 344 -----TISK----- 348
QY 472 SAGDRVTITCKASQSVSNDAVYQKPGQSKLLISYTSRYAGVPDRFSGSGYGTDTL 531
DB 349 ----- 348
QY 532 TISSVQAEADAAYVFCQDYNSTFRSGGTKEIKRADAAPTYSIFPPSSSGLTSGGASV 591
DB 349 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 375
QY 592 CFLNNFYKIDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTITKDEYERHNSYT 651
DB 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPTIMDT-DGSYFYVSKLVNQRKSNWEAGNTFI 433
QY 652 CEATHKSTSP 662
DB 434 CSVLHEFCRYP 444

RESULT 19

US-09-903-327A-2

; Sequence 2, Application US/09903327A

; Patent No. US2002016433A1

GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETED
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 456
TYPE: PRT
ORGANISM: Mouse
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2

Query Match 29.1%; Score 1023.5; DB 9; Length 456;
Best Local Similarity 37.4%; Pred. No. 4.1e-48;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQDSGPDLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQDSGPELVKPGASVKISCKASGYFTDYNNHWVKQSHGKSLWIGYIYPKGGTGY 79
QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDASAVYCARSTMTINVMYDYGQGTSTVSS 132
QY 121 AKTTPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 180
DB 133 AKTTPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGSLSSGVHTFPVQLQSD 192
QY 181 LYTSSSVTPSPSTWPTSTVTCNVAHPASSTKVDKXIVPRDSGGSPSEKSEINEKDLRKK 240
DB 193 LYTSSSVTPSPSTWPTSTVTCNVAHPASSTKVDKXIVPRDCG-----PKDVLITL 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTCAGYGVTHDNNRLTEKVKYPIINLWDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY 361 TTPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-VNSDSFGKVGQGLIVF 411
DB 290 -DVEHTAQTPREBQFNSTFRSVSELPIMHQDWLNGKEFKRVNSAAPPAPIEK----- 343
QY 412 HSEGSTVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSISLYLTTTSIVMTQTPTSLV 471
DB 344 -----TISK----- 348
QY 472 SAGDRVTITCKASQSVSNDAVYQKPGQSKLLISYTSRYAGVPDRFSGSGYGTDTL 531
DB 349 ----- 348
QY 532 TISSVQAEADAAYVFCQDYNSTFRSGGTKEIKRADAAPTYSIFPPSSSGLTSGGASV 591
DB 349 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 375
QY 592 CFLNNFYKIDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTITKDEYERHNSYT 651
DB 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPTIMDT-DGSYFYVSKLVNQRKSNWEAGNTFI 433
QY 652 CEATHK 657

Db 434 CSVLHE 439

RESULT 20

US-09-903-327A-13

Sequence 13, Application US/09903327A

Patent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erlang

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

TITLE OF INVENTION: GENE

FILE REFERENCE: 22908-1228

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/903,327A

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 493

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

OTHER INFORMATION: and EGF mature peptide

US-09-903-327A-13

Query Match 29.1%; Score 1023.5; DB 9; Length 493;

Best Local Similarity 37.4%; Pred. No. 4.4e-48;

Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVKQSPGKGLWIGRINPNNGVTLY 60

Db 20 EVLOQSGPELVKPGASVKISCKASGYFTDYNMHVKQSHGKSLWIGIYIPYKGTGY 79

QY 61 NQKFKDKATLVDSSTAYMELRLSITSDSAVYICARSTMTITNYMDYWGOGTSVTSS 120

Db 80 NQKFKSKATLTDDSSNTAYMELRLSITSDSAVYICARG-----IAYWGQGLTVTSA 132

QY 121 AKTTPSVVPLAPGSAAGTNSMTVLCGLVKGYPPEPVTVTNWGSLSGSHVHTFPVAVLQSD 180

Db 133 AKTTPSVVPLAPGSAAGTNSMTVLCGLVKGYPPEPVTVTNWGSLSGSHVHTFPVAVLQSD 192

QY 181 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240

Db 193 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVDKIVPRDCG-----235

QY 241 SELOGTALGNLKIYYNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVGLSTA 300

Db 236 CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----264

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMVGVTLDHNNRLTEKKVPINLWIDGKQ 360

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV---289

QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLIVF 411

Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----343

QY 412 HSESGSTVSVDLFDAGQYPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTFTSLV 471

Db 344 -----TISK-----348

QY 472 SAGDRVTITCKASQSVSNDVAVYQKPGQSKLLISYTSRVRAGVDRFSGSGYGTDFTL 531

Db 349 -----348

QY 532 TISSVQAEAAVYFCQDYNSPPTFGGKTLSEIKRADAAPTIVSPPSSEQLTSGASV 591

Db 349 -----KGRPKAPQVYITFPPEKQMAKDKVSLT 375

QY 592 CFLANFPKQINVKWKIDGSRQGVNLNSWTDQDSKDYSTYSMSSTLTTLTKDEYERHNSYT 651

Db 376 CMITDFFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFYKSLAVQKSNWEAGNTFI 433

QY 652 CEATHK 657

Db 434 CSVLHE 439

RESULT 21

US-09-903-327A-12

Sequence 12, Application US/09903327A

Patent No. US20020164333A1

GENERAL INFORMATION:

APPLICANT: Nemerow, Glen R.

APPLICANT: Li, Erlang

TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

TITLE OF INVENTION: GENE

FILE REFERENCE: 22908-1228

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US/09/903,327A

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 510

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

OTHER INFORMATION: and IGF-1 mature peptide

US-09-903-327A-12

Query Match 29.1%; Score 1023.5; DB 9; Length 510;

Best Local Similarity 37.4%; Pred. No. 4.4e-48;

Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVKQSPGKGLWIGRINPNNGVTLY 60

Db 20 EVLOQSGPELVKPGASVKISCKASGYFTDYNMHVKQSHGKSLWIGIYIPYKGTGY 79

QY 61 NQKFKDKATLVDSSTAYMELRLSITSDSAVYICARSTMTITNYMDYWGOGTSVTSS 120

Db 80 NQKFKSKATLTDDSSNTAYMELRLSITSDSAVYICARG-----IAYWGQGLTVTSA 132

QY 121 AKTTPSVVPLAPGSAAGTNSMTVLCGLVKGYPPEPVTVTNWGSLSGSHVHTFPVAVLQSD 180

Db 133 AKTTPSVVPLAPGSAAGTNSMTVLCGLVKGYPPEPVTVTNWGSLSGSHVHTFPVAVLQSD 192

QY 181 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240

Db 193 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVDKIVPRDCG-----235

QY 241 SELOGTALGNLKIYYNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVGLSTA 300

Db 236 CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----264

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMVGVTLDHNNRLTEKKVPINLWIDGKQ 360

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV---289

QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLIVF 411

Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK-----343

QY 412 HSESGSTVSVDLFDAGQYPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTFTSLV 471

Db 344 -----TISK-----348

QY 472 SAGDRVTITCKASQSVSNDVAVYQKPGQSKLLISYTSRVRAGVDRFSGSGYGTDFTL 531

Db 349 ----- 348

QY 532 TISSVQAEADAAVFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPSSSEQLTSGGASVV 591

Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDVKSLT 375

QY 592 CFLANFYPKDINVKWKIDGSRONGVLSWTDQDSKDYSSMSSTLTLTDEYERHNSYT 651

Db 376 CMTDFFPEDITVEMQWNGQPAEN-YKNTQIPMDT-DGSYFVYKLVNQKSNWEAGNTFI 433

QY 652 CEATHK 657

Db 434 CSVLHE 439

RESULT 22

US-09-903-327A-6

; Sequence 6, Application US/09903327A

; Patent No. US2002016433A1

; GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Erguang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; TITLE OF INVENTION: GENE

; TITLE OF INVENTION: DELIVERY

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 438

; TYPE: PRT

; ORGANISM: Mouse

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (0)...(0)

; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein

; OTHER INFORMATION: bifunctional antibody

US-09-903-327A-6

Query Match 29.0%; Score 1022.5; DB 9; Length 438;

Best Local Similarity 37.4%; Pred. No. 4.4e-48;

Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKGLEWIGRINPNNGVTLY 60

Db 20 EVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKGLEWIGRINPNNGVTLY 60

QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDSSAVYYCARSTMTITNYMDYWGQGTSTVTVSS 120

Db 80 NQKFKSKATLTDTSSNTAYMELSLTSDASAVYYCARG-----IAYWGQGLTVTVA 132

QY 121 AKTTPSPVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTIWNSSLSGGVHTFPVAVLQSD 180

Db 133 AKTTPSPVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTIWNSSLSGGVHTFPVAVLQSD 192

QY 181 LYTLSSTVTPSSVTPSEETVCNVAHPASSSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240

Db 193 LYTLSSTVTPSSVTPSEETVCNVAHPASSSTKVDKIVPRDCG----- 235

QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDFLNTLLFKGFTFGHPWYNLLVDLGSTA 300

Db 236 CKPCICTVPEVSSVFIPEPK-----PKDVLATLT----- 264

QY 301 ATSEVEGSSVDLYGAYGYQCAGGTGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360

Db 265 -----TP-KVTCVVVDIS-----KDPPEVQPSFVFD--- 289

QY 361 TTVPIDKVTYSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411

Db 361 TTVPIDKVTYSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411

Db 290 -DVEVHTAQTPREBQFNSTFRSVSELPIMHQDMLNGKEFKCRVNSAAPPAPIEK----- 343

QY 412 HSESGTSVSYDLFDAGQGYPTLLRIYRDNTTISTSTLSISLYLYTTSIVMTQPTSTLLV 471

Db 344 -----TISK----- 348

QY 472 SAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFL 531

Db 349 ----- 348

QY 532 TISSVQAEADAAVFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPSSSEQLTSGGASVV 591

Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDVKSLT 375

QY 592 CFLANFYPKDINVKWKIDGSRONGVLSWTDQDSKDYSSMSSTLTLTDEYERHNSYT 651

Db 376 CMTDFFPEDITVEMQWNGQPAEN-YKNTQIPMDT-DGSYFVYKLVNQKSNWEAGNTFI 433

QY 652 CEATHK 656

Db 434 CSVLH 438

RESULT 23

US-10-679-620-94

; Sequence 94, Application US/10679620

; Publication No. US20040110930A1

; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology

; APPLICANT: Reihl, Stephen J.

; APPLICANT: Edwards, Patricia C.

; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING

; FILE REFERENCE: 34150-004A

; CURRENT APPLICATION NUMBER: US/10/679,620

; CURRENT FILING DATE: 2003-10-03

; PRIOR APPLICATION NUMBER: 60/415,940

; PRIOR FILING DATE: 2002-10-03

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 94

; LENGTH: 700

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: pLSBC1773, see Example 14

US-10-679-620-94

Query Match 28.4%; Score 1000; DB 16; Length 700;

Best Local Similarity 36.8%; Pred. No. 1.2e-46;

Matches 242; Conservative 54; Mismatches 131; Indels 230; Gaps 11;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKGLEWIGRINPNNGVTLY 60

Db 257 QVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKGLEWIGRINPNNGVTLY 60

QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDSSAVYYCARSTMTITNYMDYWGQGTSTVTVSS 120

Db 317 DPKFQDKATITADTSNTAYLQVSLTSEDIAVYCSRNGGDFYAMDYWGQASVTVSS 376

QY 121 AKTTPSPVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTIWNSSLSGGVHTFPVAVLQSD 180

Db 377 AKTTPSPVYPLAPGSAAGTNSMVLGCLVKGYFPEPTVTIWNSSLSGGVHTFPVAVLQSD 436

QY 181 LYTLSSTVTPSSVTPSEETVCNVAHPASSSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240

Db 437 LYTLSSTVTPSSVTPSEETVCNVAHPASSSTKVDKIVPRDCG----- 479

QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDFLNTLLFKGFTFGHPWYNLLVDLGSTA 300

Db 480 -----CKPC----- 483

QY 301 ATSEVEGSSVDLYGAYGYQCAGGTGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360

Db 301 ATSEVEGSSVDLYGAYGYQCAGGTGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWDGKQ 360

Db 484 ICTVPEVSSVIF-----PPK-----PKDVTITLTPKV 512
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDFGKVGQRLIVFHSSEGSTVS 420
 Db 513 TCWVD---ISKDDPEVQ-----FS 529
 QY 421 YLDFDAQGVPTDLLRIYRDNTTISSTLSISLYLTTIVMTQTPTSLVVSAGDRVIT 480
 Db 530 WFVDDVEVHTAQTPREEOFNSTFRSVS-----ELPIMHQD----- 565
 QY 481 CKASQSVNDVAVYQKPGSKLLSYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQABD 540
 Db 566 -----WLNKDFKC-----RVNSAAPPAPIEKTIS----- 590
 QY 541 AAVYFCQDYNSTPTFGGKTLEIKRADAAPTYSIFPPSSSEOLTSGASWVCFLLNFPYK 600
 Db 591 -----KTKGRPKAPQVYTIPTTPEKEQWAKDKVSLTCTWIDTFPE 628
 QY 601 DINVKKIDGSRONGVNSWTDQSDKSTYSNSSTLTITKBEYERHNSYTCETHK 657
 Db 629 DITVEQWNGQPAEN-YKNTQPIMDT-DGSYFYSKLVQKNWEAGNTFTCSVLHE 683

RESULT 24
 US-10-071-485-90
 ; Sequence 90, Application US/10071485
 ; Publication No. US20030099648A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Buyse, Marie-Ange
 ; APPLICANT: Sablon, Erwin
 ; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
 ; TITLE OF INVENTION: SHOCK
 ; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
 ; FILE REFERENCE: INNS:015
 ; CURRENT APPLICATION NUMBER: US/10/071,485
 ; CURRENT FILING DATE: 2002-02-07
 ; PRIOR APPLICATION NUMBER: 09/485,737
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
 ; PRIOR FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: EPO 98870139.7
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: EPO 97870122.5
 ; PRIOR FILING DATE: 1997-08-18
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 711
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC
 US-10-071-485-90

Query Match 27.8%; Score 980.5; DB 14; Length 711;
 Best Local Similarity 35.3%; Pred. No. 1.5e-45;
 Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
 Db 21 QVQLVSGSELKPKGASVKISKASGYTFTDYGMMVVKQAPGQGLKMWGINTYTGESTY 80
 QY 61 NQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMITNTYMDYWGQGSTVTVSS 120
 Db 81 VDDFKGRFVFLDTSVSAAYLQISLKAEDTATYFCARGF---YAMDYWGQGTIVTVSS 137
 QY 121 AKTTPSPVPLAPGSAQAQNSMTVLCGLVKGFPEPPTVTVNSGSLSSGVHTFPVAVLQSD 180
 Db 138 ASTKGSVFPFLAPSSKSTSGTAAALCGLVKDYFPPEPPTVSMNSGALTSVHTFPVAVLQSS 197
 QY 181 -LYLSSVTVPSSTWPSSTVTCNVAPASSTKVDKKIVPRDS-----GG 224
 Db 198 GLYSLSVTVTVPSSSLGCTQYICNVNPKSNKVKRVEPKSCDKTHICTPCPAPELLGG 257

QY 225 PS-----EKSEEI-----NEKDLRKSELOGTALGNLK---QIYYN 258
 Db 258 PSVFLPPPKPKDITLMISRTPEVTCVVVDVSHEDDEVKFNWTVGVGVHNAKTKPREQYN 317
 QY 259 S-----KATTS-EK-----SADQ 271
 Db 318 STYRVSVLTVLHQDWLNGKEYCKCKVSNKALPASIETKISKAKGQPREPQVYVITLPPSREE 377
 QY 272 FLTN-----TLFLKGFETCHPMYNDLLVLDLSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
 Db 378 MTKQVSLTCLVKGFY-----SDIAVESNGOPENNYKITPPVLDSDSGSFYLYSKL-- 430
 QY 325 TPNTACMGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTIVPIDKY 368
 Db 431 TVDKSRVQOQGNVFCVSMVHEALHNYTKQSLSLSPGKLGGSQVQLVQSGSELKPKGASV 490
 QY 369 KTSKEVTVQELDLQARHYLHGKFGLYNSDFGKVGQRLIVFHSSEGSTVSVDLFDPAQ 428
 Db 491 KISCK-----ASGYTFTDYGMMVVKQAPGQGLKMWGINTYTGESTYVD--DFKG 538
 QY 429 QYPTLLRIYRDNTTISSTLSIS-----LYLYT----- 457
 Db 539 RF-----VFSLDTSVSAAYLQISLKAEDTATYFCARGFYAMDYWGQGTIVTVSSGGG 592
 QY 458 -----TSIVMTQTPTSLVVSAGDRVITTCASQSVNSDVAVYQKPGQSPKLLI 506
 Db 593 GSGGSGSGGSDIVLTQSPATMSAPGERVTLTCSASSISY-MFWYHORPGQSPRLII 651
 QY 507 SYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQAEADAAYVFCQDYNSTPTFGGQTKLEIKR 566
 Db 552 YDTSNLAGVPAFSGSGSGTSYSLTISRMEPEDEFAFYFCHQSSSYFTFGQGTKEIKR 711

RESULT 25
 US-10-410-907A-36
 ; Sequence 36, Application US/10410907A
 ; Publication No. US20030215880A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis R. Burton
 ; APPLICANT: R. Anthony Williamson
 ; APPLICANT: Gianluca Moroncini
 ; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 22908-1229
 ; CURRENT APPLICATION NUMBER: US/10/410,907A
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/371,610
 ; PRIOR FILING DATE: 2002-04-09
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: D18 Heavy Chain
 US-10-410-907A-36
 Query Match 27.8%; Score 979.5; DB 15; Length 223;
 Best Local Similarity 87.4%; Pred. No. 4.6e-46;
 Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 59
 Db 3 EVQLLESGSELKPKGASVKISKASRYTFTDYMVMWVKQSHGKRLIEWIGIYIPNTGVG 62
 QY 60 YNQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMITNTYMDYWGQGSTVTVS 119
 Db 63 YNQRFKDKATLTVDKSSSTAYMELRLSITSDSAVYICAG----FYGMDYWGQGSTVTVS 118
 QY 120 SAKTTPSPVPLAPGSAQAQNSMTVLCGLVKGFPEPPTVTVNSGSLSSGVHTFPVAVLQ 179

Db 119 SAKTTPSVYPLAPGSAQTNSMVLGCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLQY 178
 QY 180 DLYTLSSSVTPSSVTPSWPSETVTCNVAHPASSTKVDDKIVPRD 221
 Db 179 DLYTMSSSVTPSSVTPSWPSETVTCNVAHPASSTKVDDKIVPRD 220

RESULT 26
 US-10-334-235-37
 ; Sequence 37, Application US/10334235
 ; Publication No. US20040131591A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oxford Biomedica (UK) Ltd.
 ; APPLICANT: Kingsman, Alan
 ; APPLICANT: Bebbington, Christopher
 ; APPLICANT: Carroll, Miles
 ; APPLICANT: Ellard, Fiona
 ; APPLICANT: Kingsman, Susan
 ; APPLICANT: Myers, Kevin
 ; APPLICANT: Lamikandra, Abigail
 ; TITLE OF INVENTION: VECTOR SYSTEM
 ; FILE REFERENCE: 532682000920
 ; CURRENT APPLICATION NUMBER: US/10/334,235
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 10/060,585
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04317
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 09/445,375
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: mature secreted protein of 5T4 scFv, designated
 ; OTHER INFORMATION: 5T4scFv.1
 US-10-334-235-37

Query Match 27.6%; Score 972.5; DB 16; Length 243;
 Best Local Similarity 40.1%; Pred. No. 1.2e-45;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTVS 120
 Db 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTVS- 119
 QY 121 AKTTPSVYPLAPGSAQTNSMVLGCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLQSD 180
 Db 120 ----- 119
 QY 181 LYTLSSTVTPSSVTPSWPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
 Db 120 ----- 122
 QY 241 SELOGTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGKQ 360
 Db 123 ----- 132
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFLYNSDSFGKVGQVGLIVFHSSEGSTVS 420
 Db 133 ----- 134

QY 421 YDLFDAQQYPTDLLRIYRDNTTSS"SLSLSLYLYTTSIWMTOTPTPTSLLSVAGDRVTIT 480
 Db 135 -----SSIVMTQTPTFLLSVAGDRVTIT 157
 QY 481 CKASQSVNDVANYOQKPGQSPKLLISYTSRYAGVDPDRSGSGVGTDTFTLTISVQAE 540
 Db 158 CKASQSVNDVANYOQKPGQSPKLLISYTSRYAGVDPDRFGICSGYGTDTFTLTQAE 217
 QY 541 AAVYFCQDYNSPPTFGGKLEIKR 566
 Db 218 LAVYFCQDYNSPPTFGGKLEIKR 243

RESULT 27
 US-10-334-235-39
 ; Sequence 39, Application US/10334235
 ; Publication No. US20040131591A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oxford Biomedica (UK) Ltd.
 ; APPLICANT: Kingsman, Alan
 ; APPLICANT: Bebbington, Christopher
 ; APPLICANT: Carroll, Miles
 ; APPLICANT: Ellard, Fiona
 ; APPLICANT: Kingsman, Susan
 ; APPLICANT: Myers, Kevin
 ; APPLICANT: Lamikandra, Abigail
 ; TITLE OF INVENTION: VECTOR SYSTEM
 ; FILE REFERENCE: 532682000920
 ; CURRENT APPLICATION NUMBER: US/10/334,235
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 10/060,585
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04317
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 09/445,375
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 39
 ; LENGTH: 488
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide of B7-1.5T4.1
 US-10-334-235-39

Query Match 27.5%; Score 967.5; DB 16; Length 488;
 Best Local Similarity 40.0%; Pred. No. 5e-45; 13; Indels 323; Gaps 5;
 Matches 226; Conservative 3; Mismatches

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
 Db 247 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 306
 QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTVS 120
 Db 307 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTVS- 365
 QY 121 AKTTPSVYPLAPGSAQTNSMVLGCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLQSD 180
 Db 366 ----- 365
 QY 181 LYTLSSTVTPSSVTPSWPSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
 Db 366 ----- 368
 QY 241 SELOGTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 369 ----- 368
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGKQ 360
 Db 369 ----- 378

Db 2 IVMTQSHKFMSTVGDVRVSTCKASQDVNTAVAWYQKPGHSPKLLIYSASFRTYGVPR 61

QY 520 FSGSGYGTDFTLTSSVQAEDAAVYFCQDYNGPPTFGGOTKLEIKRADAAPTVSIFPPS 579

Db 62 FTGNRSGDTFTTSSVQAEDAAVYFCQDYNGPPTFGGOTKLEIKRADAAPTVSIFPPS 121

QY 580 SEQLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 639

Db 122 SEQLTSGGASVVCFLNFPKIDINVKKIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 181

QY 640 TKDEYERHNSYTCEATHKTSPIVKSFRNE 671

Db 182 TKDEYERHNSYTCEATHKTSPIVKSFRNE 213

RESULT 31

US-09-795-515-7

Sequence 7, Application US/09795515

Publication No. US20030039645A1

GENERAL INFORMATION:

APPLICANT: Adair, John R.

APPLICANT: Athwal, Diljeet S.

APPLICANT: Emtage, John S.

TITLE OF INVENTION: Humanised Antibodies

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/795,515

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/846,658

FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yatko

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0057

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 468 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-795-515-7

Query Match 27.2%; Score 957; DB 10; Length 468;

Best Local Similarity 34.7%; Pred. No. 1.8e-44;

Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

QY 1 EVQLQQSGDILVKGPGASVKISKASGYSFTGYHHWKQSPGKGLEWIGRINPENGVTLY 60

Db 20 QVQLQQSGAEELARPAGASVKMSCKASGYTFRTYTHVWKQREGQGLEWIGYINPSRGYTN 79

QY 61 NQKPKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMITNYMDYNGQGSVTVSS 120

Db 80 NQKPKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMITNYMDYNGQGSVTVSS 138

QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYPPEVTLTWNSGSLSGVHTFPVAVLQSD 180

Db 139 AKTTPPSVYPLAPVCGDITGSSVTLGCLVKGYPPEVTLTWNSGSLSGVHTFPVAVLQSD 198

QY 181 LYTSSSVTVSSWTSPSTVTCNVAHPASSTKYDKKIVPRDSGGPSPKSESEINEKDLRKK 240

Db 199 LYTSSSVTVSSWTSPSQSITCNVAHPASSTKYDKKIEPR---GPTIKPCP----- 246

QY 241 SELQGTALGNLKQIYYVNSKAITSEKSDQFLNTLLFKGFFTGHPWYNLLVDLGSTA 300

Db 247 ----- 246

QY 301 ATSEYEGSVLDYGAAYGYQCAGTPNKATCMYGGVTLHNNRLTEKKVPINLWIDCKQ 360

Db 247 -----PCKCPAPN-----LLGGPSVF----- 262

QY 361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGSTVS 420

Db 263 -----IFPPKIKDVLMI---SLSPITV 281

QY 421 YDLFDAQCGYDPTLLRIYRDNTTISSTLSISLYLTTISYMTOTPTSLLSVAGDRTVIT 480

Db 282 CVVVDVSEDDPD-----VQISWFWANVEVHTAQTOT----- 312

QY 481 CKASQSVNDVANYQOKPGQSPKLLISYTSRYAGVPRFSGSGVGTDFTLTISVQAED 540

Db 313 -----HREDYNSTLRVV----- 324

QY 541 AAVYFCQDYNSPPTFGGOTKLEIKRAD-----AAPTVSIFPPSSQLT 584

Db 325 SALPFIHQDQWMSGKEF---KCKYNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380

QY 585 SGASVVCFLNFPKIDINVKKIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 639

Db 381 KQAVTLTCWTDMPEDIYVETNNGKTELNYKTEPVLDSE-----DGSYFYMSKLURV 433

QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFRN 669

Db 434 EKXNWNERNISYSCSVVHGLNHHHTKSF 464

RESULT 32

US-10-704-352-7

Sequence 7, Application US/10704352

Publication No. US20040071693A1

GENERAL INFORMATION:

APPLICANT: Adair, John R.

APPLICANT: Athwal, Diljeet S.

APPLICANT: Emtage, John S.

TITLE OF INVENTION: Humanised Antibodies

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/704,352

FILING DATE: 07-Nov-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/795,515

FILING DATE: 28-FEB-2001

APPLICATION NUMBER: 08/846,658

FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trujillo, Doreen Yatko

REGISTRATION NUMBER: 35,719


```
;
;
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-704-352-7

Query Match      27.2%; Score 957; DB 12; Length 468;
Best Local Similarity 34.7%; Pred. No. 1.8e-44;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQSGAELARPGASVMSCKASGYTFTRYTMHWVKQSPGQLEWIGVINPSRGYTN 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSEDYAVYCARSTMTINYYMDYWGQSTVTVSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NQKFKDKATLTVDKSTTAYMELSLTSEDYAVYCARSTMTINYYMDYWGQSTVTVSS 138
QY 121 AKTTPSVVPLAPGSAQAQNSMVTGLVKGYFPEPTVTWNSSGSLSSGVHTTFAVLQSD 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 AKTTAPSVVPLAPVCGDTTGGSVTLGCLVKGTPEPTVTWNSSGSLSSGVHTTFAVLQSD 198
QY 181 LYTSSSVTPSPSTWPSSEITCNVAHPASTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 LYTSSSVTPSTWPSQSITCNVAHPASTKVDKIEPR---GPTIKPCP----- 246
QY 241 SELQGTALGNLKQIYYNKAITSSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYOCAGTGNKTCMVGVTLDHNNRLTEKKVPINLWIDGKQ 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 -----PCKCPAPN-----LLGSPSVF----- 262
QY 361 TTVPIDVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVFHSSEGSTVS 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
263 -----IPPKIKDVLMI---SLSPIVT 281
QY 421 YLFDAGQGYPTLLRIYRDNNTTISLSISLYTTSIVMTQTPTSLLSAGDRVTIT 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
282 CVVVDVSEDDPD-----VQISGFVNVNVEVHTAQIT----- 312
QY 481 CRASQSVNDVANYQKPGQSPKLLISYTSRYAGVPRDFSGSGYGTDTFTLISSVQAE 540
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
313 -----HREDYNSTLRVY----- 324
QY 541 AAVYFCQDYNPPTFGGQTKLEIKRAD-----AAPTYSIFPPSSEQLT 584
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 SALPIQHQDWSGKEF---KCKVNNKDLPAPIERTISKPGSVRAPQYVILFPPEEEMT 380
QY 585 SGASVVCFLNFPYKIDNKKIDGSEKQ-----GVLSNWTDDQSKDSTYSMSSTLT 639
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 KKQVTLTCVMTDMPEDIYVETWNTNGKTELNKNTEPVLDSD-----DGSYFMTSKLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 EKKWVTERNSYSCSVVHEGLHNNHTTKSFNR 464
```

RESULT 33

```
US-10-704-071-7
; Sequence 7, Application US/10704071
; Publication No. US20040076627A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
```

```
;
;
; Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,071
; FILING DATE: 07-Nov-2003
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-704-071-7
```

```
Query Match      27.2%; Score 957; DB 16; Length 468;
Best Local Similarity 34.7%; Pred. No. 1.8e-44;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQSGAELARPGASVMSCKASGYTFTRYTMHWVKQSPGQLEWIGVINPSRGYTN 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSEDYAVYCARSTMTINYYMDYWGQSTVTVSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NQKFKDKATLTVDKSTTAYMELSLTSEDYAVYCARSTMTINYYMDYWGQSTVTVSS 138
QY 121 AKTTPSVVPLAPGSAQAQNSMVTGLVKGYFPEPTVTWNSSGSLSSGVHTTFAVLQSD 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 AKTTAPSVVPLAPVCGDTTGGSVTLGCLVKGTPEPTVTWNSSGSLSSGVHTTFAVLQSD 198
QY 181 LYTSSSVTPSPSTWPSSEITCNVAHPASTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 LYTSSSVTPSTWPSQSITCNVAHPASTKVDKIEPR---GPTIKPCP----- 246
QY 241 SELQGTALGNLKQIYYNKAITSSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYOCAGTGNKTCMVGVTLDHNNRLTEKKVPINLWIDGKQ 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
247 -----PCKCPAPN-----LLGSPSVF----- 262
QY 361 TTVPIDVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVFHSSEGSTVS 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
263 -----IPPKIKDVLMI---SLSPIVT 281
QY 421 YLFDAGQGYPTLLRIYRDNNTTISLSISLYTTSIVMTQTPTSLLSAGDRVTIT 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
282 CVVVDVSEDDPD-----VQISGFVNVNVEVHTAQIT----- 312
QY 481 CRASQSVNDVANYQKPGQSPKLLISYTSRYAGVPRDFSGSGYGTDTFTLISSVQAE 540
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
313 -----HREDYNSTLRVY----- 324
QY 541 AAVYFCQDYNPPTFGGQTKLEIKRAD-----AAPTYSIFPPSSEQLT 584
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
325 SALPIQHQDWSGKEF---KCKVNNKDLPAPIERTISKPGSVRAPQYVILFPPEEEMT 380
QY 585 SGASVVCFLNFPYKIDNKKIDGSEKQ-----GVLSNWTDDQSKDSTYSMSSTLT 639
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
381 KKQVTLTCVMTDMPEDIYVETWNTNGKTELNKNTEPVLDSD-----DGSYFMTSKLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
434 EKKWVTERNSYSCSVVHEGLHNNHTTKSFNR 464
```

Db 282 CVVVDSEDDP-----VOISWFWNNVEVHTACTQT----- 312
 QY 481 CKASQSVNDVAVYQXPGSPKLLISYTSRYAGVDFRSGSGYGFDTLTITSSVOAED 540
 Db 313 -----HREDYNSTLRVV----- 324
 QY 541 AAVTFCQDYNPPTFGGTHLEIKRAD-----AAPTVSIFPPSSSEOLT 584
 Db 325 SALPIQHODMWSGKEF-----KCKYNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 380
 QY 585 SGGASVVCFLNFPKIDINVKWKIDGSEKQ-----GVLNSWTDQDSKDYSGMSSTLTL 639
 Db 381 KKQVTLTCWTDWDPEDIDYVWNTNGKLTNKNTEPVLDS-----DGSYFWYKLRV 433
 QY 640 TKDEYERHNSVTCATHK-TSTSPIVKSFNR 669
 Db 434 EKKWVERNSYSCSVVHGLEHNNHTKSF 464

RESULT 34
 US-10-679-620-82
 ; Sequence 82, Application US/10679620
 ; Publication No. US20040110930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Large Scale Biology
 ; APPLICANT: Reinl, Stephen J.
 ; APPLICANT: Edwards, Patricia C.
 ; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
 ; FILE REFERENCE: 34150-004A
 ; CURRENT APPLICATION NUMBER: US/10/679,620
 ; CURRENT FILING DATE: 2003-10-03
 ; PRIOR APPLICATION NUMBER: 60/415,940
 ; PRIOR FILING DATE: 2002-10-03
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 82
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p4DSHy-TOPO, see Examp1 11
 US-10-679-620-82

Query Match 27.0%; Score 952; DB 16; Length 222;
 Best Local Similarity 81.4%; Pred. No. 1.5e-44;
 Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVLOOQSGPDLVKPGASVKISKASGYSTFTGYHHWYKQSPKGLWIGRINPNNGVTLY 60
 Db 1 QVLOOQSGPELVKPGASLKLCTASGFIKDTYHHWVKRPEQGLEWIGRIYPTNGYTRY 60
 QY 61 NOKFKDKATLVKDSSTTAYMELSLTSEDSAVYVCARSTMTITNYVMYDYGQGSTVTVSS 120
 Db 61 DPKFDKATITADTSNTAYLQVSLTSEDATVYVCSRWGGDGYADYWGQASVTIVSS 120
 QY 121 AKTTPPSVYPLAPGAAQTNSMTVLGCLVKGYFPPEVTVTWNSGSLSSGVTHTPPAVLQSD 180
 Db 121 AKTTPPSVYPLAPGAAQTNSMTVLGCLVKGYFPPEVTVTWNSGSLSSGVTHTPPAVLQSD 180
 QY 181 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRD 221
 Db 181 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRD 221

RESULT 35
 US-09-900-766-4
 ; Sequence 4, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN

; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P0218050/10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus sp.
 ; US-09-900-766-4

Query Match 26.9%; Score 948; DB 10; Length 233;
 Best Local Similarity 76.4%; Pred. No. 2.5e-44;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLNTLLPKGPTG 285
 Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQDQLQHTILPKGFED 60
 QY 286 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 345
 Db 61 HSWYNDLLVDFDKDIVDKYKGVLDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
 QY 346 BEKKVPINLWDGKQTVPIDVKVTSKXEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 Db 121 BEKKVPINLWDGKQTVPLETVTKNKNVTQVELDLQARRYLOKYNLYNSDVPDGKVQ 180
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQYDFTLRLRYRDNNTTISSTLSISLYLTT 458
 Db 181 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRLRYRDNNTINSENHMDIYLYTS 233

RESULT 36
 US-10-283-838-7
 ; Sequence 7, Application US/10283838
 ; Publication No. US2003002894A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; Johan Hansson, Terje Kalland, Lars
 ; Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/10/283,838
 ; FILING DATE: 30-Oct-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692
 ; FILING DATE: August 12, 1996
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 7:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match          26.9%; Score 948; DB 14; Length 233;
Best Local Similarity 76.4%; Pred. No. 2.5e-44;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSADQFLNTLLFKGFPTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDFLQHTILFKGFPTD 60
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 61 HSWYNDLLVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARRYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWLDGKQNTVPLETVKTNKNVTYVQELDLQARRYLQEKYNLYNSDVFDGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 37
US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match          26.9%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 2.8e-44;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSADQFLNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDFLQHTILFKGFPTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 85 HSWYNDLLVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTYVQELDLQARRYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTNKNVTYVQELDLQARRYLQEKYNLYNSDVFDGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 38
US-10-267-748-113
; Sequence 113, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:

```

INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113

Query Match 26.9%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 2.8e-44;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELQGTALGNLQIYYNSKAITSEKSAQDLFTLLPKGFFTG 285
DB 25 SEKSEINEKDLRKKSELQGTALGNLQIYYNEKANTENKESHQFLQHTILFKGFFTD 84

QY 286 HPWNLLVLDLSTAAISEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOQLDLQARHYLHGKFGLYNSDSFGKVKQ 405
DB 145 EEKVPINLWDGKQNTVPLETKNKQNTVQELDLQARRYLOEKYLNLYNSDVFQKVKQ 204

QY 406 RGLIVHSSSESTVSVDLFDAGQGYPTLRIYRDNTTISTSLISLYLTT 458
DB 205 RGLIVHTSTSPSYNDLFGAGQGYVNTLLRIYRDNTKNTINSENHIDIYLYTS 257

RESULT 39
US-10-281-479A-24
; Sequence 24, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. US20030133932A1e = Synthetic
US-10-281-479A-24

Query Match 26.8%; Score 945; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 3.7e-44;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

QY 453 LLYLT---TSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQQKPGQSPKLLISYT 509

DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQDVGTAVAVYQQKPGQSPKLLIYWA 72
QY 510 SSRVAGVDPFRFSGSGYGTDFLTITSSVQAEAAVYFCQDDYNSPPTFGGGTKLEIKRADA 569
DB 73 SIRHTGVDPFRFTGSGSGTDFLTITSNVQSEDLADYFCQY-YSSYRTFGGTFKLEIKRADA 131
QY 570 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKDIINWKIDGSEKQNGVLSNWTQDQSKDS 629
DB 132 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKDIINWKIDGSEKQNGVLSNWTQDQSKDS 191
QY 630 TYSMSSTLTLTQDEYERINSYTCETHTKTSTSPVKSFNRE 671
DB 192 TYSMSSTLTLTQDEYERINSYTCETHTKTSTSPVKSFNRE 233

RESULT 40
US-10-275-180A-24
; Sequence 24, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U5
; CURRENT APPLICATION NUMBER: US/10/275,180A
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./No. US20030190687A1e =
; OTHER INFORMATION: Synthetic Construct
US-10-275-180A-24

Query Match 26.8%; Score 945; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 3.7e-44;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

QY 453 LLYLT---TSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQQKPGQSPKLLISYT 509
DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQDVGTAVAVYQQKPGQSPKLLIYWA 72
QY 510 SSRVAGVDPFRFSGSGYGTDFLTITSSVQAEAAVYFCQDDYNSPPTFGGGTKLEIKRADA 569
DB 73 SIRHTGVDPFRFTGSGSGTDFLTITSNVQSEDLADYFCQY-YSSYRTFGGTFKLEIKRADA 131
QY 570 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKDIINWKIDGSEKQNGVLSNWTQDQSKDS 629
DB 132 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKDIINWKIDGSEKQNGVLSNWTQDQSKDS 191
QY 630 TYSMSSTLTLTQDEYERINSYTCETHTKTSTSPVKSFNRE 671
DB 192 TYSMSSTLTLTQDEYERINSYTCETHTKTSTSPVKSFNRE 233

RESULT 41
US-10-286-132A-24
; Sequence 24, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.

; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030198637A1e = Synthe
US-10-286-132A-24

Query Match 26.8%; Score 945; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 3.7e-44;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

QY 453 LYLVT--TSIVNTQPTSLLSAGDRVTITCKASQSVSNDAVYQQKFGQSPKLLISYT 509
DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGRVSITCKASQDVGTAFAVYQQKFGQSPKLLIYA 72

QY 510 SSRVAGVDFRFSGGVGTFTLTISVQAEADAIVYCCQDYNPPTFGGKLEIKRADA 569
DB 73 STRHTGVDFRFTSGSGGTFTLTISNVQSEDLADYFCQQ-YSSYRTFGGKLEIKRADA 131

QY 570 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLSNWTDDQSKDS 629
DB 132 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLSNWTDDQSKDS 191

QY 630 TYSMSSTLTLDKDEYRHRNSYTCATHKTSTSPVKSFRNE 671
DB 192 TYSMSSTLTLDKDEYRHRNSYTCATHKTSTSPVKSFRNE 233

RESULT 42
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmalie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match 26.8%; Score 944; DB 12; Length 233;
Best Local Similarity 76.3%; Pred. No. 4.2e-44;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELSQGTALGNLKOIYYNKAITSSEKSAQDQTLNTLLFKGFFTG 286
DB 2 EKSEINEKDLRKSELSQGTALGNLKOIYYNKAITSSEKSHDQFLQHTILFKGFFTDH 61

QY 287 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHNNRLTE 346
DB 62 SWYNDLLVDFDSKDIDVKYKGKVDLYGAYGYOCAGTGNKTACMYGGVTLHNNRLTE 121

QY 347 EKKVPINLWIDGKQTTVPIDKVTSSKEVTYQELDLQARHYLHGKFGLYNSDSFGKVQR 406
DB 122 EKKVPINLWIDGKQTTVPLETVTKNKNTVQELDLQARHYLQEKYLYNSDVFQKVQR 181

QY 407 GLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISSTLSISLYTT 458
DB 182 GLIVFHTSTPSVNYDLFGAQQYSNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 43
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 26.5%; Score 935; DB 9; Length 257;
Best Local Similarity 75.5%; Pred. No. 1.4e-43;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELSQGTALGNLKOIYYNKAITSSEKSAQDQTLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELSQGTALGNLKOIYYNKAITSSEKSHDQFLQHTILFKGFFTN 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGKVDLYGAYGYOCAGTGNKTACMYGGVTLHNNRLT 144

QY 346 EKKVPINLWIDGKQTTVPIDKVTSSKEVTYQELDLQARHYLHGKFGLYNSDSFGKVQ 405
DB 145 EKKVPINLWIDGKQTTVPLETVTKNKNTVQELDLQARHYLQEKYLYNSDVFQKVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISSTLSISLYTT 458

Db 205 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNTKNTSENHMDIYLYTS 257

RESULT 44

US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match 26.5%; Score 935; DB 10; Length 257;
Best Local Similarity 75.5%; Pred. No. 1.4e-43;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTWLFLKGFPTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTWLFLKGFPTG 84
QY 286 HPWYNDLAVDLSGAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLAVDLSGAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNTKNTSENHMDIYLYTS 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNTKNTSENHMDIYLYTS 257

RESULT 45

US-10-679-620-118
; Sequence 118, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinal, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC2523, see Example 6
US-10-679-620-118

Query Match 26.3%; Score 926; DB 16; Length 451;
Best Local Similarity 34.0%; Pred. No. 8.4e-43;
Matches 236; Conservative 59; Mismatches 129; Indels 270; Gaps 15;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSTFTDTHVHWKQRPQGLWIGFISPGNGDIRY 60

Db 1 EVQLQSGAELVKPGASVKISKASGYSTFTDTHVHWKQRPQGLWIGFISPGNGDIRY 60
QY 61 NQKFKDKATLTVDKSTTAYMELASLTSEDGAVYYCARSTMI--TNYVMDYWGQSTVTV 118
Db 61 NEKFKDKATLTADKSSSTAYMQLNSLTSEDGAVYFCKESFYVYDDNY--GDYWGQGTTLTV 119
QY 119 SSAKTPPSVPLAPGASAAQNSMTWLTCLVKGYPPEYTVTWNSGSLSSGVHFFPAVLQ 178
Db 120 SSAKTAPSVPLAPGASAAQNSMTWLTCLVKGYPPEYTVTWNSGSLSSGVHFFPAVLQ 179
QY 179 SDLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLR 238
Db 180 SDLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKKIEPR---GPTIKPCP----- 229
QY 239 KXSELOGTALGNLKOIYYNKAITSSEKSDADQFLTWLFLKGFPTGHPWYNDLVDLGS 298
Db 230 ----- 229
QY 299 TAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTBEKKVPINLWIDG 358
Db 230 -----PCKCPAPN-----LLGGPSVF----- 245
QY 359 KQTTVPIDKVTSKKEVTQVQELDLQARHYLHGKFGLYNSDSFGKVKQGLVHFSSEGST 418
Db 246 -----IPPKIKDVLMI---SLSPI 262
QY 419 VSYDLFDAQQGVPTDILLRIYRDNTTISSTLSISLYLTTIVMTQTPTSLLSAGDRVT 478
Db 263 VTCVVDVSEDDPD-----VOISFWVNNVEVHTAQOT----- 295
QY 479 ITCKASQSVNDVAVYQKQSGPKLLISYTSRYAGVDPDRFSGSGYGTDTLTLTSSVQA 538
Db 296 -----HREDYNSLTLEV-- 307
QY 539 EDAAVYFCQDYNPSPTFGGKTKLEIKRAD-----AAPTYSIIPPSSEQ 582
Db 308 --SALPIQHDWMSGKEF---KCKVNNKDLFAPERTISKPKGSVRAPQVYVLPPEE 361
QY 583 LTSGGASVVCFLNFPKIDNVKWKIDGSEQN-----GVLSNMTDQDSKDSYMSSTL 637
Db 362 MTKKQVTLTCMTDMPEDIVYEWNTNNGKTELYNKTEPVLDS-----DGSIFMYSKL 414
QY 638 TLTKDEYERHNSYTCETHK--TSTSPIVKSNRN 670
Db 415 RVEKKNNWERNYSYSCSVVHGLNHHHTTKSFHS 448

RESULT 46

US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match 26.3%; Score 925; DB 14; Length 257;
Best Local Similarity 75.1%; Pred. No. 5.1e-43;

```

Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSADOFNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAKTENKESHDQFROHTILFKGFFTD 84
QY 286 HPYNLDLVLGSLTAATSEYEGSVLDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVRFDSKDIYDKYKGGKVDLYGAYAGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 204
QY 406 RGLVHSSSGSTVSYDLFPAQOQYPTLLRIYRDNTTISSTSLSLYLYTT 458
Db 205 RGLVHSTPEPSVNYDLFGAQOQYNTLLRIYRDNTINSENHDIILYITS 257

RESULT 47
US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/982,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match 26.1%; Score 921; DB 14; Length 233;
Best Local Similarity 75.0%; Pred. No. 7.5e-43;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKKSELOQTALGNLKOIYYNSKAITSEKSADOFNTLLFKGFFTG 286
Db 2 EKSEINEKDLRKKSELOQTALGNLKOIYYNEKAKTENKESHDQFROHTILFKGFFTDH 61
QY 287 PWNDDLVLGSLTAATSEYEGSVLDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTE 346
Db 62 SWYNDLLVRFDSKDIYDKYKGGKVDLYGAYAGYOCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 347 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 406
Db 122 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 181
QY 407 RGLVHSSSGSTVSYDLFPAQOQYPTLLRIYRDNTTISSTSLSLYLYTT 458
Db 182 RGLVHSTPEPSVNYDLFGAQOQYNTLLRIYRDNTINSENHDIILYITS 233

RESULT 48
US-10-216-484-11
; Sequence 11, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haryuyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru

```

```

; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-11

Query Match 26.0%; Score 915; DB 14; Length 238;
Best Local Similarity 81.3%; Pred. No. 1.6e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVSND----VAVYQKPGQSPKLLISYTSR 512
Db 19 TGDIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDYMNWYQKPGQPKLLIYAASNL 78
QY 513 YAGVDFRFGSGGYGTDFTLTITSSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPT 572
Db 79 ESGIPARFSGSGGTDFTLNIHPVEEEDAATYYCQSNEDPRTFEGGKTKLEIKRADAAPT 138
QY 573 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 632
Db 139 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 198
QY 633 MSSTLTITKDEYERHNSYTCETHKTSPTPIVKSFNENE 671
Db 199 MSSTLTITKDEYERHNSYTCETHKTSPTPIVKSFNENE 237

RESULT 49
US-10-384-933-11
; Sequence 11, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haryuyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-11

Query Match 26.0%; Score 915; DB 14; Length 238;
Best Local Similarity 81.3%; Pred. No. 1.6e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVSND----VAVYQKPGQSPKLLISYTSR 512
Db 19 TGDIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDYMNWYQKPGQPKLLIYAASNL 78
QY 513 YAGVDFRFGSGGYGTDFTLTITSSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPT 572
Db 79 ESGIPARFSGSGGTDFTLNIHPVEEEDAATYYCQSNEDPRTFEGGKTKLEIKRADAAPT 138

```

QY 573 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 632
DB 139 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 198
QY 633 MSSTLTITKDEYERHNSYTCETHKTSTSPVKSFNRE 671
DB 199 MSSTLTITKDEYERHNSYTCETHKTSTSPVKSFNRE 237

RESULT 50

US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Evguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match 25.9%; Score 912; DB 9; Length 238;
Best Local Similarity 81.3%; Pred. No. 2.4e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVSAAGRVITTCASQSVSND-----VAWYQKPGSQKLLISYTSR 512
DB 19 TGDIVLTQSPASLAVSLQRATISCKASQSDYDGDSTVMWYQKPGSQKLLIYAAANL 78
QY 513 YAGVDPDRSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTGGGTGKLEIKRADAAPT 572
DB 79 ESGIPARFSGSGGTDFLTINHPVEEEDAAATYCCQTNEDPWTEGGGTGKLEIKRADAAPT 138
QY 573 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 632
DB 139 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 198
QY 633 MSSTLTITKDEYERHNSYTCETHKTSTSPVKSFNRE 671
DB 199 MSSTLTITKDEYERHNSYTCETHKTSTSPVKSFNRE 237

RESULT 51

US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND

COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match 25.8%; Score 908; DB 8; Length 257;
Best Local Similarity 74.2%; Pred. No. 4.3e-42;
Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSEKQGTALGNLKKIYYNEKAKTENKESHDOFFQHTILFKGFTD 285
DB 25 SEKSEINEKDLRKSEKQGTALGNLKKIYYNEKAKTENKESHDOFFQHTILFKGFTD 84
QY 286 HPWYNDLLVLDLSTAATSEYEGSSVDLYGAVYGCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVRFDSKDIVDKYKGGKVDLYGAVAGYGCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 346 EKKYVPINLWIDKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EKKYVPINLWIDKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLLRIYRDNNTTISSTLSLSLYLYTT 257

RESULT 52

US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 25.6%; Score 903; DB 8; Length 233;
Best Local Similarity 73.7%; Pred. No. 7.2e-42;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLTNLLFKGFFTH 286
DB 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKANTENKESHDQFQHTILFKGFFTH 61
QY 287 PWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 346
DB 62 SWYNDLLVDFDSKDIYDKYKXKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLMDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 406
DB 122 EKKVPINLMDGKQNTVPLETVKTNKXNTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181
QY 407 GLIVFHSSGSGTVSYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTT 458
DB 182 GLIVFHTSTPSVNYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTT 233

RESULT 53
US-10-281-479A-23
Sequence 23, Application US/10281479A
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
APPLICANT: LeBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1e = Synthe
US-10-281-479A-23

Query Match 25.6%; Score 900.5; DB 14; Length 462;
Best Local Similarity 33.1%; Pred. No. 2.1e-41;
Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;
QY 1 EVQLQQSGFDLVKPCASVKISKASGYFTGYNMHWKQSPKGLWIGRINPNNGVTLY 60
DB 20 EVMLVESGGGLVKPGSLKLSAASGFTFSSVYVMSVRQTPEKLEWVATISSGGSYTY 79
QY 61 NQKFKDKATLLVDKSSITAYMELSLTSEDSAVYCAR--STMITNYMDYWGOGTSVT 118
DB 80 PDSVKGREFTIISRDNAKNTLYLQMSLSRSEDYAMYCARGDSMITT---DYWGOGTTLTV 136
QY 119 SSAKTTTPSVYPLAPGSAQAQTNMVTLCGLVKGYFPEPPTVTWNSGSLSSGVHTFPVAVLQ 178
DB 137 SSAKTTTPSVYPLAPGSAQAQTNMVTLCGLVKGYFPEPPTVTWNSGSLSSGVHTFPVAVLQ 196
QY 179 SLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVKKIVPRDSGSGPSEKSEKSEINEKDLR 238
DB 197 SLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVKKIVPRDCG----- 241
QY 239 KKSELQGTALGNLQIYYVNSKAITSEKSDAQFLTNLLFKGFFTHGHPWYNDLLVDLGS 298
DB 242 --KPCICTVPEVSVIFPPK-----PKDVLTLTL----- 270
QY 299 TAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLMDG 358
DB 271 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD- 295
QY 359 KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLI 409
DB 296 ---DVEVHTAQTPREQFNSFTFRSVSELPFTHQDNLNGKEFKCRVNSAFAFPPIEX--- 349
QY 410 VFHSSGSGTVSYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTTISVMTQTPTSL 469
DB 350 -----TISKT----- 354
QY 470 LVSAGDRVITTCASQSVSNDVAMVQKPGSPKLLISYTSRVSAGVDPFRFSGSGYGTDF 529
DB 355 ----- 354
QY 530 TLTISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGAS 589
DB 355 -----KGRKAPQVYTIPTPKQNAKDKVS 379
QY 590 VVCFLNFFPKDINVWKIDGSEKQNGVNSWTDQDSKDYSSMSSTLTITKDEYERHNS 649
DB 380 LTCMITDFFEDITVEQWNGQPAEN-YKNTQPTIMDT-DGSYFVYKLVNYSKQNSWEAGNT 437
QY 650 YTCETHK 657
DB 438 FTSVLHE 445

RESULT 54
US-10-286-132A-23
Sequence 23, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LeBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED

; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
 ; FILE REFERENCE: 21085.002907
 ; CURRENT APPLICATION NUMBER: US/10/286.132A
 ; CURRENT FILING DATE: 2003-01-22
 ; PRIOR APPLICATION NUMBER: US 60/346,402
 ; PRIOR FILING DATE: 2001-11-01
 ; PRIOR APPLICATION NUMBER: PCT/US01/14151
 ; PRIOR FILING DATE: 2001-05-02
 ; PRIOR APPLICATION NUMBER: US 60/201,344
 ; PRIOR FILING DATE: 2000-05-02
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 462
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030198637A1e = Synthetic
 US-10-286-132A-23

Query Match 25.6%; Score 900.5; DB 14; Length 462;
 Best Local Similarity 33.1%; Pred. No. 2.1e-41;
 Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;

QY	1	EVQLQQSGDPLVKPGASVKISKASGYSFTGYMHWKQSPGKGLWIGRINPNNGVTLY	60
Db	20	EVMLVESGGGLVKPGSLKLSAASGFTFSYVMSVWVQTPEKLEWVAITSSGGSYYT	79
QY	61	NOKFKDKATLVDSKSTTAYMELRSLSLSEDSAAVYCAR--STMITNYVMDYWGQTSVTV	118
Db	80	PDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYCARRGDSMITT---DYWGQGTTLTV	136
QY	119	SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPVVTWNSGSLSGVHTFPVAVLQ	178
Db	137	SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPVVTWNSGSLSGVHTFPVAVLQ	196
QY	179	SDLYTLSSSVTPSWSEFVTCNVAHPASSTKVDKIVPRDGGSGSEKSEINEKDLR	238
Db	197	SDLYTLSSSVTPSWSEFVTCNVAHPASSTKVDKIVPRDCG-----	241
QY	239	KKSELQGTALGNLKIYYNKAITSSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGS	298
Db	242	--CKPCICTVPEVSVFIFPPK-----PKDVLITL-----	270
QY	359	KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLI	409
Db	296	---DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLWNGKEFKCRVNSAAPPAPIEK---	349
QY	410	VFHSSEGSVSYDLFPAQGGVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSL	469
Db	350	-----TISK-----	354
QY	470	LVSAGDRVITTCASQSVSNDAVANYQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTFD	529
Db	355	-----	354
QY	530	TLTISVQAEDAAVFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIIPPSSEQITSGGAS	589
Db	355	-----KGRPKAPQVVTIPPPKQKQAKDKVVS	379
QY	590	VVCFLNFPKIDINVKWIDGSEKQNGVLSNWTDDSKDSTYSMSSTLTTLTKDEYERHNS	649
Db	380	LTCMTIDFFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVSKLVQKSNWEAGNT	437
QY	650	YTCEATHK 657	
Db	438	FTCSVLHE 445	

RESULT 55
 US-10-275-180A-23
 ; Sequence 23, Application US/10275180A
 ; Publication No. US20030190687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The UAB Research Foundation
 ; APPLICANT: Zhou, Tong
 ; APPLICANT: Ichikawa, Kimihisa
 ; APPLICANT: Kimberly, Robert P.
 ; APPLICANT: Koopman, William J.
 ; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
 ; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
 ; FILE REFERENCE: 21085.002905
 ; CURRENT APPLICATION NUMBER: US/10/275,180A
 ; CURRENT FILING DATE: 2002-10-31
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 464
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030190687A1e =
 ; OTHER INFORMATION: Synthetic Construct
 US-10-275-180A-23

Query Match 25.6%; Score 900.5; DB 14; Length 464;
 Best Local Similarity 33.1%; Pred. No. 2.1e-41;
 Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;

QY	1	EVQLQQSGDPLVKPGASVKISKASGYSFTGYMHWKQSPGKGLWIGRINPNNGVTLY	60
Db	20	EVMLVESGGGLVKPGSLKLSAASGFTFSYVMSVWVQTPEKLEWVAITSSGGSYYT	79
QY	61	NOKFKDKATLVDSKSTTAYMELRSLSLSEDSAAVYCAR--STMITNYVMDYWGQTSVTV	118
Db	80	PDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYCARRGDSMITT---DYWGQGTTLTV	136
QY	119	SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPVVTWNSGSLSGVHTFPVAVLQ	178
Db	137	SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPVVTWNSGSLSGVHTFPVAVLQ	196
QY	179	SDLYTLSSSVTPSWSEFVTCNVAHPASSTKVDKIVPRDGGSGSEKSEINEKDLR	238
Db	197	SDLYTLSSSVTPSWSEFVTCNVAHPASSTKVDKIVPRDCG-----	241
QY	239	KKSELQGTALGNLKIYYNKAITSSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGS	298
Db	242	--CKPCICTVPEVSVVIFPPK-----PKDVLITL-----	270
QY	299	TAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPIINLWIDG	358
Db	271	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-295	295
QY	359	KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLI	409
Db	296	---DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLWNGKEFKCRVNSAAPPAPIEK---	349
QY	410	VFHSSEGSVSYDLFPAQGGVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSL	469
Db	350	-----TISK-----	354
QY	470	LVSAGDRVITTCASQSVSNDAVANYQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTFD	529
Db	355	-----	354
QY	530	TLTISVQAEDAAVFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIIPPSSEQITSGGAS	589
Db	355	-----KGRPKAPQVVTIPPPKQKQAKDKVVS	379
QY	590	VVCFLNFPKIDINVKWIDGSEKQNGVLSNWTDDSKDSTYSMSSTLTTLTKDEYERHNS	649
Db	380	LTCMTIDFFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVSKLVQKSNWEAGNT	437

```
QY 650 YTCETHK 657
Db 438 FTCVLHE 445

RESULT 56
US-10-679-620-80
; Sequence 80, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679, 620
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 80
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Murine [p9E10LT-TOPO, see Example 3]
US-10-679-620-80

Query Match 25.4%; Score 894; DB 16; Length 218;
Best Local Similarity 80.6%; Pred. No. 2.1e-41;
Matches 174; Conservative 13; Mismatches 25; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVN---DVAWYQKPGQSPKLLISYTSRYAG 515
Db 2 IVLTQSPASLAVSLGORATISCRASEVDNFGFMMWFQKPGQPKLLIYAIISNRSG 61

QY 516 VPDPSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGKLEIKRADAAPTYSI 575
Db 62 VPARFSGSGGTDFSLNIHPVEEDDPAMYFCQQTKEVPWTFGGTKLEIKRADAAPTYSI 121

QY 576 FPSSQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 635
Db 122 FPSSQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 181

QY 636 TLTLTKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 182 TLTLTKDEYERHNSYTCETHKTSPIVKSFNNE 217

RESULT 57
US-10-679-620-116
; Sequence 116, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679, 620
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2003-10-03
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 116
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL799, see Example 5
US-10-679-620-116

Query Match 25.4%; Score 894; DB 16; Length 712;
Best Local Similarity 80.6%; Pred. No. 7.7e-41;
Matches 174; Conservative 13; Mismatches 25; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVN---DVAWYQKPGQSPKLLISYTSRYAG 515
Db 2 IVLTQSPASLAVSLGORATISCRASEVDNFGFMMWFQKPGQPKLLIYAIISNRSG 63

QY 519 RPSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGKLEIKRADAAPTYSI 578
Db 62 RPSGSGGTYSYSLTISSEMEADAAATYCHQYHRSPLTFGAGTKLEIKRADAAPTYSI 121

QY 579 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 638
Db 122 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 181

QY 639 LTKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 182 LTKDEYERHNSYTCETHKTSPIVKSFNNE 214

RESULT 59
US-10-679-620-122
; Sequence 122, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
US-10-679-620-122

Query Match 25.3%; Score 890.5; DB 16; Length 215;
Best Local Similarity 80.8%; Pred. No. 3.2e-41;
Matches 172; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVND-VAWYQKPGQSPKLLISYTSRYAG 518
Db 2 IVLTQSPASLAVSLGERVTMTCTASSSVSSSYFHWYQKPGSSPKLWYTTSLASGVA 61

QY 519 RPSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGKLEIKRADAAPTYSI 578
Db 62 RPSGSGGTYSYSLTISSEMEADAAATYCHQYHRSPLTFGAGTKLEIKRADAAPTYSI 121

QY 579 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 638
Db 122 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 181

QY 639 LTKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 182 LTKDEYERHNSYTCETHKTSPIVKSFNNE 214

RESULT 59
US-10-679-620-122
; Sequence 122, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
US-10-679-620-122
```

```

; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 122
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL1792, see Example 6
US-10-679-620-122

Query Match      25.3%; Score 890.5; DB 16; Length 483;
Best Local Similarity 80.8%; Pred. No. 7.8e-41;
Matches 172; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 450 IWTQTPTSLVLSAGDRTITCKASQSVND-VAWYQKQKQSPKLLISYTSRYAGVDPD 518
DB 2 IVLTQSPALMSASLGERVTMTCTASSVSSSYFHWYQKQKQSPKLLIYTTISNLASGVA 61

QY 519 RFSGSGYGTDTLTISVQAEADAAYVFCQDYNPPPTFGGKLEIKRADAAPTTSIFPP 578
DB 62 RFSGSGSTSYSLTISWEADAATYCHQVRSPLTFGAGTKLEKRAADAAPTTSIFPP 121

QY 579 SSEQLTSGGASVGVFLNFPKIDINVKWKIDGSRQNGVLSNWDQDSKSTYSMSSTLT 638
DB 122 SSEQLTSGGASVGVFLNFPKIDINVKWKIDGSRQNGVLSNWDQDSKSTYSMSSTLT 181

QY 639 LTKDEYERHNSYTCETHKSTSPVKSFNNE 671
DB 182 LTKDEYERHNSYTCETHKSTSPVKSFNNE 214

RESULT 60
US-10-291-265-335
; Sequence 335, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-335

Query Match      25.1%; Score 885; DB 15; Length 363;
Best Local Similarity 30.6%; Pred. No. 1.1e-40;
Matches 205; Conservative 56; Mismatches 82; Indels 328; Gaps 5;

QY 1 EVOLQSGDPLVKGASVKISKASGYSTGYMHWKQSPKGLWIGTRINPNNGVTLY 60
DB 20 EVOLLESGLVQPGSLRLSCAASGFTTSSFSMSWRQAPKGLWSSISGSGTYY 79

```

```

QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDGAVVYCARSTMITNKMVDYWGQGTSTVSS 120
DB 80 ADSVAGRTTIISRDNSKNTLYIQMNSLRAEDTAVYCAKFPF-----YFDYWGQGTSTVSS 135
QY 121 AKTTPPSVYPLAPGSAQAQNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFFAVLQSD 180
DB 136 G----- 136
QY 181 LYTSSSVTPSSSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEBINEKDLKK 240
DB 137 ----- 136
QY 241 SELOGTALGNLKIYYNNSKAITSEKSAQDLTNLLFKGFFTHGHPWYNLLVDLQSTA 300
DB 137 ----- 136
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 137 -----DSS-----GGSS----- 143
QY 361 TTVPIDKVKTSKKEVTVOELDLQARHVLHGKFLYNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 144 -----VTVSSDIQ----- 152
QY 421 YDLFAQGYPTLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTSLIYSAGDRTIT 480
DB 153 -----MTQSPSTLSASVGDRTIT 171
QY 481 CKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVDPDFSGSGYGTDTLTISVQAEAD 540
DB 172 CKASQSVNLAWYQKQKQKAPKLLIYKASLESQVPSRFSGSGGTDTLTISLQPD 231
QY 541 AAVYFCQDYNPPPTFGGKLEIKRADAAPTTSIFPSSQSLTSGGASVGVFLNFPK 600
DB 232 FATYTCQVYVYPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNFPYR 291
QY 601 DINVKWKIDGSRQNGVLSNWDQDSKSTYSMSSTLTLTDEYERHNSYTCETHKST 660
DB 292 EAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHKLYACEVTHQGLS 351

QY 661 SPIVKSFNNE 671
DB 352 SPVTKSFNNE 362

RESULT 61
US-10-679-620-78
; Sequence 78, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 78
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Murine [p9E10Hy-TOPO, see Example 3]
US-10-679-620-78

Query Match      25.1%; Score 884.5; DB 16; Length 451;
Best Local Similarity 33.6%; Pred. No. 1.5e-40;
Matches 223; Conservative 57; Mismatches 147; Indels 237; Gaps 12;

QY 1 EVOLQSGDPLVKGASVKISKASGYSTGYMHWKQSPKGLWIGTRINPNNGVTLY 60

```



```

; SEQ ID NO 34
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Light Chain
US-10-410-907A-34

Query Match      24.6%; Score 866.5; DB 15; Length 215;
Best Local Similarity 79.2%; Pred. No. 6.5e-40;
Matches 168; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 460 IVMQTPTSLVSGADRVTTICKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDR 519
DB 4 LVLTQSPAFMSASPEKVTMTCSASSV-NYMHVYQKSGTSPKRYDYTSKLAGVPEAR 62

QY 520 FSGSGYGTDTLTSSVQAEAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFPPPS 579
DB 63 FSGSGGTYSYSLTSSMEADAATYVYQKSSNPTTGGGTKLEIKRADAAPTYSIFPPS 122

QY 580 SEQLTSGASVVCFLNFPKIDINVKKIDGSRQNGVLNSWTDQDSKSTYSMSSTLT 639
DB 123 SEQLTSGASVVCFLNFPKIDINVKKIDGRQRQNGVLNSWTDQDSKSTYSMSSTLT 182

QY 640 TKDEYERHNSYTCRATHKTSPIVKSFRNE 671
DB 183 TEDEYERHNSYTCRATHKTSPIVKSFRNE 214

RESULT 64
US-10-159-006-30
; Sequence 30, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanba, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-30

Query Match      24.5%; Score 863.5; DB 14; Length 472;
Best Local Similarity 34.0%; Pred. No. 2.3e-39;
Matches 227; Conservative 57; Mismatches 142; Indels 241; Gaps 18;

QY 1 EVQLQQSGDPLVKPGASVKISKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQQSGDPLVKPGASVKMSKTSRYTFTTEYTHHWKQSGKLEWIGRINPNNGIPNY 79

QY 61 NQKFKDKATLVKDSSTTAYMELSLTSEDSAVYVCARSTMTINY----VMDYWGQSTSV 116
DB 80 NQKFKGRATLVKGSSTTAYMELSLTSEDSAVYFCARRRYAYGDEGHANDYWGQSTSV 139

QY 117 TVSSAKTTPPSVYPLAPGSAQAQTSNMTVLGLVKRGYFPEPVYTVNWSGSLSSGVHTFP 176
DB 140 TVSSSS-TKGPSVYPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSNWSGSLTSGVHTFP 198

```

```

QY 177 IQSD-LYTLSSSVTVPSWSPSETVTCNVAHPASTKVKDKIVPRDGGPSEKSEINEK 235
DB 199 LQSSGLYSLSSVTVFSSSLGTQYICNVNHPKNTKVDKKEPKSC-----245
QY 236 DLKKSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFTGHPWYNDLLVD 295
DB 246 -----DKTHCTPCPCAPPELLGGPSVF--LPPKP--KDTLM--277
QY 296 LGSTAATSEYEGSSVDLYGAYYQCAGGTGNKTAQMYGVTLHDNNRLTEKKVPINLW 355
DB 278 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWY 303
QY 356 IDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVEHSE 415
DB 304 VDG-----VEVHNAKTPREEQ-----YNSTY---RVSVLTVLHQDW 338
QY 416 GSTSYDLDFAQGGVYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLLSVAGD 475
DB 339 LAGKEY-----344
QY 476 RVTTICKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTLTLS 535
DB 345 -----RCKVY-----NKALPAP-----TEKTSKAKGP-----368
QY 536 VQAEADAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGASVVCFLN 595
DB 369 -----REPOVYTLPPSREEMTKNQVSLTCLVK 395
QY 596 NFYPKIDINVKKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTTLTKDEYERHNSY 650
DB 396 GFYPSDIAVWEWSNGQPNNTKTPPVLDSD-----DGSFFLYSKLTVDKSRWQGGNVF 448
QY 651 TCEATHK 657
DB 449 SCSVMHE 455

RESULT 65
US-09-910-059-131
; Sequence 131, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, &
; TITLE OF INVENTION: Their Therapeutic use in an Adopt System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match      24.3%; Score 855.5; DB 9; Length 473;
Best Local Similarity 72.9%; Pred. No. 6.2e-39;
Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;

```

QY 1 EVQLQSGEDLVKPGASVKISKASGYSTGYIMHWKSPGKGLIEWIGRI-NPNNGVTL 59
Db 243 EYKLVESGGGLVQPGGSLRLSCLATSGFTFTDYIMNWVRQPPGKALEWLGFIGNKANGYTT 302
QY 60 -YNQKFKDQATLVKDSSTAYNELSLTSEDSAVYCARSTMTIYNYMDYKGGTSTVTV 118
Db 303 EYSASVKGFTISRDKSQSILYLQMTLRAEDSATYYCTDRGLRFY-FDWGQGITITV 361
QY 119 SSAKTTTPPSVYPLAPGSAQTSMTVLGCLVKGYPEPVPVTVTWNSGSLSSGVHTFPVAVLQ 178
Db 362 SSAKTTTPPSVYPLAPGSAQTSMTVLGCLVKGYPEPVPVTVTWNSGSLSSGVHTFPVAVLQ 421
QY 179 SLYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKIVPRDSG 223
Db 422 SLYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKIVPRDCG 466

RESULT 66
US-09-795-515-5
; Sequence 5, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 01-MAY-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-5

Query Match 24.2%; Score 852.5; DB 10; Length 235;
Best Local Similarity 74.9%; Pred. No. 4.2e-39;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSISLYLYTTSIVMTQPTPSLLVSGADRVITTCASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIRSGQVILVTCSPAIMASPGKVTMTCSASSSVY-MNWIYQKSGTSPKRWYD 71
QY 509 TSSRYAGVDPFRFGSGYGTDFLTISVQAEAAVYFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131
QY 569 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDIINVKWKIDGSRQNGVLSNWTDDQSKD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131

QY 569 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDIINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 TAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDIINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYMSSTLTLTDKDEYERHNSYTCETHTKTSTSPIVKSFNENE 671
Db 192 STYMSSTLTLTDKDEYERHNSYTCETHTKTSTSPIVKSFNENE 234
RESULT 67
US-10-704-352-5
; Sequence 5, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-704-352-5

Query Match 24.2%; Score 852.5; DB 12; Length 235;
Best Local Similarity 74.9%; Pred. No. 4.2e-39;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSISLYLYTTSIVMTQPTPSLLVSGADRVITTCASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIRSGQVILVTCSPAIMASPGKVTMTCSASSSVY-MNWIYQKSGTSPKRWYD 71
QY 509 TSSRYAGVDPFRFGSGYGTDFLTISVQAEAAVYFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131
QY 569 AAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDIINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 TAPTIVSIFPPSSQELTSGGASVVCFLNNFYPKDIINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYMSSTLTLTDKDEYERHNSYTCETHTKTSTSPIVKSFNENE 671

Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTKSTSPVKSFNENE 234
 |||

RESULT 68

US-10-704-071-5
 ; Sequence 5, Application US/10704071
 ; Publication No. US20040076627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Adair, John R.
 ; Athwal, Diljeet S.
 ; Emtage, John S.
 ; TITLE OF INVENTION: Humanised Antibodies
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10704,071
 FILING DATE: 07-Nov-2003
 CLASSIFICATION: (D)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,658
 FILING DATE: 01-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Irujillo, Doreen Yanko
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CARP-0057
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 235 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-704-071-5

Query Match 24.2%; Score 852.5; DB 16; Length 235;
 Best Local Similarity 74.9%; Pred. No. 4.2e-39;
 Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
 QY 449 LSISLYLTTGIVTQTPTSLVAGDRVTITCKASOSVNDVAVYQCKPGQPKLLISY 508
 Db 13 ISAVIISRGQIVITQSPAINMSAPGKVTWTCASSSVY-MNMYQCKSGTSPKRWYD 71
 QY 509 TSSRYAGVPDFSGGYGTDTFTLTSSVQAEAAVYFCQDDYNSPPTFGGKTLEIKRAD- 568
 Db 72 TSKLASGVPAHFRGSGGTSYSLTISGWEADAATYTCQWSSNPFPTFGSGTKLEINRAD 131
 QY 569 AAPTYSIIPPSSEQLTSCGASVCFNNFYKDTINVKWIDGSRQGVLSNMTDQDSKD 628
 Db 132 TAPTYSIIPPSSEQLTSCGASVCFNNFYKDTINVKWIDGSRQGVLSNMTDQDSKD 191
 QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTKSTSPVKSFNENE 671
 Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTKSTSPVKSFNENE 234

RESULT 69

US-10-467-546-4

; Sequence 4, Application US/10467546
 ; Publication No. US20040096901A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gregorio Aversa
 ; APPLICANT: Frank Kolbinger
 ; APPLICANT: Jose M. Carballido Herrera
 ; APPLICANT: Andras Aszodi
 ; APPLICANT: Jose W. Saldanha
 ; APPLICANT: Bruce M. Hall
 ; TITLE OF INVENTION: Therapeutic binding molecules
 ; FILE REFERENCE: PCT/EP02/01420
 ; CURRENT APPLICATION NUMBER: US/10/467,546
 ; CURRENT FILING DATE: 2003-08-08
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 448
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; NAME/KEY: MISC FEATURE
 ; OTHER INFORMATION: Amino acid sequence of chimeric heavy chain
 ; US-10-467-546-4

Query Match 24.2%; Score 852; DB 16; Length 448;

Best Local Similarity 33.5%; Pred. No. 9e-39;
 Matches 222; Conservative 58; Mismatches 145; Indels 238; Gaps 17;
 QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVLOQSGPELVKPGASVKMSCKASGYFTTNYIIHWKQSPGKLEWIGYENPNHGTY 60
 QY 61 NQKFKDKATLVDKSSTTAYMELSLTSEDGAVYCARSTMTITVYWDVWQCGHSTVSS 120
 Db 61 NEKFKRATLTADKSSNTAYMDLSLTSEDGAVYCARSGPYAWF--DTWQGGTIVTVSS 118
 QY 121 AKTTPSVVPLAPGSAAGTNSMTVTLGCLVKGYPPEPTVTWNSGSLSSGVHTFPFAVLQSD 180
 Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPTVSWNSGALTSGVHTFPFAVLQSS 178
 QY 181 -LYTLSSSVTVPSSTWPTSETVTCNVAHPASSTKVDKXIVPRDSGGSPSEKSEINEKDLRK 239
 Db 179 GLYSLSVVTVPPSSSLGTQTVICNVNHPKSTKVDKRVPEKSC----- 221
 QY 240 KSELQGTALGNLKOIYYNNSKAITSSSEKSAQFLNTLTLEKFFTGHPWYNDLLVDLST 299
 Db 222 -----DKTHTCPCPAPELGGPSVF--LPFPKP--KDTLM----- 253
 QY 300 AATSEYEGSSVDLYGAVYCYQCAGGTGNTACTMGVTLHDNNRLTEPKKVPINLWIDGK 359
 Db 254 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 282
 QY 360 QTTVPIDKVKTSKKTQVQELDLQARHYLHGKFGLYNSDSFGGKQVQGLIIVFHSSEGSTV 419
 Db 283 ---VEVHNAKTKPREEQ-----YNSY---RVVSYLTVLHQDWLNGK 318
 QY 420 SYDLFDAQQQYPTDLLRIYRDNTTISSTLSLSLYLTTSITWMTQTPSTLLVSAGDRVTI 479
 Db 319 EY----- 320
 QY 480 TCKASQSVNDVAVYQCKPGQSPKLLISYTSRVAGVPRDFSGSGYGTDTFTLTSSVQAF 539
 Db 321 CKKVS-----NKALPAP---IEKTSKAKGP----- 344
 QY 540 DAAVYFCQDDYNSPPTFGGKTLEIKRADAAPTYSIIPPSSEQLTSCGASVVCFLNFP 599
 Db 345 -----REPQVTLTPSREEMTKQVSLTCLVKGYFP 375
 QY 600 KDINVKWKIDGSRQK-----GVLSNMTDQDSKSTYSMSSTLTITKDEYERHNSYTC 654
 Db 376 SDIAVENWESNGQPNYNTTPPVLDSE-----DGSFFLYSKLTVDKSRWQQGNVFCGV 428
 QY 655 THK 657

Db 429 MHE 431

RESULT 70

US-10-378-567-2

; Sequence 2, Application US/10378567

; Publication No. US2004006208A1

; GENERAL INFORMATION:

; APPLICANT: KARPUSAS, MICHAEL

; APPLICANT: HSU, YEN-MING

; APPLICANT: TAYLOR, FREDERICK R.

; APPLICANT: ZHENG, ZHONGLI

; TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND

; FILE OF INVENTION: CD154, AND USE THEREOF IN DRUG DESIGN

; FILE REFERENCE: A096CON1

; CURRENT APPLICATION NUMBER: US/10/378,567

; CURRENT FILING DATE: 2003-02-28

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 60/276,452

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/229,933

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO 2:

; LENGTH: 448

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: humanized 5c8 heavy chain amino acid

US-10-378-567-2

Query Match 24.1%; Score 849; DB 15; Length 448;

Best Local Similarity 33.5%; Pred. No. 1.3e-38;

Matches 222; Conservative 60; Mismatches 143; Indels 238; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWYKQSPGKLEWIGRIINPNNGVTLY 60

Db 1 QVLOVSGAEVVKPGASVKLSCKASGYFTSYMYWVWYKQAPGQGLEWIGINPNNGDTNF 60

QY 61 NQKFKDKATLVDSKSTTAYMELRLSITSEDSAVVYCARSTMTITNYVMDYWGQSTVTYSS 120

Db 61 NEKFKSKATLVDSKASTAYMELSLRSDTAVYICRSDGND--MDSWGQGLTVTYSS 118

QY 121 AKTTPSPVPLAPGSAQAQNSMTLCLVKGYFPEPVTVVNSGSLSSGVHTFPAVLQSD 180

Db 119 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVVNSGALTSGVHTFPAVLQSS 178

QY 181 -LYTLSSSVTPSSSTWPSSETVTCNAHPASSTKVDKKIIPRDSGGPSEKSEINEKDLRK 239

Db 179 GLYLSSTVTPSSSLGDTQYICNVNHPKSTKVDKKVEPKSC----- 221

QY 240 KSELQGTALGNLKIYYNYSKAITSSSEKADQFLNTLLFKGFTGHFWYNDLLVLDLST 299

Db 222 -----DKHTCCPCPAPELLOGPSVF--LFPKP--KDTLM----- 253

QY 300 AATSEYEGSSVDLYGAYYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359

Db 254 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNVDG-- 282

QY 360 QTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNSSDFGKVGQGLIVFHSSEGSTV 419

Db 283 ---VEVHNAKTPREEQ-----YNSTY---RVVSVLTVLHQDWLNGK 318

QY 420 SYDLFDAQCGQPTLLRIYRDNTTISSTLSLSLYLTYSIVMTPTPTSLAVSAGDRTVI 479

Db 319 EY----- 320

QY 480 TCKASQSVNDVAWYQCKPQSKLLISYTSRYAGVDPDRFSGSGYGTDTLTITSSVQAE 539

Db 429 MHE 431

US-10-291-265-804

; Sequence 804, Application US/10291265

; Publication No. US20030232054A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; APPLICANT: Tang et al

; FILE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides

; CURRENT APPLICATION NUMBER: US/10/291,265

; CURRENT FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 09/491,404

; PRIOR FILING DATE: 2000-01-25

; PRIOR APPLICATION NUMBER: 09/617,746

; PRIOR FILING DATE: 2000-07-17

; PRIOR APPLICATION NUMBER: 09/631,451

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 09/633,870

; PRIOR FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 944

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 804

; LENGTH: 384

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-291-265-804

Query Match 23.9%; Score 841.5; DB 15; Length 384;

Best Local Similarity 30.2%; Pred. No. 2.9e-38;

Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWYKQSPGKLEWIGRIINPNNG-VTL 59

Db 20 EVQLVESGGGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSGLSGGSGSTY 79

QY 60 YNOKFKDKATLVDSKSTTAYMELRLSITSEDSAVVYCARSTMTITNYVMDYWGQSTVTVS 119

Db 80 YADSVKGRFTISRDNKGTLYLQNSLRADDTARYCAKG-----GVELA 124

QY 120 SAKTTPSPVPLAPGSAQAQNSMTLCLVKGYFPEPVTVVNSGSLSSGVHTFPAVLQS 179

Db 125 STK----- 127

QY 180 DLYTLSSSVTPSSSTWPSSETVTCNAHPASSTKVDKKIIPRDSGGPSEKSEINEKDLRK 239

Db 128 -----PSSIW----- 132

QY 240 KSELQGTALGNLKIYYNYSKAITSSSEKADQFLNTLLFKGFTGHFWYNDLLVLDLST 299

Db 133 -----RLNPIRY-----WYFDLW--GGTLL 150

QY 300 AATSEYEGSSVDLYGAYYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359

Db 151 VTSSGGGSS-----CGS-----GGAS----- 167

QY 360 QTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNSSDFGKVGQGLIVFHSSEGSTV 419

Db 168 ----- 167

```

QY 420 SYDLFDAQQYPTDLLRIYRDNTTISSTLSLSISLYLTTSIVMTQPTSLVAGDRVTI 479
Db 168 -----TGEIVLTQSPGTLSLSPGERATL 190
QY 480 TCKASQSVND-VAMVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 538
Db 191 SCRASQSVSSSYLAWYQKQAPRLLIYGASRATGIPDRFSGSGGTDTFTLTISRLEP 250
QY 539 EDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFY 598
Db 251 EDFAVYCCQYGGSPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFY 310
QY 599 PKDINVKWKIDGRQNGVLSNMTDQSDSTYSMSSTLTLTDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQ 370
QY 659 STSPIVKSFNENE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 72
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

```

```

Query Match 23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLQQSGFDLVKPGASVKISKASGYSTGYTHHWKQSPKGLGWGRINPNNG-VTL 59
Db 20 EVLQVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWVSGLSGSGSTY 79
QY 60 YNQKFKDQATLVKDSSTTAYNVELSLTSEDSAVYVCARSTMITNYMDYMGQGTSTVTS 119
Db 80 YADSVKGRFTISRDNSKGTLYQMNSLRADDTARYCAKG-----GVELA 124
QY 120 SAKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPVTVTVNSGSLSSGVTHTPPAVLQS 179
Db 125 STK----- 127
QY 180 DLYTLSSSVTPSPSPWPSETVTCNVAHPASSTKVDKIVPRDSCGPSEKSEBINEKDLRK 239
Db 128 -----PSSIW----- 132
QY 240 KSELQGTALGNLKOIYYNKAITSSEKSAQDLTLLFKGFTGHPWYNDLLVDLGGST 299
Db 133 -----RLNPIRY-----WYFDLW-GQGTLL 150

```

```

QY 300 AATSEYEGSSVDLYGAYGYQACGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGK 359
Db 151 VTVSGDGGSS-----GGAS----- 167
QY 360 QTTVPIDKVTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTV 419
Db 168 ----- 167
QY 420 SYDLFDAQQYPTDLLRIYRDNTTISSTLSLSISLYLTTSIVMTQPTSLVAGDRVTI 479
Db 168 -----TGEIVLTQSPGTLSLSPGERATL 190
QY 480 TCKASQSVND-VAMVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 538
Db 191 SCRASQSVSSSYLAWYQKQAPRLLIYGASRATGIPDRFSGSGGTDTFTLTISRLEP 250
QY 539 EDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFY 598
Db 251 EDFAVYCCQYGGSPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFY 310
QY 599 PKDINVKWKIDGRQNGVLSNMTDQSDSTYSMSSTLTLTDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQ 370
QY 659 STSPIVKSFNENE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 73
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806

```

```

Query Match 23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLQQSGFDLVKPGASVKISKASGYSTGYTHHWKQSPKGLGWGRINPNNG-VTL 59
Db 20 EVLQVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWVSGLSGSGSTY 79
QY 60 YNQKFKDQATLVKDSSTTAYNVELSLTSEDSAVYVCARSTMITNYMDYMGQGTSTVTS 119
Db 80 YADSVKGRFTISRDNSKGTLYQMNSLRADDTARYCAKG-----GVELA 124
QY 120 SAKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPVTVTVNSGSLSSGVTHTPPAVLQS 179
Db 125 STK----- 127
QY 180 DLYTLSSSVTPSPSPWPSETVTCNVAHPASSTKVDKIVPRDSCGPSEKSEBINEKDLRK 239

```

```
Db      128      |||||-----PSSIW-----132
Qy      240 KSELQGTALGNLKOIYYNNSKAITSEKSGADQFLNTLLFKGFTGHPWYNDLLVDLQST 299
Db      133      |||||-----RNPYR-----WYFDLW-CQGT 150
Qy      300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGK 359
Db      151 VTVSSGCGSS-----GGAS-----167
Qy      360 QTTVPIDKVKTSKEVTQVQELDLQARHLYHGKFLYNSDSFGKVGQGLIVFHSSEGSTV 419
Db      168      |||||-----GGAS-----167
Qy      420 SYDLFDAQGQYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQTPTSLIVSAGDRVTI 479
Db      168      |||||-----TGEIVLTQSPGTLSPGERATL 190
Qy      480 TKASQSVSND-VAMVYQKQPGQPKLLISVTSRYAGVDPFRSGSGYGTDFTLTISVVOA 538
Db      191 SCRASQSVSSYLAWYQKQPGQAPRLIYGCASRATGIDPRFSGSGGTDFTLTISRLEP 250
Qy      539 EDAVYFCQDYNPPTFGGQTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFY 598
Db      251 EDPVAVYCCQYGGSPPTFGQGTQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFY 310
Qy      599 PKDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMSSTLTLLKDEYERHNSYTCEATHKT 658
Db      311 PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSSLSSTLTLSKADYERHKVYACEVTHQG 370
Qy      659 STSPVTKSFNRNE 671
Db      371 LSSPVTKSFNRGE 383
```

```
RESULT 74
US-10-291-265-807
; Sequence 807, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 807
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-807
```

```
Query Match      23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

Qy      1 EVOLQSGDPLVKPGASVKISCKASQSYFTGYVMHWKQSPKGLEWIGRIPNNG-VTL 59
Db      20 EVOLVESGGGLVQPGGSLRLSCLASGFTTSSVAMSWVRQAPKGLEWVSGLSGGSSTY 79
Qy      60 YKQKFKDKATLTVDKSTTAYMELRSLTSEDGAVYYCARSTMTITNYMDWQGGTSTVTS 119
```

```
Db      80 YADSVKGFITSRDNSKGTLYLQNSLRADDTARYYCAKG-----GVELA 124
Qy      120 SAKTTPPSVYPLAPGSAQAQTNMVMVTLGLVKGYFPEPVTVTWNSGSLSSGVVHTPPAVLQS 179
Db      125 STK      |||||-----127
Qy      180 DLYTLSSSVTVPSSTWPFSETVTCNVAHPASSTKVDDKXIVPRDSGGPSEKSEEINEKDLRK 239
Db      128      |||||-----PSSIW-----132
Qy      240 KSELQGTALGNLKOIYYNNSKAITSEKSGADQFLNTLLFKGFTGHPWYNDLLVDLQST 299
Db      133      |||||-----RNPYR-----WYFDLW-CQGT 150
Qy      300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGK 359
Db      151 VTVSSGCGSS-----GGAS-----167
Qy      360 QTTVPIDKVKTSKEVTQVQELDLQARHLYHGKFLYNSDSFGKVGQGLIVFHSSEGSTV 419
Db      168      |||||-----GGAS-----167
Qy      420 SYDLFDAQGQYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQTPTSLIVSAGDRVTI 479
Db      168      |||||-----TGEIVLTQSPGTLSPGERATL 190
Qy      480 TKASQSVSND-VAMVYQKQPGQPKLLISVTSRYAGVDPFRSGSGYGTDFTLTISVVOA 538
Db      191 SCRASQSVSSYLAWYQKQPGQAPRLIYGCASRATGIDPRFSGSGGTDFTLTISRLEP 250
Qy      539 EDAVYFCQDYNPPTFGGQTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFY 598
Db      251 EDPVAVYCCQYGGSPPTFGQGTQVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFY 310
Qy      599 PKDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMSSTLTLLKDEYERHNSYTCEATHKT 658
Db      311 PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSSLSSTLTLSKADYERHKVYACEVTHQG 370
Qy      659 STSPVTKSFNRNE 671
Db      371 LSSPVTKSFNRGE 383
```

```
RESULT 75
US-10-216-484-143
; Sequence 143, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 143
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-143
```

```
Query Match      23.5%; Score 827.5; DB 14; Length 470;
Best Local Similarity 32.5%; Pred. No. 2.1e-37;
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 26.5729 Seconds
(without alignments)
1305.563 Million cell updates/sec

Title: US-09-900-766-1
Perfect score: 3522
Sequence: 1 EVQLQSGPDLVKPGASVKI.....EATHKTSPIVKSNRNES 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/2/1aa/5A-COMB.pep: *
2: /cgn2_6/prodata/2/1aa/5B-COMB.pep: *
3: /cgn2_6/prodata/2/1aa/6A-COMB.pep: *
4: /cgn2_6/prodata/2/1aa/6B-COMB.pep: *
5: /cgn2_6/prodata/2/1aa/6C-COMB.pep: *
6: /cgn2_6/prodata/2/1aa/6D-COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108.5	31.5	489	5	PCT-US95-11405-35
2	1107	31.4	233	4	US-08-695-692B-8
3	1107	31.4	257	3	US-08-486-099-112
4	1107	31.4	257	3	US-08-360-107A-122
5	1107	31.4	257	3	US-08-484-223B-112
6	1107	31.4	257	3	US-08-919-597-112
7	1107	31.4	257	3	US-08-475-668A-112
8	1107	31.4	257	3	US-08-485-551A-112
9	1107	31.4	257	3	US-08-471-913A-112
10	1107	31.4	257	3	US-08-485-264A-112
11	1107	31.4	257	4	US-08-474-349A-112
12	1107	31.4	257	4	US-08-470-896-112
13	1107	31.4	257	4	US-08-485-546A-112
14	1059.5	30.1	445	1	US-08-353-400-33
15	1059.5	30.1	464	1	US-08-353-400-36
16	1040	29.5	226	3	US-08-896-933-24
17	1040	29.5	226	4	US-09-314-235-24
18	980.5	27.8	711	4	US-09-485-737B-90
19	966	27.4	468	2	US-08-116-247-7
20	960	27.3	212	2	US-08-737-129A-2
21	957	27.2	468	2	US-08-303-569B-7
22	957	27.2	468	4	US-09-795-515-7
23	953.5	27.1	223	5	PCT-US94-14106-51
24	948	26.9	233	4	US-08-695-692B-7
25	948	26.9	233	4	US-08-486-099-113
26	948	26.9	233	3	US-08-360-107A-123
27	948	26.9	233	3	US-08-484-223B-113

28	948	26.9	257	3	US-08-919-597-113	Sequence 113, App
29	948	26.9	257	3	US-08-475-668A-113	Sequence 113, App
30	948	26.9	257	3	US-08-485-551A-113	Sequence 113, App
31	948	26.9	257	3	US-08-471-913A-113	Sequence 113, App
32	948	26.9	257	3	US-08-485-264A-113	Sequence 113, App
33	948	26.9	257	4	US-08-474-349A-113	Sequence 113, App
34	948	26.9	257	4	US-08-470-896-113	Sequence 113, App
35	948	26.9	257	4	US-08-485-546A-113	Sequence 113, App
36	944.5	26.8	233	1	US-08-353-400-37	Sequence 37, Appl
37	944	26.8	233	1	US-08-446-918A-4	Sequence 4, Appl
38	944	26.8	233	2	US-08-580-806-4	Sequence 4, Appl
39	941.5	26.7	219	1	US-08-353-400-34	Sequence 34, Appl
40	933	26.5	222	2	US-08-737-129A-6	Sequence 6, Appl
41	931.5	26.4	232	3	US-08-896-933-23	Sequence 23, Appl
42	931.5	26.4	232	4	US-09-314-235-23	Sequence 23, Appl
43	925	26.3	257	4	US-09-144-776B-2	Sequence 2, Appl
44	921	26.1	233	4	US-09-144-776B-4	Sequence 4, Appl
45	915.5	26.0	254	2	US-08-792-824-10	Sequence 10, Appl
46	915.5	26.0	254	2	US-08-792-824-13	Sequence 13, Appl
47	909.5	25.8	254	2	US-08-792-824-4	Sequence 4, Appl
48	909.5	25.8	254	2	US-08-792-824-7	Sequence 7, Appl
49	904.5	25.7	238	3	US-09-152-545-4	Sequence 4, Appl
50	903.5	25.7	447	6	5455030-1	Patent No. 5455030
51	901	25.6	218	5	PCT-US94-14106-57	Sequence 57, Appl
52	898	25.5	211	4	US-09-170-769A-8	Sequence 8, Appl
53	897.5	25.5	223	5	PCT-US94-14106-55	Sequence 55, Appl
54	895	25.4	215	2	US-08-737-129A-8	Sequence 8, Appl
55	892.5	25.3	599	1	US-08-442-542-18	Sequence 18, Appl
56	892.5	25.3	599	1	US-08-765-469-18	Sequence 18, Appl
57	889.5	25.3	235	4	US-09-423-439-58	Sequence 58, Appl
58	889.5	25.3	235	4	US-09-011-769A-23	Sequence 23, Appl
59	878	24.9	213	2	US-08-737-129A-4	Sequence 4, Appl
60	873	24.8	647	4	US-09-423-439-60	Sequence 60, Appl
61	872	24.8	236	2	US-08-792-824-3	Sequence 3, Appl
62	872	24.8	236	2	US-08-792-824-9	Sequence 9, Appl
63	872	24.8	236	2	US-08-792-824-12	Sequence 12, Appl
64	872	24.8	453	4	US-09-301-593-18	Sequence 18, Appl
65	864	24.5	218	5	PCT-US94-14106-61	Sequence 61, Appl
66	863.5	24.5	472	4	US-09-301-593-30	Sequence 30, Appl
67	861	24.4	215	4	US-09-170-769A-4	Sequence 4, Appl
68	858	24.4	234	5	PCT-US94-07659-4	Sequence 4, Appl
69	855.5	24.3	250	4	US-09-011-769A-21	Sequence 21, Appl
70	855.5	24.3	473	4	US-09-171-945-131	Sequence 131, Appl
71	852.5	24.2	235	2	US-08-303-569B-5	Sequence 5, Appl
72	852.5	24.2	235	2	US-08-116-247-5	Sequence 5, Appl
73	852.5	24.2	235	4	US-09-795-515-5	Sequence 5, Appl
74	850.5	24.1	200	6	5189147-8	Patent No. 5189147
75	841	23.9	454	2	US-07-934-373C-22	Sequence 22, Appl
76	841	23.9	454	3	US-08-437-842B-22	Sequence 22, Appl
77	841	23.9	454	4	US-08-146-206C-22	Sequence 22, Appl
78	841	23.9	454	4	US-09-705-686-22	Sequence 22, Appl
79	841	23.9	454	5	PCT-US93-07833-22	Sequence 22, Appl
80	840	23.9	206	6	5189147-9	Patent No. 5189147
81	834.5	23.7	217	5	PCT-US94-14106-59	Sequence 59, Appl
82	831.5	23.6	247	5	PCT-US94-07659-2	Sequence 2, Appl
83	830	23.6	233	2	US-08-792-824-6	Sequence 6, Appl
84	828.5	23.5	235	3	US-08-444-644-28	Sequence 28, Appl
85	828.5	23.5	235	4	US-08-232-246A-28	Sequence 28, Appl
86	827.5	23.5	215	6	5455030-3	Patent No. 5455030
87	826.5	23.5	235	3	US-08-444-644-42	Sequence 42, Appl
88	826.5	23.5	235	4	US-08-232-246A-42	Sequence 42, Appl
89	825.5	23.4	235	3	US-08-444-644-19	Sequence 19, Appl
90	825.5	23.4	235	4	US-08-232-246A-19	Sequence 19, Appl
91	819	23.3	234	2	US-07-690-192-2	Sequence 2, Appl
92	818.5	23.2	472	4	US-09-301-593-43	Sequence 43, Appl
93	812	23.1	467	2	US-07-916-098A-45	Sequence 45, Appl
94	811.5	23.0	233	3	US-08-444-644-33	Sequence 33, Appl
95	811.5	23.0	233	4	US-08-232-246A-33	Sequence 33, Appl
96	802	22.8	255	2	US-07-690-192-4	Sequence 4, Appl
97	802	22.8	452	3	US-09-027-449-71	Sequence 71, Appl
98	802	22.8	452	3	US-09-036-985-71	Sequence 71, Appl
99	802	22.8	452	4	US-09-121-952A-71	Sequence 71, Appl
100	802	22.8	452	4	US-09-234-340A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

PCT-US95-11405-35

Sequence 35, Application PC/TUS9511405

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PHOSPHOROUS-32 LABELING OF ANTIBODIES

TITLE OF INVENTION: FOR CANCER THERAPY

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11405

FILING DATE: 18-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,103

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 19733/599/IMIN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-11405-35

Query Match 31.5%; Score 1108.5; DB 5; Length 489;

Best Local Similarity 37.1%; Pred. No. 2.4e-66;

Matches 249; Conservative 60; Mismatches 156; Indels 207; Gaps 7;

QY 1 EVQLQQSGDPLVKPGASVKISKASGYSGFTGYNHWYKQSPGKLEWIGRINPNNGVTLY 60

DB 23 EVQLVESGGGVQPGSRILRSCSASGDFDTYXXXXXWVRQAPGKLEWIGXXXXXXX 82

QY 61 NQKFKDALTLDKSSITAYMELRSLTSEDSAVYCARSTWITNYVDYWGQGSTVTVSS 120

DB 83 XXXXXXRFTISRDAKNTFLQMDSLRPEDTGVYFCA-SXXXXXXXWGQGPPTVSS 141

QY 121 AKTPPSVYPLAPGSAAGTNSMVTGLGVKGYFPEPVTVTNWNSGSLSSGVHTFPVQLQSD 180

DB 142 ASTKGPSVFPPLAPSGSKTSGTALGCLVKDYPPEPVTVSNWNSGALTSVHTFPVQLQSS 201

QY 181 -LYTLSSVTVPSSTWSPSETVTCNVAHPASTKVDKKIIPRDSGGPSEKSEENKDLRK 239

DB 202 GLYSLSSVTVTPSSSLGTTQTCVNNKPSNTKVDKKVEP----- 241

QY 240 KSELQGTALGNLKQIYYNNSKAITSSSEKADQFLTNLLFKGPFTHGHPWYNLLVDLGS 299

DB 242 -----KSCD----- 245

QY 300 AATSEYEGSSVDLYGAYYGYQACAGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGK 359

Db 246 ----- 245

QY 360 QTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFLGNSDSFGGKVGQRGLIVFHSSEGSTV 419

DB 246 -----KT-----HTCPPCPM 255

QY 420 SYDLFDAQQQYPTLLRIYRDNNTTSSLSLSLSLYLYTTISVTMTPTSLLSVSAGDRVIT 479

DB 256 KYLL-----PTAAGLLLLAQAQAMADQLTQSPSSLSASVGDRAVIT 297

QY 480 TCKASQSVSNVDVAMVYQQKPGSPKLLISYTSRVAGVDPDRFSGSGYGFDTLTSSVQAE 539

DB 298 TCXXXXXXXWYQQKPGKAPKLLIYXXXXXXGVPDRFSGSGSGTDFFTTSSLOPE 357

QY 540 DAAYVFCQDDYNSPPTFGGKLEIKRADAAPTYSIRPPSSSEQLTSGASVVCFLNNFYP 599

DB 358 DIATYICXXXXXX-XXFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYP 416

QY 600 KDINVKWKIDGSEKQNGVLSNWTQDQSDKSTYSMSSTLTLTQDEYRHNSTYCEATHKTS 659

DB 417 REAKVQMKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGL 476

QY 660 TSPIVKSFNRNE 671

DB 477 SSPVTKSFNRGE 488

RESULT 2

US-08-695-692B-8

Sequence 8, Application US/08695692B

Patent No. 651499

GENERAL INFORMATION:

APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten.

APPLICANT: Johan Hansson, Terje Kalland, Lars

APPLICANT: Abrahamson and Goran Forsberg

TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS

TITLE OF INVENTION: AND THEIR USE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pravel, Hewitt, Kimball & Krieger

STREET: 1177 West Loop South, 10th Floor

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77027-9095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/695,692B

FILING DATE: August 12, 1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9601245-5

FILING DATE: March 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Krieger, Paul E.

REGISTRATION NUMBER: 25,886

REFERENCE/DOCKET NUMBER: 4,986/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-695-692B-8

Query Match 31.4%; Score 1107; DB 4; Length 233;

Best Local Similarity 89.7%; Pred. No. 1.2e-66; Mismatches 15; Indels 0; Gaps 0;
Matches 209; Conservative 9;

QY 226 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 1 SEKSEINEKDLRKKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVLDGSKATNKYKGVLDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNNTTISSTLSISLYLTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNNTTINSENHLIDLYLTT 233

RESULT 3
US-08-486-099-112
; Sequence 112, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 25 SEKSEINEKDLRKKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSKATNKYKGVLDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNNTTISSTLSISLYLTT 458
Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNNTTINSENHLIDLYLTT 257

RESULT 4
US-08-360-107A-122
; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-122

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 25 SEKSEINEKDLRKKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84

QY 286 HPWYNDLLVDLGSKDTATNKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDTATNKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 5

US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223B-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSDQFLTWLLPKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSDQFLTWLLPKGFFTG 84
QY 286 HPWYNDLLVDLGSKDTATNKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345

DB 85 HPWYNDLLVDLGSKDTATNKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 6

US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054285
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-919-597-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSDQFLTWLLPKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSSSEKSDQFLTWLLPKGFFTG 84
QY 286 HPWYNDLLVDLGSKDTATNKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345

Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 257

RESULT 7
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 458

Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 257

RESULT 8
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNTTSSLSLSLYTT 257

Sequence 112, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSISLYTT 257

RESULT 11
US-08-474-349A-112
Sequence 112, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:

Sequence 112, Application US/08479193A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
EPSTEIN-BARR VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSISLYTT 257

RESULT 10
US-08-485-264A-112

APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSELOGTALGNLKOIYYNSKAITSEKSDADQFLTWLLFKGFTG 285
DB 25 SEKSEINEKDLRKKSELOGTALGNLKOIYYNEKAITENKESDQFLTWLLFKGFTG 84
QY 286 HPWYNDLLVLDLGSATATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDLGSADATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
DB 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTISSTLSISLYLTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTISSENHLIDLYLTT 257

RESULT 14
US-08-353-400-33
Sequence 33, Application US/08353400
Patent No 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-33

Query Match 30.1%; Score 1059.5; DB 1; Length 445;
Best Local Similarity 37.5%; Pred. No. 4.1e-63;
Matches 250; Conservative 61; Mismatches 107; Indels 249; Gaps 14;
QY 1 EYQLQSGPDLVKGASVKISCKASGYSTGYMHWVKQSPCKGLEWIGRINPNNGVTLY 60
DB 1 QYQLQSGPDLVKGASVKISCKASGYSTGYMHWVKQSPCKGLEWIGRINPNNGVTLY 60
QY 61 NQFKDKATLTVDKGSTTAYMELRLSTSEDSAVYYCARSTMI-TNYVMYMGQGTSTVTS 119
DB 61 NEKFKKATLTVDKGSTTAYMELRLSTSEDSAVYYCARERAYGYDDANDYMGQGTSTVTS 120
QY 120 SAKTTPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGHTTFAVLQS 179
DB 121 SAKTTPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGHTTFAVLQS 180
QY 180 DLYTLSSSVTPSPSTWPTSETVTCNVAHPASSTKVDKIVPRDGG----- 224
DB 181 DLYTLSSSVTPSPSTWPTSETVTCNVAHPASSTKVDKIVPRDGG----- 224
QY 240 KSELOGTALGNLKOIYYNSKAITSEKSDADQFLTWLLFKGFTGHPWYNDLLVDLGS 299
DB 225 -CKPICITVPEVSSVFIPPK-----PKDVLITL----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKYPINLWIDGK 359
DB 254 -----TP-KVTCVVVDIS-----KDDPEVQFSMFVD-- 278
QY 360 QTTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIV 410
DB 279 --DVEVHTAQTOPREBQFNSTFRSVSELPINHQDMLNGCKFKCRVNSAAFPAPIEK--- 332
QY 411 FHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTISSTLSISLYLTTISIVMTQTPTSL 470
DB 333 -----TISKT----- 337
QY 471 VSAGDRAVTITCKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVPDRFSGSGYDPT 530
DB 338 ----- 337
QY 531 LTISVQAEADAAYFCQDDYNSPPTFGGQTKLEIKRADAAPTIVSIFPSSSQTSGGASV 590
DB 338 -----KGRPKAPQVYVTPPKQMAKDKVSL 363
QY 591 VGLANNFKDINVKWKIDGSEKQNGVLSWTDQSDKSTYSMSSTLTTLTKDEYERHSY 650
DB 364 TCMITDFFPFDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVQSNWEAGNTF 421
QY 651 TCEATHK 657
DB 422 TCSVLHE 428

RESULT 15
US-08-353-400-36

EARLIER APPLICATION NUMBER: 07/416,530
 EARLIER FILING DATE: 1989-10-03
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 24
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-314-235-24

Query Match 29.5%; Score 1040; DB 4; Length 226;
 Best Local Similarity 85.2%; Pred. No. 3.4e-62;
 Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

229 SEEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDQFLNTLLFKGFTGHPW 288
 1 SEEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDQFLNTLLFKGFTGHPW 60
 289 YNDLLVDLSTAAATSEYEGSSVDLYGAYGQCAGGTPNKACMYGGVTLHDNNRLTEEK 348
 61 YNDLLVDLSTAAATSEYEGSSVDLYGAYGQCAGGTPNKACMYGGVTLHDNNRLTEEK 119
 349 KVPINLWIDGKQTTVPIDKVTSSKEVTQELDLQARHLYHGKFLYNSDSFGKQVORGL 408
 120 ---VAKWIDGKQTTVPIDKVTSSKEVTQELDLQARHLYHGKFLYNSDSFGKQVORGL 176
 409 IVFHSSEGSTVSVDLFDAGQYPTDLRIYRDNNTISSTLSISLYLYTT 459
 177 IVFHSSEGSTVSVDLFDAGQYPTDLRIYRDNNTISSTLSISLYLYTT 226

RESULT 18
 US-09-485-737B-90
 ; Sequence 90, Application US/09485737B
 ; Patent No. 6350860
 ; GENERAL INFORMATION:
 ; APPLICANT: Buysse, Marie-Ange
 ; APPLICANT: Sablon, Edwin
 ; TITLE OF INVENTION: INTERPERON-GAMMA-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
 ; FILE REFERENCE: INNS:015
 ; CURRENT APPLICATION NUMBER: US/09/485,737B
 ; CURRENT FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
 ; PRIOR FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: EPO 98870139.7
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: EPO 97870122.5
 ; PRIOR FILING DATE: 1997-08-18
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 711
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC
 US-09-485-737B-90

Query Match 27.8%; Score 980.5; DB 4; Length 711;
 Best Local Similarity 35.3%; Pred. No. 1.4e-57;
 Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;

1 BVQLQQSQPDLVKPGASVKISKASGYSFTGYNMHWKQSPGKLEWIGRINPNNGVTLY 60
 21 QVQLVQSGSELKFGASVKISKASGYSFTGYNMHWKQSPGKLEWIGRINPNNGVTLY 80
 61 NQKFKDKATLVDSKSTAYNELSLTSEDSAVTYCARSTWITNYVDYWGQGTSTVVS 120
 81 VDDFKGREFVSLDTSVSAAYLQISLKAEDTATYFCARRGF---YANDYWGQGTSTVVS 137
 121 AKTAPPSPVPLAPGASAAQTNSMVTGLCLVKGFPEPTVTWNSGSLSSGVTTPPAVLQSD 180

138 ASTKGPSVEFLAPASKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 197
 181 -LYTSSSVTVPSSTWPESTVTCNVAHPASSTKVDKIKIVPRDS-----GG 224
 198 GLYSLSVVTVFSSSLGTQYICNVNHPKSNKVDKRVKPEKSCDKHTHCPCPAPPELLGG 257
 225 PS-----EKSEEEI-----NEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDQFLNTLLFKGFTGHPW 258
 258 PSVFLFPKPKDQTLMSRTPEVTGVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPREEQYN 317
 259 S-----KAITSS-EK-----SADQ 271
 318 STYRVSVTVLHQDLNKGKEYKCKVSKALPASIEKTIISKAKQGPPEPVYTLPPSREE 377
 272 FLTN-----TLLFKGFTGHPWYNDLLVDLSTAAATSEYEGSS---VDLYGAYGQCAGG 324
 378 MTKNQVSLTCLVKGFV-----SDIAVEWESNGQPNVYKTPPVLDSDGSGFFLYSKL-- 430
 325 TPNKACMYGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTTVPIDKY 368
 431 TVDKSRWQGNVFSVSMVHEALHNHYTOKSLSPKLGSGSQVOLVOSGSELKPKGASV 490
 369 KTSKKEVTQELDLQARHLYHGKFLYNSDSFGKQVORGLIVFHSSEGSTVSVDLFDAGQ 428
 491 KISK-----ASGYTFDYGWVWVQAPGQGLKMGWINTYTGESTVVD--DFKG 538
 429 QPDTLLRIYRDNNTISSTLSIS-----LYLYT----- 457
 539 RP-----VFSLDTSVSAAYLQISLKAEDTATYFCARRGFYAMDYWGQGTSTVTSVSGG 592
 458 -----TSIVMTQTTSLYSAGDRVTITCKASQSVSNDVAMVYQKPGQSPKLLI 506
 593 GSGGSGSGSGSDIVLTQSPATMSAPGERVLTCSASSISY-MFWYHQRPGQSPRLII 651
 507 SYTSRYAGVPRFSGSGYGTFTLTISVQAEDAAVYFCQDYNPSPTFGGKLEIKR 566
 652 YDTSNLAGVPARFSGSGSTSYSLTISRMPEDEPATYFCHQSSSYPTFGGKLEIKR 711

RESULT 19
 US-08-116-247-7
 ; Sequence 7, Application US/08116247
 ; Patent No. 5929212
 ; GENERAL INFORMATION:
 ; APPLICANT: Jolliffe, Linda K.
 ; APPLICANT: Zivin, Robert A.
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Athwal, Diljeet S.
 ; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/116,247
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/743,377
 ; FILING DATE: 10-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paintin, Francis A.
 ; REGISTRATION NUMBER: 19,386
 ; REFERENCE/DOCKET NUMBER: CARP-0011

```
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 468 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-116-247-7

Query Match      27.4%; Score 966; DB 2; Length 468;
Best Local Similarity 34.9%; Pred. No. 7.7e-57;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHWVKQSPKGLIEWIGRINPNNGVTLY 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 20 QVLOQSGAELARPGASVKMSCKASYTFTYTMHWKQRPQGLEWIGYINPSRGYNY 79
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMITNYMDYWGQTSVTYSS 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYICAR-STYDHYCLDYWGQGTTLTVSS 138
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPPEVITVWNSGSLSSGVHTFPVQLQSD 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 139 AKTTPSVVPLAPVCGDTTGSSTVLGCLVKGYFPPEVITVWNSGSLSSGVHTFPVQLQSD 198
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 LYTLSSTVTPSTWSEVITCNVAHPASTKVDKIVPRDGGSPSEKSEENKDLRKK 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 LYTLSSTVTPSTWSPQSITCNVAHPASTKVDKIEPR--GPTIKFCP----- 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 241 SELQGTALGNLKIYYNNAKITSSEKSDQFLTNTLLFKGFTTGHWPYNDLLVLGSTA 300
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 ----- 246
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 301 ATSEYEGSSVDLYGAYGYCCAGGTENKTAQMGVTLHDNNRLTEKKVPIINLWIDGK 360
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 -----PKCPADN-----LLGSPSE----- 262
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKGLNDSFGKQVQGLIVFHSSEGSTVS 420
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 -----IPPKIKDVLMI-----SLSPVIT 281
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 421 YDLFDAQGOVPTLLRIYRDNLTTSISLSILYLTTSIVMTQTPTSLLSAGDRVIT 480
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 282 CVVDVSEDDPD-----VQISWFVNNVEVHTAQCT----- 312
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQAED 540
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 313 -----HREDYNSTRVV----- 324
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 541 AAVYFCQDYNSPPTFGGKTLEIKRAD-----AAPTVISIPPSSEQLT 584
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 325 SALPIQHQDWSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 585 SGASVYCFLLNFPKIDNVKWKIDGSEKQ-----GVLNSWTDQDSKDSYMSSTLT 639
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 381 KKQVTLTCMTDFMPEDIVVETNNGKTELNVKNTPEVLDS-----DGSYFMYSKLRV 433
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 640 TKDEYERHNSYCEATHK-TSTSPVVKSENR 669
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 434 EKQNWERNYSYSCSVVHGLNHHHTKSPSR 464
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 20
US-08-737-129A-2
/ Sequence 2, Application US/08737129A
/ Patent No. 585816
/ GENERAL INFORMATION:
/ APPLICANT: Ikuo FUJII et al.
/ TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
/ TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
/ NUMBER OF SEQUENCES: 8
```

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Wenderoth, Lind & Ponack
/ STREET: 805 Fifteenth Street, N.W., #700
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/737,129A
/ FILING DATE: No. 585816member 15, 1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warren M. Cheek, Jr.
/ REGISTRATION NUMBER: 33,367
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-8850
/ TELEFAX:
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 212 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-737-129A-2

Query Match      27.3%; Score 960; DB 2; Length 212;
Best Local Similarity 84.7%; Pred. No. 7e-57;
Matches 183; Conservative 11; Mismatches 14; Indels 8; Gaps 1;

QY 6 QSGDPLVKPGASVKISKASGYSTGYMHWVKQSPKGLIEWIGRINPNNGVTLYNQKFK 65
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 2 ESGTLEAKPGASVKMSCKASYTFTSYMHWKQRPQGLEWIGYINPSTDYTYIQKFK 61
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 66 DKATLTVDKSTTAYMELRLSTSDSAVYICARSTMITNYMDYWGQTSVTYSSAKTTP 125
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 62 DKATLTADKSSSTAYMQLSSLTSDSAVYICV-----MKDYWGQTSVTYSSAKTTP 113
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 126 PSVYPLAPGSAQAQNSMTVLGCLVKGYFPPEVITVWNSGSLSSGVHTFPVQLQSDLYT 185
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 PSVYPLAPGSAQAQNSMTVLGCLVKGYFPPEVITVWNSGSLSSGVHTFPVQLQSDLYT 173
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 SSVTPSPSTWSEVITCNVAHPASTKVDKIVPRD 221
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 SSVTPSPSTWSEVITCNVAHPASTKVDKIVPRD 209
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 21
US-08-303-569B-7
/ Sequence 7, Application US/08303569B
/ Patent No. 5859205
/ GENERAL INFORMATION:
/ APPLICANT: Adair, John R.
/ APPLICANT: Athwal, Diljeet S.
/ APPLICANT: Emtage, John S.
/ TITLE OF INVENTION: Humanised Antibodies
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
/ STREET: One Liberty Place - 46th Floor
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: USA
```

ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,569B
 FILING DATE: 07-SEP-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yato
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CARP-0032
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 468 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-303-569B-7

Query Match 27.2%; Score 957; DB 2; Length 468;
 Best Local Similarity 34.7%; Pred. No. 3.1e-56;
 Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;
 QY 1 EVOLQCSGPDVAVKPCASVKISKAGSYFTGYVHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 QVQLQCSGAELARPGASVKMSCKASGYFTTRYTHWVKRQPGQLEWIGINPSRGVTNY 79
 QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYICARSTMTINYMDYWGQGTSTVSS 120
 DB 80 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYICAR-STYDDHYCLDYWGQGTSTVSS 138
 QY 121 AKTTPPSVYPLAPGSAQTSMVTGLCVKGYFPPEVTVTNWNSGLSSGVHTTFAVLQSD 180
 DB 139 AKTTAPSVYPLAPVCGDGTGSSVTLGLCVKGTFFPEVTLTNWNSGLSSGVHTTFAVLQSD 198
 QY 181 LYTLSSTVTPSSWPSSTVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240
 DB 199 LYTLSSTVTPSSWPSSTVTCNVAHPASSTKVDKIEPR---GPTIKPCP----- 246
 QY 241 SELOQTALGNLKQIYYNYSKAITSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
 DB 247 ----- 246
 QY 301 ATSEYEGSSVDLYGAYGYCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 DB 247 -----PKCQAPN-----LLGSPSVF----- 262
 QY 361 TTVPIDKVKTSKREVTQELDQARHYLHGKFGLYNSDSFGKQVQGLIVFHSESGSTVS 420
 DB 263 -----IPPKIKDVLMI---SLSPIT 281
 QY 421 YDLFDAQOQYPTLLRIYRONTTISSTSLSTSLYLYTTSIVMTQPTSLVLSAGDRVTIT 480
 DB 282 CVVVDVSEDDPD-----VQLSWFVNNVEVHTAQQTQ----- 312
 QY 481 CKASQSVSNDAVWYQKQPGQSKLLISYTSRYAGVDFRFGSGGQGTDFTLTISSVQAE 540
 DB 313 -----HREDYNSTLRV----- 324
 QY 541 AAVYFCQDYNSPTFFGGTGLEIKRAD-----AAVTYIFPPSSEQLT 584
 DB 325 SALPIQHODMWSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
 QY 585 SGGASVVCFLANFYPKOINVKWKIDGSRQN-----GVLSWTDQDSDKSTYSMSLTLL 639
 DB 381 KKQVTLTCMVDTFEPEDIVVENTNGKTELNYKNTEPVLDS-----DGSYFMYSKLRV 433

QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFNR 669
 DB 434 EKKWVVERNSYSCSVVHEGLHNNHTTKSFNR 464
 RESULT 22
 US-09-795-515-7
 ; Sequence 7, Application US/09795515
 ; Patent No. 6632927
 ; GENERAL INFORMATION:
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Achwal, Diljeet S.
 ; TITLE OF INVENTION: Humanised Antibodies
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/795,515
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/846,658
 ; FILING DATE: 01-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Trujillo, Doreen Yato
 ; REGISTRATION NUMBER: 35,719
 ; REFERENCE/DOCKET NUMBER: CARP-0057
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 468 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-795-515-7

Query Match 27.2%; Score 957; DB 4; Length 468;
 Best Local Similarity 34.7%; Pred. No. 3.1e-56;
 Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;
 QY 1 EVOLQCSGPDVAVKPCASVKISKAGSYFTGYVHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 QVQLQCSGAELARPGASVKMSCKASGYFTTRYTHWVKRQPGQLEWIGINPSRGVTNY 79
 QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYICARSTMTINYMDYWGQGTSTVSS 120
 DB 80 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYICAR-YDDHYCLDYWGQGTSTVSS 138
 QY 121 AKTTPPSVYPLAPGSAQTSMVTGLCVKGYFPPEVTVTNWNSGLSSGVHTTFAVLQSD 180
 DB 139 AKTTAPSVYPLAPVCGDGTGSSVTLGLCVKGTFFPEVTLTNWNSGLSSGVHTTFAVLQSD 198
 QY 181 LYTLSSTVTPSSWPSSTVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240
 DB 199 LYTLSSTVTPSSWPSSTVTCNVAHPASSTKVDKIEPR---GPTIKPCP----- 246
 QY 241 SELOQTALGNLKQIYYNYSKAITSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
 DB 247 ----- 246

QY 301 ATSEYEGSSVDLYGAYVYQACAGTGNKATCMYGVTLHDNNRLTEBKVPINLWIDGKQ 360
 Db 247 -----PCKCPAEN-----LLGGSVF----- 262
 QY 361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDPSGGKVQGLIVFHSSEGSTVS 420
 Db 263 -----IPPKIKDVLMI-----SUSPIVT 281
 QY 421 YDLFDAGQVPTLLRIYRDNMTTSSISLSISLYTTSIVMTQTPTSLVSAGDRVTIT 480
 Db 282 CVVDVSDDEDD-----VQISFVANNVEVHTAQOT----- 312
 QY 481 CKASQSVNSDVANVYQKPGSPKLLISYSSRAGVDFRPSGSGYGTDTLLTSSVQARD 540
 Db 313 -----HREDYNSTLRV----- 324
 QY 541 AAVYFQOQDYNSPPTFGGTGKLEIKRAD-----AAPTIVSIPPSSEQLT 584
 Db 325 SALPIQHDMWSKEP-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
 QY 585 SGGASVVCFLNNYPKDKVWKIDGSERON-----GVLSNWTQDQSKDSTYSMSSTLT 639
 Db 381 KKQVTLTCMVTDMPEDIVYEWMTNNGKTELNYKNTFVLDS-----DGSYFMYSKLRV 433
 QY 640 TKDEYERHNSYCEATHK-TSTSPIVKSENR 669
 Db 434 EKGWERNISYSCSVVHEGLNHHHTTKFSR 464

RESULT 23
 PCT-US94-14106-51
 ; Sequence 51, Application PC/TUS9414106
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Process for Generating Specific Antibodies
 ; NUMBER OF SEQUENCES: 61
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII (text)
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: PCT/US94/14106
 ; CLASSIFICATION:
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 223 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US94-14106-51

Query Match 27.1%; Score 953.5; DB 5; Length 223;
 Best Local Similarity 83.0%; Pred. No. 2e-56;
 Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;
 QY 1 EVOLQSGPDLVKPGASVATSKASGYFTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVOLQSGPDLVKPGASVATSKATGYTLSSYWLWVKSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQFKDKAILTVDKSSTTAYMELRSLTSDSVAIYCARSTMTINY--VMDYWGQGSTVT 118
 Db 61 NQFKDKAITFTVDTSSNTAYMQLSLTSDSVAIYCARSD-YGNYGDEYWGQGSTV 119
 QY 119 SSAKTTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEVTVTWNSGSLSSGVHTTFAVLQ 178
 Db 120 SSAKTTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEVTVTWNSGSLSSGVHTTFAVLQ 179
 QY 179 SDLYTLSSSVYTPSSWPSETVTCNVAHPASSTKVDKIVPRD 221
 Db 180 SDLYTLSSSVYTPSSWPSETVTCNVAHPASSTKVDKIVPRD 222

RESULT 24
 US-08-695-692B-7
 ; Sequence 7, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692B
 ; FILING DATE: August 12, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-695-692B-7

Query Match 26.9%; Score 948; DB 4; Length 233;
 Best Local Similarity 76.4%; Pred. No. 5e-56;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEETNEKDLRKSELOQTALGNLKOIYYVNSKAITSSSEKADQFLTNTLLFKGFTG 285
 Db 1 SEKSEETNEKDLRKSELOQTALGNLKOIYYVNSKAITSSSEKADQFLTNTLLFKGFTG 60
 QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYVYQACAGTGNKATCMYGVTLHDNNRLT 345
 Db 61 HSWYNDLLVDFSDKIDVKYKGVKVDLYGAYVYQACAGTGNKATCMYGVTLHDNNRLT 120
 QY 346 BEKVPINLWIDGQOTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDPSGGKVQ 405
 Db 121 BEKVPINLWIDGQONTVPLETVTNKNKNVTVQELDLQARHYLHGKFGLYNSDPSGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQVPTLLRIYRDNMTTSSISLSISLYT 458
 Db 191 RGLIVFHTSTPVSVDLFDAGQVNTLLRIYRDNMTTSSISLSISLYT 233

RESULT 25
 US-08-486-099-113
 ; Sequence 113, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELGQTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELGQTALGNLKOIYYNEKAKTENKESHQDFLOHTILFKGFTD 84

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSDKDIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 405
DB 145 BEKKVPINLWDGKQTTVPLETVKTKNKNTVQELDLQARHYLQEKYLYNSDVFDCVKQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAGQYPTDLRLIYRDNTTISSTLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 26
US-08-107A-123
Sequence 123, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELGQTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELGQTALGNLKOIYYNEKAKTENKESHQDFLOHTILFKGFTD 84

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSDKDIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 405
DB 145 BEKKVPINLWDGKQTTVPLETVKTKNKNTVQELDLQARHYLQEKYLYNSDVFDCVKQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAGQYPTDLRLIYRDNTTISSTLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 27
US-08-484-223B-113
Sequence 113, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.

;; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
;; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;; TITLE OF INVENTION: TRANSMISSION
;; NUMBER OF SEQUENCES: 245
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,223B
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7872-029
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 257 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-484-223B-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAQOFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHQFLQHTILFKGFFTD 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 144

QY 346 BEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLQEKYLYNSDSVFDGKVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSLSLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 28
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION

;; NUMBER OF SEQUENCES: 273
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/919,597
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470,896
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7872-020
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 113:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 257 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-919-597-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAQOFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHQFLQHTILFKGFFTD 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 144

QY 346 BEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLQEKYLYNSDSVFDGKVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSLSLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 29
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/475.668A
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDQFLTNLLPKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESHQFLQHTILFKGFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYSGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGGVDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHLYHKGFLYNSDSFGKQV 405
DB 145 BEKKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARLYQEKYLNYSDFDGVQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKNTINSENHMDIYLTS 257

RESULT 30
US-08-485-551A-113
Sequence 113, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/485.551A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDQFLTNLLPKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESHQFLQHTILFKGFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYSGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGGVDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHLYHKGFLYNSDSFGKQV 405
DB 145 BEKKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARLYQEKYLNYSDFDGVQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKNTINSENHMDIYLTS 257

RESULT 31
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: Protein
; US-08-471-913A-113

```

```

Query Match      26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQLNTLLEKGFPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFPTD 84
QY 286 HPWNLLVLDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTCACMGVTLHDNNRLT 345
Db 85 HSNYNLLVDFDSKDIVDKYKGVKVDLYGAYGYQCAGGTPNKTCACMGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGQTTPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYLYNSDVFDPGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGVNTLLRIYRDNKTINSENHHDIDLYLTS 257

```

```

RESULT 32
US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-113

```

```

Query Match      26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQLNTLLEKGFPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFPTD 84
QY 286 HPWNLLVLDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTCACMGVTLHDNNRLT 345
Db 85 HSNYNLLVDFDSKDIVDKYKGVKVDLYGAYGYQCAGGTPNKTCACMGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGQTTPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYLYNSDVFDPGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGVNTLLRIYRDNKTINSENHHDIDLYLTS 257

```

```

RESULT 33
US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995

```

```

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-113

Query Match          26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQDQFLQHTILFKGFTD 84
QY 286 HPWYNDLLVLDLGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKYGKVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKVPINLWLDGKQNTVPLETVTKNKNVTQVELDLQARRYLOEKYLYNSDVFQGVQ 204
QY 406 RGLIVFHSEGSTVSVDLFDAGQGYPTLLRIYRDNNTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 34
US-08-470-896-113
; Sequence 113, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-113

Query Match          26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQDQFLQHTILFKGFTD 84
QY 286 HPWYNDLLVLDLGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKYGKVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKVPINLWLDGKQNTVPLETVTKNKNVTQVELDLQARRYLOEKYLYNSDVFQGVQ 204
QY 406 RGLIVFHSEGSTVSVDLFDAGQGYPTLLRIYRDNNTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 35
US-08-485-546A-113
; Sequence 113, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGYQCAGTTPNKATCMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSKOIVDKYKGGKVDLYGAYYGYQCAGTTPNKATCMYGGVTLHDNNRLT 144

QY 345 EEKKVPINLWDGKQTTVPIDVKTSKKEVTVQELDLQARHLYHGKFGLYNSDSFGKVQ 405
DB 145 EEKKVPINLWDGKQNTVLETVKTNKNVTVOELDLQARRYLQEKYINLYNSDVFQGVQ 204

QY 406 RGLIVFHSSEGSVSYDLDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNTKINSENHIDILYLYTS 257

RESULT 36
US-08-353-400-37
Sequence 37, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-37

Query Match 26.8%; Score 944.5; DB 1; Length 239;
Best Local Similarity 78.1%; Pred. No. 8.9e-56;
Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTSLSLSLYLYTT-----SIVMTQTPTSLVSAGDRVTITCKASQSVND-----VAVY 494
DB 3 SQAQVILLLLWVGTCGDIWVSQSPSSLAVSAGEKVTMSCKSSQLNSRTRKNLYLAWY 62

QY 495 QQKPGQSPKLLISYTSRGYAGVDRFSGSGYGTDTLTITISVQAEDAAYVFCQDYNSPP 554
DB 63 QQRPGQSPKLLIYWASTRTSGVDRFTGSGSGTDTLTITISVQAEDLAIYYCKQSY-TLR 121

QY 555 TFGGKTLEIKRADAAFTVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 614
DB 122 TFGGKTLEIKRADAAFTVSIFPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQ 181

QY 615 NGVLNSWTDQDSKSTYSMSSTLTLTIDKDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
DB 182 NGVLNSWTDQDSKSTYSMSSTLTLTIDKDEYERHNSYTCETHKTSTSPIVKSFNRNE 238

RESULT 37
US-08-446-918A-4
Sequence 4, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 9.3e-56;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTG 286
DB 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTDH 61

QY 287 FWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGYQCAGTTPNKATCMYGGVTLHDNNRLTE 346
DB 62 SWYNDLLVDFDSKOIVDKYKGGKVDLYGAYYGYQCAGTTPNKATCMYGGVTLHDNNRLTE 121

QY 347 EKKVPINLWDGKQTTVPIDVKTSKKEVTVQELDLQARHLYHGKFGLYNSDSFGKVQ 406
DB 122 EKKVPINLWDGKQNTVLETVKTNKNVTVOELDLQARRYLQEKYINLYNSDVFQGVQ 181

QY 407 GLIVFHSSEGSVSYDLDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTT 458
DB 182 GLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNTKINSENHIDILYLYTS 233

RESULT 38
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match 26.8%; Score 944; DB 2; Length 233;
Best Local Similarity 76.3%; Pred. No. 9,3e-56;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKSELOCTALGNLQIYYNNSKATTSSEKSAOQFLNTLLFKGFTGH 286
Db 2 EKSEINEKDLRKSELOCTALGNLQIYYNNSKATTSSEKSHDQFLQHTILFKGFTDH 61
QY 287 PWYNDLLVDLSTAASTSEVESSVDLYCAVYGCAGTGNKTCMYGGVTLHDNNLTE 346
Db 62 SWYNDLLVDFDSKIDVKYKGVLDLYGAYGYCAGTGNKTCMYGGVTLHDNNLTE 121
QY 347 EKKVPINLWIDKQTTVPIDKVTISKKEVTVQELDQARHYLHGKFGLYNSDSFGKVQR 406
Db 122 EKKVPINLWIDKQNTVLETVKINKNVTYQELDQARRYLQEKYLNLSNDSVDFGKVQR 181
QY 407 GLIVHSSEGVTSVDLFDAGQVPTLLRLRYRNTTISLSISLYLTT 458
Db 182 GLIVHTSTPSVNDLFGAGQVSNLTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 39
US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-34
Query Match 26.7%; Score 941.5; DB 1; Length 219;
Best Local Similarity 83.0%; Pred. No. 1.3e-55;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;
QY 460 IVMTOTPSLLVSAGDRVTITCKASQSVND-----VANYQKPGQSPKLLIYSTSR 513
Db 2 IVMSQSPSSLAVSAGEKVTMSCKSSQLNSTRKNYLAWYQORPGQSPKLLIYWASTRT 61
QY 514 AGVPRFSGSGVGTDTLTITSSVQAEAAVYFCQDYNSTPTFGGTTKLEIKRADAAPT 573
Db 62 SGVPRFTGSGSGGTDTLTITSSVQAEADAIYCKQSY-TLATFGGTTKLEIKRADAAPT 120
QY 574 SIFPPSSQELTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDSTYS 633
Db 121 SIFPPSSQELTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDSTYS 180
QY 634 SSTLTLTDKDEYERHNSYTCETHKTSTSPIVKSENRNE 671
Db 181 SSTLTLTDKDEYERHNSYTCETHKTSTSPIVKSENRNE 218
RESULT 40
US-08-737-129A-6
; Sequence 6, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Porack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-129A-6

Query Match 26.5%; Score 933; DB 2; Length 222;
Best Local Similarity 82.6%; Pred. No. 4.7e-55;
Matches 180; Conservative 12; Mismatches 24; Indels 2; Gaps 1;
QY 6 QSGPDLVKPGASVKISKCKAGSYFTGYMHVWVKQSPGKLEWTGRINPNNGVTLNQKPK 65
DB 2 ESGPELVKPGSVTIISKAGSYFTTSMWNVQRPGQGLEWIGRIYPGSGDNNYNGKPK 61
QY 66 DKATLTWKSSTTAYMELSLTSEDGAVVYCAR--STMITNVYMDYWGQGTSTVTVSSAKT 123
DB 62 VKATLTAEKRSSTVYIHLSSLTSDVSAVFCARPHYDYSVAMDWGGQGTSTVTVSSAKT 121
QY 124 TPGSVYPLAPGSAQNSMTVLCGLVKGYFPEPTVTWNSGSLSSGVHTFPVAVLQSDLYT 183
DB 122 TPGSVYPLAPGSAQNSMTVLCGLVKGYFPEPTVTWNSGSLSSGVHTFPVAVLQSDLYT 181
QY 184 LSSSVTPSPSTWPSSEVTTCNVAPASSTKVKKIVPRD 221
DB 182 LSSSVTPSPSTWPSSEVTTCNVAPASSTKVKKIVPRD 219

RESULT 41

US-08-896-933-23
Sequence 23, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match 26.4%; Score 931.5; DB 3; Length 232;
Best Local Similarity 76.0%; Pred. No. 6.3e-55;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNSKAITSEKSADQFLNTLLFKGPFPTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQFL-HTILFKGPFPTD 59
QY 286 HPWYNDLLVLDGTAATSEVSGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
DB 60 HSWYNDLLVDFDSKQIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVKQ 405
DB 120 EEKVPINLWLDGKQNTVPLETKNKNVTVOELDPQARRYLOEKYNLYNSDVFQKVKQ 179

QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPDTLRIYRDNTTISSTLSISLYLYTT 458
DB 180 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRIYRDNKTINSENMHIDIYLYTS 232

RESULT 42

US-09-314-235-23
Sequence 23, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-04-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23
LENGTH: 232
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-314-235-23

Query Match 26.4%; Score 931.5; DB 4; Length 232;
Best Local Similarity 76.0%; Pred. No. 6.3e-55;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNSKAITSEKSADQFLNTLLFKGPFPTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQFL-HTILFKGPFPTD 59
QY 286 HPWYNDLLVLDGTAATSEVSGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
DB 60 HSWYNDLLVDFDSKQIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVKQ 405
DB 120 EEKVPINLWLDGKQNTVPLETKNKNVTVOELDPQARRYLOEKYNLYNSDVFQKVKQ 179
QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPDTLRIYRDNTTISSTLSISLYLYTT 458
DB 180 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRIYRDNKTINSENMHIDIYLYTS 232

RESULT 43

US-09-144-776B-2
Sequence 2, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army WPMC -504 Scott Street
MCWR-JA (Charles H. Harris-Patent
Atty)

```

; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 26.3%; Score 925; DB 4; Length 257;
Best Local Similarity 75.1%; Pred. No. 2e-54;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 84
QY 286 HPYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 44
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCWR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA

; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 26.3%; Score 925; DB 4; Length 257;
Best Local Similarity 75.1%; Pred. No. 2e-54;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 84
QY 286 HPYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 BEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 45
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYER, ELDEFRAMI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESS: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 26.1%; Score 921; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 3.2e-54;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 286
Db 2 EKSEINEKDLRKSELOQTALGNLQIYYNYSKAITSEKSDAQLTNTLLFKGPTG 61
QY 287 HPYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 346
Db 62 SYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 121
QY 347 EKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 406
Db 122 EKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 181
QY 407 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 45
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYER, ELDEFRAMI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESS: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 431-96
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-824-10

Query Match 26.0%; Score 915.5; DB 2; Length 254;
Best Local Similarity 79.2%; Pred. No. 8.3e-54;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;
QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
DB 23 EVQLQSGAELVKPGASVKLSCTASGFIKDTFMHWVKQRPQGLEWIGRIDPANGNTEY 82
QY 61 NQKFKDKATLVDKSTTAYMELRSITSDSAVYICARSTMTITNYMDYWGQTSVTYSS 120
DB 83 DPKFGKATITADTSSNTVNLQSLTSEDTAVYICASGGELG---FPYWGQGLTVTVA 139
QY 121 AKTTPSVYPLAPGSAQTNSMTVLCGLVKGYFPEPVTITWNSGSLSSGVHTFPVAVLQSD 180
DB 140 AKTTPSVYPLAPGSAQTNSMTVLCGLVKGYFPEPVTITWNSGSLSSGVHTFPVAVLQSD 199
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRD--SGG 224
DB 200 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCTSGG 245

RESULT 46
US-08-792-824-13
Sequence 13, Application US/08792824
Patent No. 5932449
GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHYEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Chemical and Biological Defense
ADDRESSEE: Command
STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
STATE: MD
COUNTRY: U.S.
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908

REFERENCE/DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-824-13

Query Match 26.0%; Score 915.5; DB 2; Length 254;
Best Local Similarity 79.2%; Pred. No. 8.3e-54;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;
QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
DB 23 EVQLQSGAELVKPGASVKLSCTASGFIKDTFMHWVKQRPQGLEWIGRIDPANGNTEY 82
QY 61 NQKFKDKATLVDKSTTAYMELRSITSDSAVYICARSTMTITNYMDYWGQTSVTYSS 120
DB 83 DPKFGKATITADTSSNTVNLQSLTSEDTAVYICASGGELG---FPYWGQGLTVTVA 139
QY 121 AKTTPSVYPLAPGSAQTNSMTVLCGLVKGYFPEPVTITWNSGSLSSGVHTFPVAVLQSD 180
DB 140 AKTTPSVYPLAPGSAQTNSMTVLCGLVKGYFPEPVTITWNSGSLSSGVHTFPVAVLQSD 199
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRD--SGG 224
DB 200 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCTSGG 245

RESULT 47
US-08-792-824-4
Sequence 4, Application US/08792824
Patent No. 5932449
GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHYEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Chemical and Biological Defense
ADDRESSEE: Command
STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
STATE: MD
COUNTRY: U.S.
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-792-824-4
Query Match 25.8%; Score 909.5; DB 2; Length 254;
Best Local Similarity 78.8%; Pred. No. 2.1e-53;
Matches 178; Conservative 15; Mismatches 28; Indels 5; Gaps 2;
QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTFGYVHWYKQSPGKLEWIGRINPNNGVTLY 60
DB 23 EVQLQQSGAELVKPGASVKLSCTASGFIKDTFMHWYKQSPGKLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLVKSSITAYNELRLSLSDSAVYICARSTMTINYNVDYWGQGTSTVTS 120
DB 83 DPKFGKATITADTSSNTVNLQSLSLSDSAVYICASGGELG---PPYWGQGTTLVISA 139
QY 121 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 180
DB 140 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 199
QY 181 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDCTSGG 245
QY 121 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 180
DB 140 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 199
QY 181 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDCTSGG 245
RESULT 48
US-08-792-824-7
; Sequence 7, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHVEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM #31-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-7
Query Match 25.8%; Score 909.5; DB 2; Length 254;
Best Local Similarity 78.8%; Pred. No. 2.1e-53;
Matches 178; Conservative 15; Mismatches 28; Indels 5; Gaps 2;
QY 1 EVQLQQSGPDLVKPGASVKISCKASGYSTFGYVHWYKQSPGKLEWIGRINPNNGVTLY 60

DB 23 EVQLQQSGAELVKPGASVKLSCTASGFIKDTFMHWYKQSPGKLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLVKSSITAYNELRLSLSDSAVYICARSTMTINYNVDYWGQGTSTVTS 120
DB 83 DPKFGKATITADTSSNTVNLQSLSLSDSAVYICASGGELG---PPYWGQGTTLVISA 139
QY 121 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 180
DB 140 AKTTPPSVYPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGVHTFPVQLQSD 199
QY 181 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDCTSGG 245
RESULT 49
US-09-192-545-4
; Sequence 4, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799979570
; CURRENT APPLICATION NUMBER: US/09/192,545
; EARLIER FILING DATE: 1998-11-13
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-4
Query Match 25.7%; Score 904.5; DB 3; Length 238;
Best Local Similarity 79.5%; Pred. No. 4.2e-53;
Matches 175; Conservative 18; Mismatches 22; Indels 5; Gaps 2;
QY 457 TTSIVMTQTPTSLIYAGDRVTITCKASQSV--SND---VAVYQKPGQSKLLISYTS 511
DB 18 SSDVLTQTPLSLPVLGDSQISCRSQSIVHSGNTYLEWYLOKPGQSKLLIYKVS 77
QY 512 RVAGVDPDRFSGSGYGTDTFTLTISVQAEADAAYFCQDYNSPPTFGGTTKLEIKADAAP 571
DB 78 RFGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQSHVPLTFGAGTKLEKADAAP 137
QY 572 TVSIIPPSSEQLTSGGASVVCFLNNFYPKDINVKKIKDSEBQNGVLNSWTDQDSKSTY 631
DB 138 TVSIIPPSSEQLTSGGASVVCFLNNFYPKDINVKKIKDSEBQNGVLNSWTDQDSKSTY 197
QY 632 SMSSTLTLTDEYERHNSYTCATHKTSPTVKSFNNE 671
DB 198 SMSSTLTLTDEYERHNSYTCATHKTSPTVKSFNNE 237
RESULT 50
5455030-1
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990

```
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:1
; LENGTH: 447
; 5455030-1

Query Match      25.7%; Score 903.5; DB 6; Length 447;
Best Local Similarity 32.9%; Pred. No. 1.1e-52;
Matches 222; Conservative 69; Mismatches 121; Indels 263; Gaps 15;

QY 1 EVOLQSGPDLVPCGASVKLSCKASGYFTGYMHVVKQSPGKGLWIGRINPNNGVTLY 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLVESGGDLVPCG-SLKLSCAAGFTFISYGMVWQTPDKRLEWVATISSGTYTY 59
QY 61 NQFKOKATLTVDKSSTTAYMELRSITSEDSAVYYCAR---STMITN-YVMDVWGQTSV 116
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 PDSVKGRFTISRDNAKNTLYLQMSGLSKSEDTANYICARRITTVLLDYDYANDVWGQTSV 119
QY 117 TVSSAKTTPSVYPLAPGSAQNSMVTGLCLVKGYFPEPVVTVNWSGLSSGVHTFPAPV 176
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 TVSSAKTTPSVYPLAPGSAQNSMVTGLCLVKGYFPEPVVTVNWSGLSSGVHTFPAPV 179
QY 177 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTVDKKIIPRDSGGPSEKSEELNEXD 236
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTVDKKIIPRDCG----- 226
QY 237 LRKKSLOQTALGNLQKIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDL 296
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 ----CKPCICTPEVSSVFIFPPK-----PKDVLITL----- 255
QY 297 GSTAATSEVGGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLTEKKVPINLMI 356
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 -----TP-KVTCVVVDIS-----KDDPEVQFSWFV 279
QY 357 DGRQTTVPIDKVKTSKEV-----TVQELDLQARHLHGKFGLYNSDS--FGGKVQRG 407
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
280 D----DVEVHTAGTQPREQFDSSTSVSELPLMHQDWLNGKEFKRVDASAAPAPIEK- 334
QY 408 LIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRNTTISSTLSISLYLTTISVMTQPT 467
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
335 -----TISKT----- 339
QY 468 SLLVSAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRRVAGVDPDRFGSGYGT 527
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 ----- 339
QY 528 DFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPIPPSEQLTSGG 587
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 -----KGRPKAPQVYTIPTPPKEQVAKDX 362
QY 588 ASVVCFLNPFYKDIYVKKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTTLTKD 642
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
363 VSLTCMTDFFPDIDTIVQWDGQPAENYKNTQRIKNT-----DGSYFYVSKLDVQKS 415
QY 643 EVERHNSYTCETHK 657
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 NWEAGTFTICSVLHE 430

RESULT 51
PCT-US94-14106-57
; Sequence 57, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-14106-57

Query Match      25.6%; Score 901; DB 5; Length 218;
Best Local Similarity 80.6%; Pred. No. 6.4e-53;
Matches 174; Conservative 9; Mismatches 29; Indels 4; Gaps 1;

QY 460 IVMQTPTSLVLSVAGDRVTITCKASQSVND---VAVYQKPGQPKLLISYTSRYAG 515
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 IVMQTSPASLAVSLGQRATISCRVRQSVSTSSHSHMYQKPGQPKLLIKYASNLESG 61
QY 516 VPDFSGSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSI 575
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 VPARFSGSGSGTDTFTLNHPVEEEDTATYYCOHSWEIPTYTFGGGKTKLEIKRADAAPTIVSI 121
QY 576 FPPSEQLTSGGASVVCFLANNFYKDIYVKKIDGSRQNVLSNWTDDQSKDSTYSMS 635
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 FPPSEQLTSGGASVVCFLANNFYKDIYVKKIDGSRQNVLSNWTDDQSKDSTYSRSS 181
QY 636 TLTLTKDYEYRHSNYTCETHKSTSPIVKSFNRNE 671
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 TLTLTKDYEYRHSNYTCETHKSTSPIVKSFNRNE 217

RESULT 52
US-09-170-769A-8
; Sequence 8, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Murine
; US-09-170-769A-8

Query Match      25.5%; Score 898; DB 4; Length 211;
Best Local Similarity 81.4%; Pred. No. 9.7e-53;
Matches 171; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 462 MTQPTSLVLSVAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFS 521
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTQPTSLVLSVAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFS 60
QY 522 GSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPIPPSE 581
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPIPPSE 120
QY 582 QLTSGGASVVCFLANNFYKDIYVKKIDGSRQNVLSNWTDDQSKDSTYSMSSTTLTK 641
```

```
Db 121 QLTGGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLTITK 180
Qy 642 DEYERHNSYTCETHKSTSPIVKSFNRNE 671
Db 181 DEYERHNSYTCETHKSTSPIVKSFNRNE 210

RESULT 53
PCT-US94-14106-55
; Sequence 55, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-55

Query Match 25.5%; Score 897.5; DB 5; Length 223;
Best Local Similarity 79.4%; Pred. No. 1.1e-52;
Matches 177; Conservative 12; Mismatches 31; Indels 3; Gaps 2;

Qy 1 EVQLQSGFDFLVKPGASVKISCKASGYSTFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGAELMPPGASVKISCKATGYTLSSSLWLEWVKSPGHLGIEWIGELFCGSGAHY 60
Qy 61 NQKFKDKATLVDRGSTTAYMELSLTSEDSAVYICARSTMITNY--VMDYWGQGSTVTV 118
Db 61 NEKFKGKATFTVDSSNTAYMQLSLTSEDSAVYICARGD-YGNYGDFDYWGQGLTV 119
Qy 119 SSKATTPSVYPLAPGSAQAQNSMWTICLVKGFPPPTVWNSGSLSGVHTFPVAVLQ 178
Db 120 FSAKTPSSVYPLAAGSAQAQNSMWTICLVKGLPEPTVWNSGSLSGVHTFPVAVLQ 179
Qy 179 SDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRD 221
Db 180 SDLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRD 222

RESULT 54
US-08-737-129A-8
; Sequence 8, Application US/08737129A
; Patent No. 585816
; GENERAL INFORMATION:
; APPLICANT: IKUO FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTISELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 585816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-8

Query Match 25.4%; Score 895; DB 2; Length 215;
Best Local Similarity 80.2%; Pred. No. 1.6e-52;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 460 IVMTOTPTSLVSGDRVTITCKASQSVSNVDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 2 LVMTQTPSSMYASLGERVTITCKASQDINIVLWFPQKPGKSPKALIVRTNGLVDGVPSR 61
Qy 520 FSGSGYGTFTLTISVQAEADAIVFCQDYNSTPPTFGGKLEIKRADAAPTVSIPTPS 579
Db 62 FSGSGGQDYSLTISLSEYEDMGIVYCLQYDFEFTFGGKLEIKRADAAPTVSIPTPS 121
Qy 580 SGLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLT 639
Db 122 SGLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLT 181
Qy 640 TKDEYERHNSYTCETHKSTSPIVKSFNRNE 671
Db 182 TKDEYERHNSYTCETHKSTSPIVKSFNRNE 213

RESULT 55
US-08-442-542-18
; Sequence 18, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Kozziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
```

```

: GENERAL INFORMATION:
: APPLICANT: Carozzi, Nadine B.
: APPLICANT: Koziel, Michael G.
: TITLE OF INVENTION: Antibodies which Bind to Insect Gut
: TITLE OF INVENTION: Proteins and their Use
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/765,469
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: FILING DATE: 08/267,641
: ATTORNEY/AGENT INFORMATION:
: NAME: Spruill, W. Murray
: REGISTRATION NUMBER: 32,943
: REFERENCE/DOCKET NUMBER: CGC 1750
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-541-8615
: TELEFAX: 919-541-8689
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 599 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-765-469-18

Query Match 25.3%; Score 892.5; DB 3; Length 599;
Best Local Similarity 32.4%; Pred. No. 8.7e-52;
Matches 219; Conservative 73; Mismatches 118; Indels 265; Gaps 16

Qy 1 EVOLQSGPDLVRFPGASVKISCKASGYSGFTGYMHVWKQSPGKLEWIGRI--NPNGVT 58
Db 155 QVKLQESGGGLVQPKGSLKSCASGFTFNPNWVRQAPGKLEWVARIRSKSNYAT 214
Qy 59 LYNQKFKDKATLIVDKSSSTAYMELRSLTSEDGAVYYCARSTMITNYMDYWGQTSVTV 118
Db 215 SYGDSVKDRFTVSRDSSQSMFYLGNNLKTEDTAMYICVR---VVGAMDYWGQTSVTV 271
Qy 119 SSARKTTPPSVYPLAPG--SAAQTNMSWTLGCLVKGYPEPVTVTWNSGSLSSGVHTTPAV 176
Db 272 SSARKTTPPSVYPLAPGSRSAQTNMSWTLGCLVKGYPEPVTVTWNSGSLSSGVHTTPAV 331
Qy 177 LQSDLYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKKIVPRDSGSPSEKSEINEKD 236
Db 332 LQSDLYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKKIVPRDCG----- 378
Qy 237 LRKSELOQTALGNLKOIYYNSKAITSSSEKSDQFLTNTLLFKGFTGHFWNDLLVDL 296
Db 379 -----CRPCICTVPEVSVSFIFPPK-----PRDVLITL----- 407
Qy 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTBKKVPINLWI 356
Db 408 -----TP-KYTCVVVDIS-----KDDPEVQFSWFV 431
Qy 357 DGKQTTPVIDKVTSKKEV-----TVQELDLOARHYLHGK-FGL-YNSDSFGGKVGQR 407
Db 432 D----DVEVHTAQTPREEQFNSTFASVSELPMHQDWLNGKEFKCIVNSGAAPPAIEK- 486
Qy 408 LIVFHSSEGTSTVDYLFDAOGYVDDTLRIVRDNNTTISSTLSSTSLVLYTTSIMTCTPT 467

```

QY	357	DGQQTWTFIDKATSKKEV-----TVSELDQARHYLEKQ-FGL-YNDSDFGKRVQ	407
Db	432	D-----DVEHTAQTPREEQFNSTFRSVSELPVHQDLWLNKGFKCRVNSAAPPTKE-	486
QV	408	LIVFHSSGSGTAVDVFDAOGVYDDTLRTVRYDNTTISSTLSLSIYLYTTTSLVMTQPT	467

Db 487 -----TISK----- 491
 Qy 468 SLLVSGDRVTITCKASQSVNDVAVYQKPGQSKLLISYTSRVAGVDRFSGSGYGT 527
 Db 492 ----- 491
 Qy 528 DFTLTSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRADAPTYSIFPPSSEQUTSGG 587
 Db 492 -----KGRPKAPOVYTIPTTPEQMAKDK 514
 Qy 588 ASVVCFLNNFYKPDINVKWKIDGSEON-----GVLSWTDQDSKDYSGMSSTLTITKD 642
 Db 515 VSLTCMTIDFPEDITVWQNGQPAENYKNTQPIMT-----NGSYFYVSKLNVQKS 567
 Qy 643 EYERHNSYTCBATHK 657
 Db 568 NWEAGNTFTCSVLHE 582

RESULT 57

US-09-423-439-58
 ; Sequence 58, Application US/09423439
 ; Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

BLAKEY, David Charles

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-NO. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 58:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-423-439-58

Query Match 25.3%; Score 889.5; DB 4; Length 235;
 Best Local Similarity 77.1%; Pred. No. 4.1e-52;
 Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

Qy 449 LSISLYLTTSIVMTQTPTSLVLSAGDRVTITCKASQSVNSNDVAVYQKPGQSKLLISY 508
 Db 13 ISASVIMSRGQTVLSQSPAILSGPCKVTMTCRASSSVTY-IHWYQKPGSSPKSWIYA 71
 Qy 509 TSSRVAGVDRFSGSGYGTDTLTITSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRAD 568
 Db 72 TSNLASGVPAFPSSGSGYGTSLTISRVEADAAVYCOHWSKRPPTFGGTYKLEIKRAD 131
 Qy 569 AAPTYSIFPPSSEQUTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 628

Db 132 AAPTYSIFPPSSEQUTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 191
 Qy 629 STYSMSSTLTITCKEYERHNSYTCBATHKTSPIVKSFNRE 671
 Db 192 STYSMSSTLTITCKEYERHNSYTCBATHKTSPIVKSFNRE 234

RESULT 58

US-09-011-769A-23
 ; Sequence 23, Application US/09011769A
 ; Patent No. 6436691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKEY, David C.

DAVIES, David H.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-011-769A-23

Query Match 25.3%; Score 889.5; DB 4; Length 235;

Best Local Similarity 77.1%; Pred. No. 4.1e-52;

Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

Qy 449 LSISLYLTTSIVMTQTPTSLVLSAGDRVTITCKASQSVNSNDVAVYQKPGQSKLLISY 508
 Db 13 ISASVIMSRGQTVLSQSPAILSGPCKVTMTCRASSSVTY-IHWYQKPGSSPKSWIYA 71
 Qy 509 TSSRVAGVDRFSGSGYGTDTLTITSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRAD 568
 Db 72 TSNLASGVPAFPSSGSGYGTSLTISRVEADAAVYCOHWSKRPPTFGGTYKLEIKRAD 131
 Qy 569 AAPTYSIFPPSSEQUTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 628
 Db 132 AAPTYSIFPPSSEQUTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 191
 Qy 629 STYSMSSTLTITCKEYERHNSYTCBATHKTSPIVKSFNRE 671

Db 192 STYMSSTLTITLKDEYERHNSYTCETHKTSPIVKSFRNE 234

RESULT 59
US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 5865816
; GENERAL INFORMATION:
; APPLICANT: IKUO FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885916member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-737-129A-4

Query Match 24.9%; Score 878; DB 2; Length 213;
Best Local Similarity 81.1%; Pred. No. 2.1e-51;
Matches 172; Conservative 13; Mismatches 25; Indels 2; Gaps 2;

QY 460 IWTQPTSLYSAGDRVTITCKASQSVNDVAVYQKQSPKLLISVTSRYAGVDR 519
Db 2 LVMTQPALMSAPGKWTMCASSISY-NHWYQKQKPTPKRWIYKTSKLTSGVPAR 60

QY 520 FSGSGYGTFTLTISVQAEAAVYFCQDDYNSPPTFGGKTKLEIKRADAAPTIVSIFPPS 579
Db 61 FSGSGSGTSFSLTISMEAEADATVYCHQ-RSSYPTFGGKTKLEIKRADAAPTIVSIFPPS 119

QY 580 SEQLTSGGASVUCFLNFPKQINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSSTLT 639
Db 120 SEQLTSGGASVUCFLNFPKQINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSSTLT 179

QY 640 TKDEYERHNSYTCETHKTSPIVKSFRNE 671
Db 180 TKDEYERHNSYTCETHKTSPIVKSFRNE 211

RESULT 60
US-09-423-439-60
; Sequence 60, Application US/09423439
; Patent No. 6339070

GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 647 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-423-439-60

Query Match 24.8%; Score 873; DB 4; Length 647;
Best Local Similarity 37.3%; Pred. No. 1.9e-50;
Matches 247; Conservative 66; Mismatches 184; Indels 166; Gaps 27;

QY 1 EVOIQSGPDLVKPGASVKISKASGYSTGYVYHWTQSPKGLWIGRI-NPENGVTIL 59
Db 20 EVKLVEGSGGLVQPGGSLRUSCATSGTFTDYNNWVRQPPGKALEWLGIFGNKANGYTT 79

QY 60 -YNQKFKDKATLTVDKSSTTAYMELRLTSDTSVAVYCARSTMTNVMYWGQSTVTV 118
Db 80 EYSASVKRFTISRDKSQSLYLQMTLRAEDSATYICTDRGLRFY-FDYWGQSTLTIV 138

QY 119 SSAKTTPSVVPLAPGSAQAQNSMVTLCGLVKGYFPPEPVTVMNSGSLSGVHTFPVAVLQ 178
Db 139 SSAKTTPSVVPLAPGSAQAQNSMVTLCGLVKGYFPPEPVTVMNSGSLSGVHTFPVAVLQ 198

QY 179 SDLTYLASSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRD-----SGGPSE 227
Db 199 SDLTYLASSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIVPRDCCGGGGGGGGGGGSG 258

QY 228 KSEBI-----NE-----KDLRKSEIQ-GT-----ALGNLKKIYYNKAITSSEKS 268
Db 259 KRDNVLFQAATDEQPAVTKITLKVNIETGTGDAEGIAAGNFLEAKNLGFTVTRSKS 318

QY 269 ADQFLTNILFKGFTGHPWYNDLL-----VDLGSTAAATSEYEGSSVDLYGAYYQCA 322
Db 319 AGLVVGNDIV--GKIKRGGKNLLMGMHMDTVLKGILAKAPFVREGDKAYG-----P 369

QY 323 GGTENKACMYGG--VTLHNNRLTEKKVPINLWIDGKQTTVFIDKVKTSKKEVTVOEL 380
Db 370 GIADDK-----GGNAVILHTLKLL-----KEYGYRD- 395

QY 381 DLQARHYLHGKFG----LYNSDSFGGKVGQRLIVFHSSEGSTVSYDLFDAGQGVPTLLR 436
Db 396 -----YGTITVLFNTD-----BEKGSFGSRDLIQBEAKLADYVLS 430

QY 437 IYRDNVTISSTLSLSILYLTTSIWMQT-----PTSLYSAGDRVTITC 481

Db 431 F--BPTSAGDEKLSLG-----TSGIAYQVNVITGKASHAGRAPELGVNALVEASDLVLRM 484
QY 482 KASOSVSN-DVAVTQOQKPGQSKLLISYTS-----SRVAGVDPDRSGSGYGTDFTLTSSV 536
Db 485 NIDDKAKVLRFNWTIAKAGVNSNIPASATLNADRYA-----RNEDFDAAMKTL 534
QY 537 QAEDAAVVFQODY-----NSPPTFG--GOTKLEIKRA-----DAAPTVAIFPPSSBQLT 584
Db 535 ZERAQOKKLPEADVIVTRGRPAFNAEGGKLVLDKAVAYYKEAGTGLGV-----EERT 589
QY 585 SGG 587
Db 590 GGG 592

RESULT 61
US-08-792-824-3
; Sequence 3, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEB, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-3

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 166; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNSDVAVYQOQKPGQSKLLISYTSRYAGVDPDR 519
Db 24 IQMTQSPASLSASVGETVTITCRASGNHNYLAWYQOQKSPQLLVYNAKTLADGVPSR 83
QY 520 FSGSGYGTDFTLTISVQAEADAAYVFCQDYNPSPTFGGKLEIKRADAAPTVAIFPPS 579
Db 84 FSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTWTFGGTKLEIKRADAAPTVAIFPPS 143
QY 580 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQNGVLNSWTDQDSDKSTYSMSSTLTL 639
Db 144 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQNGVLNSWTDQDSDKSTYSMSSTLTL 203

RESULT 63
US-08-792-824-12
; Sequence 12, Application US/08792824

QY 640 TKDEVERHNSYTCETHKTSPIVKSFNRNE 671
Db 204 TKDEVERHNSYTCETHKTSPIVKSFNRNE 235

RESULT 62
US-08-792-824-9
; Sequence 9, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEB, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-9

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 166; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNSDVAVYQOQKPGQSKLLISYTSRYAGVDPDR 519
Db 24 IQMTQSPASLSASVGETVTITCRASGNHNYLAWYQOQKSPQLLVYNAKTLADGVPSR 83
QY 520 FSGSGYGTDFTLTISVQAEADAAYVFCQDYNPSPTFGGKLEIKRADAAPTVAIFPPS 579
Db 84 FSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTWTFGGTKLEIKRADAAPTVAIFPPS 143
QY 580 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQNGVLNSWTDQDSDKSTYSMSSTLTL 639
Db 144 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQNGVLNSWTDQDSDKSTYSMSSTLTL 203

RESULT 63
US-08-792-824-12
; Sequence 12, Application US/08792824

Patent No. 5932449
GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHVEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Chemical and Biological Defense
ADDRESS: Command
STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
STATE: MD
COUNTRY: U.S.
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-824-12

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 165; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
QY 460 IVMQTPTLLVNSAGDRVITKASQSVNDVAVYQKFGQPKLLISTSSRYAGVDR 519
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 520 FSGSGYGTDFLTLSISSVQAEADAVYFCQDYNAPPTFGGGTKLEIKRADAAPTIVSIFPPS 579
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 580 SEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLSNWDQDSKDYMSSTLT 639
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 640 TKDEYERHNSYTCEATHKSTSTPIVKSFNRE 671
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83

RESULT 64

US-09-301-593-18
Sequence 16, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301.593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 18
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-18

Query Match 24.8%; Score 872; DB 4; Length 453;
Best Local Similarity 34.1%; Pred. No. 1.4e-50;
Matches 227; Conservative 56; Mismatches 143; Indels 240; Gaps 17;
QY 2 VLOQSGPDLVPGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLN 61
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 62 QKFKDKATLTVDKSTTAYMELRLSTSEDSAVYCARSTMITNY----VMDYWGQGSVT 117
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 61 QKFKGRATLTVGKSSSTAYMELRLSTSEDSAVYCARRIAYGYDEGHAMDYWGQGSVT 120
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 118 VSSAKTTPPSVYPLAPGSAATNSMTLGLVKGYPFEPVTVTWNSSLSGSLSSVHTFFAVL 177
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 121 VSSASTKGPSVFPPLAPSKSTSGGTAALGLVLDYFPFVTVSWNSGALTSVHTFFAVL 180
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 178 QSD-LYTLSSSVTPSSWPSETVTCNVHPASTKVDKIVPRDSGGSPSEKSEINEKD 236
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 181 QSSGLYSLSSVTVFSSSLGTQTYICNVNHPKSTKVDKVEPKSC----- 226
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 237 LRKXSELQGTALGNLKQIYYNNSKAITSSSEKSAQOFLTNTLLFGFTGHPWYNLLVDL 296
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 297 GSTAATSEYEGSSVDLYGAYYQACGTPNKTACMYGGVTLHDNNRLTEKKYPINLWI 356
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 357 DGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVFHSSEG 416
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 417 STVSYDLFDAQGYPDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLLSVAGDR 476
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 321 NGKEY----- 325
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 477 VTITCKASQSVSNDVAVYQKFGQPKLLISYTSRRVAGVDPDRPSGSGYGTDFLTITSSV 536
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 326 ---XCKVS-----NKALPAP---TEKTSKAKGP----- 349
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 537 QAEDAAVFCQDYNAPPTFGGGTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNN 596
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 350 -----REFQVYTLPPSREEMTKQVSLTCLVKG 377
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 597 FYPKIDINVKWKIDGSRQN-----GVLSNWDQDSKDYMSSTLTLTDEYERHNSYT 651
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 378 FYPSDIAVESNGQPPENNYKTTTPVLDS-----DGSFELYSKLTIVDKSRWQGNVFS 430
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 652 CEATHK 657
Db I Q M T Q P A S L S A G V E T I T C R A S G N I H L A W Y Q K G S P Q L L V Y N A K T L A D G V R 83
QY 431 CSVMHE 436

RESULT 65
PCT-US94-14106-61
Sequence 61, Application PC/TUS9414106
GENERAL INFORMATION:
APPLICANT:

Matches 168; Conservative 11; Mismatches 31; Indels 4; Gaps 1;
 QY 462 MTOTPTSLVAGDRVTITCKASQSVNDV----AWQKPGQSPKLLISYSSRVAGVP 517
 Db 1 MTQSPASLAVSLQRPAPYCRASESDSYNSFLHWYQKPGPPKLLIYRASNLQSGIP 60
 QY 518 DFGSGGYGDTFTLTSSVQAEAAVYFCQDYNSPFTFGGKLEIKRADAAPTYSIIP 577
 Db 61 ARFSGSGRTDFTLTINPVEADVAATYCCQSNEDPTTSGGKLEIKRADAAPTYSIIP 120
 QY 578 PSSEQLTSGGASVVCFLNNFYKIDINVKWIDGSRQNGVLNWTDDSKDSTYSMSSTL 637
 Db 121 PSSEQLTSGGASVVCFLNNFYKIDINVKWIDGSRQNGVLNWTDDSKDSTYSMSSTL 180
 QY 638 TLTKDEYERHNSYTCETHKTSPIVKSFNRE 671
 Db 181 TLTKDEYERHNSYTCETHKTSPIVKSFNRE 214

RESULT 68
 PCT-US94-07659-4
 ; Sequence 4, Application PC/TUS9407659
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Peter
 ; APPLICANT: Gross, Mitchell
 ; APPLICANT: Jonak, Zdenka L.
 ; APPLICANT: Theisen, Timothy
 ; APPLICANT: Hurler, Mark
 ; APPLICANT: Jackson, Jeffrey R.
 ; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
 ; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
 ; TITLE OF INVENTION: Disorders in Man
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation - Corp.
 ; ADDRESSEE: Intellectual Property
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07659
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/090,534
 ; FILING DATE: 09-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REFERENCE/DOCKET NUMBER: P50171-1
 ; TELEPHONE: (610) 270-5024
 ; TELEFAX: (610) 270-5090
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-07659-4

Query Match 24.4%; Score 858; DB 5; Length 234;
 Best Local Similarity 72.9%; Pred. No. 5.2e-50;
 Matches 157; Conservative 19; Mismatches 39; Indels 4; Gaps 1;
 QY 447 TSLISILYLYTT-----SIVMTPTSLVAGDRVTITCKASQSVNDVAVYQKPGQSP 502

Db 5 TOVLALLLWLTGARCIDQMTQSPASLSASVGEVTVITCRASGNIHNLVYQKQKQSP 64
 QY 503 KLLISYSSRVAGVDPDRPSGSGYGTDTFTLTSSVQAEAAVYFCQDYNSPFTFGGKTL 562
 Db 65 QLLVYNAKTLADGVPSRPSGSGSTQYSLKINSIQPEDFGSYQCQHFWSIPIYTFGGGKTL 124
 QY 563 EIKRADAAPTYSIIPPSSEQLTSGGASVVCFLNNFYKIDINVKWIDGSRQNGVLNWT 622
 Db 125 EIKRADAAPTYSIIPPSSEQLTSGGASVVCFLNNFYKIDINVKWIDGSRQNGVLNWT 184
 QY 623 DQSKDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNRE 671
 Db 185 DQSKDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFNRE 233

RESULT 69
 US-09-011-769A-21
 ; Sequence 21, Application US/09011769A
 ; Patent No. 6436691
 ; GENERAL INFORMATION:
 ; APPLICANT: SLATER, Anthony M.
 ; BLAKEY, David C.
 ; DAVIES, David H.
 ; HENNAM, John F.
 ; HENNEQUIN, Laurent F.A.
 ; MARSHAM, Peter R.
 ; DOWELL, Robert I.
 ; TITLE OF INVENTION: Chemical Compounds
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, LLP
 ; STREET: 1100 New York Ave., N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 Mb disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/011,769A
 ; FILING DATE: 13-Feb-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB96/01975
 ; FILING DATE: 13-AUG-1996
 ; APPLICATION NUMBER: GB 9612295.7
 ; FILING DATE: 12-JUN-1996
 ; APPLICATION NUMBER: GB 9611019.2
 ; FILING DATE: 25-MAY-1996
 ; APPLICATION NUMBER: GB 9516810.0
 ; FILING DATE: 16-AUG-1995
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 250 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 US-09-011-769A-21

Query Match 24.3%; Score 855.5; DB 4; Length 250;
 Best Local Similarity 72.9%; Pred. No. 8.4e-50;
 Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;
 QY 1 EVQLQQSGPDLVQPCASVKISKASGYSTGYMHWVQKSPGKLEWIGRI-NFNNGVTL 59
 Db 20 EVKLVEGGGLVQPGGRLRISCATSGFTFTDYNNWVQPPGKALEWLGIGNKASYTT 79
 QY 60 -YNQKFKDKATLTVDKSTTAYMELRSLTSDSDSAVYVCARSTMTINYMDYWGQGTSTV 118

```
Db 80 EYSASVKGRTISRDKSQSILYLQWNTLRAEDSATYCTDRGLRFY-FDYWGQGTTLTV 138
QY 119 SSAKTPPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 178
Db 139 SSAKTPPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 198
QY 179 SDLYTLSSSVTPSPSTPSEVTCNVNVAHPASSTKVDKKIVPRDSG 223
Db 199 SDLYTLSSSVTPSPSTPSEVTCNVNVAHPASSTKVDKKIVPRDCG 243

RESULT 70
US-09-171-945-131
; Sequence 131, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Monoclonal Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171.945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-131

Query Match 24.3%; Score 855.5; DB 3; Length 473;
Best Local Similarity 72.9%; Pred. No. 1.9e-49;
Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;

QY 1 EVQLQSGPDLVKPGASVKISCKASGYSTFTGYMHVWVKQSPGKLEWIGRI-NPNNGVTIL 59
Db 243 EYKLVESGGGLVQPGGSLRLSCLATSGFTFTDYNNWVRQPPGKALEWLGFIGNKANGYTT 302
QY 60 -YNQKFKDKATLVTDKSTTAYMELRSLTSDSAVYVCARSTMITNYMDYWGQGTSTVTV 118
Db 303 EYSASVKGRTISRDKSQSILYLQWNTLRAEDSATYCTDRGLRFY-FDYWGQGTTLTV 361
QY 119 SSAKTPPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 178
Db 362 SSAKTPPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 421
QY 179 SDLYTLSSSVTPSPSTPSEVTCNVNVAHPASSTKVDKKIVPRDSG 223
Db 422 SDLYTLSSSVTPSPSTPSEVTCNVNVAHPASSTKVDKKIVPRDCG 466
```

```
RESULT 71
US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
```

```
; GENERAL INFORMATION:
; APPLICANT: Agair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Etage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-303-569B-5

Query Match 24.2%; Score 852.5; DB 2; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 449 LSIISLYTTSIVMTQTPTSLLSVAGDRVITTCASQSVSNDVAVYQKPGQSPKLLISY 508
Db 13 ISAVIISRGQIVLTQSPALMSASPEKVTMTCSASSSVY-MNYYQKSGTSPKRWIYD 71
QY 509 TSSRAGVPDFRFGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGKLEIKLAD 568
Db 72 TSLASGVPAHFRGSGSGTSYSLTISGMEADDAATYQCQWSSNFTTSGSGTKLEINRAD 131
QY 569 AAPTIVSIPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEFQNGVLNSWTDQDSK 628
Db 132 TAPTIVSIPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEFQNGVLNSWTDQDSK 191
QY 629 STYSMSSTLTLDKDYERHNSYTCETHKTSPIVKSFNRE 671
Db 192 STYSMSSTLTLDKDYERHNSYTCETHKTSPIVKSFNRE 234

RESULT 72
US-08-116-247-5
; Sequence 5, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-116-247-5

Query Match 24.2%; Score 852.5; DB 2; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 449 LSISLYLTTISIVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIISRGQIVLTQSPAIMSASPGKVTMTCSASSSVSY-MNMYQQSGTSPKRWIYD 71
QY 509 TSSRYAGVDPFRFGSGGYGDTFTLTISVQAEADAAYVFCQDYNPPTFGGKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYCCQWSSNPFTFGSGTKLEINRAD 131
QY 569 APTVSIFFPSSBQLTSGGASVVCFLNNFPKDIIVKWKIDGSRQGVNSWTDQDSKD 628
Db 132 TAPTIVSIFFPSSBQLTSGGASVVCFLNNFPKDIIVKWKIDGSRQGVNSWTDQDSKD 191
QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNRNE 234

RESULT 73
US-09-795-515-5
; Sequence 5, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-795-515-5

Query Match 24.2%; Score 852.5; DB 4; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 449 LSISLYLTTISIVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIISRGQIVLTQSPAIMSASPGKVTMTCSASSSVSY-MNMYQQSGTSPKRWIYD 71
QY 509 TSSRYAGVDPFRFGSGGYGDTFTLTISVQAEADAAYVFCQDYNPPTFGGKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEADAATYCCQWSSNPFTFGSGTKLEINRAD 131
QY 569 APTVSIFFPSSBQLTSGGASVVCFLNNFPKDIIVKWKIDGSRQGVNSWTDQDSKD 628
Db 132 TAPTIVSIFFPSSBQLTSGGASVVCFLNNFPKDIIVKWKIDGSRQGVNSWTDQDSKD 191
QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKSFNRNE 234

RESULT 74
5189147-8
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSEN, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEORODIMERIC T LYMPHOCYTE RECEPTOR
; ANTIBODY
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 8:
; LENGTH: 200
; 5189147-8

Query Match 24.1%; Score 850.5; DB 6; Length 200;
Best Local Similarity 78.3%; Pred. No. 1.4e-49;
Matches 170; Conservative 13; Mismatches 17; Indels 17; Gaps 3;

QY 1 EVQLQQSGPDLVKEPGASVKISCKASGYSTFGYYHWYKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQQSGAELVRAGSSVKSKASGYTFTSYGINVYKQRPQGQLEWIGYINPGNGVINY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYVCARSTWITNYVMYDYGQGTSTVTSS 120
Db 61 NEKEFGKXTLLTVDKSSSTAYMQLRSLTSEDSAVYFCARS-----HYYG-----G 104
QY 121 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYPEPVTVTWNSGLSSGSHVHTFPAVLQSD 180
Db 105 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYPEPVTVTWNSGLSSGSHVHTFPAVLQSD 164
QY 181 LYTLLSSSVTPSPSTWPSSETVTCNVHPASSSTKVDKKI 217
```

Db 165 TY-LSSSVTPSPRPSETVTCNVAHPASSTKVDK1 200
 RESULT 75
 US-07-934-373C-22
 ; Sequence 22: Application US/07934373C
 ; Patent No. 5821337
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul J. Carter
 ; APPLICANT: Leonard G. Presta
 ; TITLE OF INVENTION: Immunglobulin Variants
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934,373C
 ; FILING DATE: 21-Aug-1992
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/05126
 ; FILING DATE: 15-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0709P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-07-934-373C-22

Query Match 23.9%; Score 841; DB 2; Length 454;
 Best Local Similarity 33.2%; Pred. No. 1.7e-48;
 Matches 222; Conservative 58; Mismatches 146; Indels 242; Gaps 18;
 QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLY 60
 Db 1 QVQLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLY 60
 QY 61 NQKFKDKATLVKDSSTAYMELSLTSEDGAVYCARSTWITNY-----VMDYWGQGS 115
 Db 61 NQKFKDKATLVKDSSTAYMELSLTSEDGAVYCARSTWITNY-----VMDYWGQGS 115
 QY 116 VTVSSAKTTPPSVPLAPGSAQINSVMYTLGLVKLVYFPEPTVTWNSSGSLSSGVHTFPA 175
 Db 120 VTVSSAKTTPPSVPLAPGSAQINSVMYTLGLVKLVYFPEPTVTWNSSGSLSSGVHTFPA 175
 QY 176 VLQSD-LYTLSSSVTPSPSTVTCNVAHPASSTKVDKVIIPRDSGGPSEKSEBINE 234
 Db 180 VLQSSGLYSLSSVTPSPSSLTGTQYICNVNHPKSNITKVDKVEPKSC----- 227
 QY 235 KDLRKKSSELTALGNLQIYYNYSKAITSSKSAQDLTNTLLPKGFFTCHPWYNLLV 294
 Db 228 -----DKHTTCTPCPAPELLGGPSVF--LFPKP--KDTLM 259

QY 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNRLTEKKVPINL 354
 Db 260 -----ISRPEVT-CVVVDVS-----HEDPEVFNW 284
 QY 355 WIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVGORGLIVFHSS 414
 Db 285 YVDG----VEVHNAKTPREEQ-----YNSTY--RVSVLTVLHOD 319
 QY 415 EGSSTVSYDLFDAQGGYPTLLRIYEDNTTISTSTLSLSLYLYTTSIVMTQPTSLVSAG 474
 Db 320 WLNGKEY----- 326
 QY 475 DRVTITCKASQSVSNDVAWYQOKPQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTIS 534
 Db 327 -----KCKVS-----NKALPAP--LEKTIKAKGP----- 350
 QY 535 SVQAEADAIFYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFL 594
 Db 351 -----REPQVYTLPPSREEMTKNQVSLTCLV 376
 QY 595 NNFYPKDINVKWKIDGSEKQ-----GVLSNWTQDQSKDSTYSMSSTLTLTAKDEYERHNS 649
 Db 377 KGFYPSDIAVEWESNGQPNKYKTPPVLD-----DGSFFLYSKLTVDKSRWQGNV 429
 QY 650 YTCEATHK 657
 Db 430 FSCSVWHE 437
 Search completed: August 12, 2004, 13:34:01
 Job time : 33.5729 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 7.37083 Seconds
(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEKDLRKSEKLG.....RDNTTISSTLSLSLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 78:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	90.9	257	2 A28179	enterotoxin E prec
2	948	77.8	257	2 A28664	enterotoxin A prec
3	918	75.4	260	2 C89384	enterotoxin P [imp
4	611	50.2	258	2 A33953	enterotoxin D prec
5	420.5	34.5	258	2 H89668	enterotoxin Sen [i
6	372.5	30.6	260	2 E89969	enterotoxin SeO [i
7	311	25.5	240	2 C89991	extracellular ente
8	296.5	24.3	242	2 C89969	extracellular ente
9	284.5	23.4	266	2 S11885	enterotoxin C3 - S
10	282	23.2	239	2 D89969	enterotoxin SEM [i
11	277.5	22.8	266	2 A60114	enterotoxin C-2 pr
12	269.5	22.1	251	1 S23659	enterotoxin type A pr
13	268.5	22.0	266	1 ENSAB6	enterotoxin B prec
14	263.5	21.6	266	1 ENSAC1	enterotoxin C-1 pr
15	253.5	20.8	236	2 S18783	enterotoxin type A pr
16	251.5	20.6	236	2 S18789	enterotoxin A precurs
17	248.5	20.4	236	2 S18786	enterotoxin type A pr
18	241	19.8	258	2 G89968	extracellular ente
19	220	18.1	250	1 A28152	streptococcal pyro
20	190	15.6	136	2 A89969	enterotoxin YENT2
21	178	14.6	157	2 A89942	hypothetical prote
22	155.5	12.8	235	2 A30509	enterotoxin C precurs
23	115	9.4	62	2 H89941	hypothetical prote
24	100	8.2	234	1 XCSA51	toxic shock syndro
25	98	8.0	133	2 B89969	enterotoxin Yent1
26	98	8.0	227	2 G89967	enterotoxin 14 [impor
27	96	8.0	234	2 B89992	toxic shock syndro
28	96	7.9	552	2 T41863	chitinase chi-A or
29	94	7.7	231	2 D89807	enterotoxin 11 [impor

30	94	7.7	979	2 JQ0894	Pil5 protein - Myc
31	91.5	7.5	993	2 A61905	outer membrane sec
32	1634	7.5	1634	2 B64410	DNA-directed DNA p
33	88	7.2	419	1 C53312	thymidine phosphor
34	543	7.2	543	2 A53310	phoromone cad1 bin
35	88	7.2	788	2 A71076	hypothetical prote
36	87.5	7.2	1946	2 A61449	hypothetical prote
37	87	7.1	914	2 TC8081	probable myrosinas
38	87	7.1	988	2 TC8102	myrosinase-binding
39	86.5	7.1	722	2 E71403	hypothetical prote
40	86.5	7.1	1449	2 T30857	glucosyltransferas
41	86	7.1	1388	2 T38720	chromodomain helic
42	85.5	7.0	638	2 AH0340	putative autotransp
43	85.5	7.0	1449	2 T30552	glucosyltransferas
44	85	7.0	1090	2 AG1749	glycosidase homolo
45	84.5	6.9	443	2 S23771	outer membrane por
46	84	6.9	232	2 F89807	exotoxin 13 [impor
47	83.5	6.9	282	2 A41025	aspartilopepsin I
48	83.5	6.9	292	2 B89807	exotoxin 9 [impor
49	83	6.8	226	2 G89806	exotoxin 6 [impor
50	83	6.8	444	2 H83624	probable porin PA0
51	83	6.8	2893	2 A64556	toxin-like outer m
52	82.5	6.8	328	2 F64187	p-aminobenzoate sy
53	82.5	6.8	455	2 S39663	aminopeptidase hom
54	82.5	6.8	600	1 D65000	NADH dehydrogenas
55	82.5	6.8	600	2 B91025	NADH dehydrogenase
56	82.5	6.8	600	2 C85869	NADH dehydrogenase
57	82	6.7	123	2 E84752	hypothetical prote
58	82	6.7	466	2 S36209	dep protein precur
59	82	6.7	631	2 S70908	transferrin-bindin
60	82	6.7	644	2 T33730	hypothetical prote
61	82	6.7	745	2 D82568	conserved hypothet
62	82	6.7	843	2 H72204	pullulanase - Ther
63	82	6.7	888	2 C90595	hypothetical prote
64	81.5	6.7	227	2 C89808	exotoxin 15 [impor
65	81.5	6.7	374	2 AH1903	hypothetical prote
66	81.5	6.7	1269	2 A90267	proteinase related
67	81.5	6.7	2288	2 T29939	hypothetical prote
68	81	6.7	411	2 AI1161	flagellar hook pro
69	81	6.7	411	2 AI1520	flagellar hook pro
70	81	6.7	611	2 T15410	hypothetical prote
71	81	6.7	992	2 T28421	probable DNA-direc
72	81	6.7	2167	2 A71489	cell wall-associat
73	80.5	6.6	1395	2 S25937	gene atpA intron 1
74	80.5	6.6	1704	2 A55426	gingipain R (EC 3 .
75	80.5	6.6	1883	2 C82875	hypothetical prote
76	80	6.6	345	2 A64370	adenylosuccinate s
77	80	6.6	411	2 B69006	phosphoglycerate k
78	80	6.6	501	2 C86460	probable cytochrom
79	80	6.6	1151	2 A45226	integrin alpha-1 c
80	80	6.6	2044	2 AB1180	probable peptidogl
81	80	6.6	2902	2 C71953	toxin-like outer m
82	79.5	6.5	445	2 E86440	probable chloropla
83	79.5	6.5	637	2 S36523	El protein - human
84	79.5	6.5	692	2 B64381	hypothetical prote
85	79	6.5	453	2 D71084	probable phospho-s
86	79	6.5	478	2 F90497	hypothetical prote
87	79	6.5	490	2 D82668	dihydrolipoamide d
88	79	6.5	551	2 C72865	chitinase - Autogr
89	79	6.5	1025	2 S69790	fibronectin-bindin
90	79	6.5	1518	2 A44811	glucosyltransferas
91	79	6.5	3890	2 C89921	hypothetical prote
92	78.5	6.4	232	2 S89807	exotoxin 12 [impor
93	78.5	6.4	396	2 S56954	protein YBR162C ho
94	78.5	6.4	413	2 S59650	hypothetical prote
95	78.5	6.4	468	2 T25475	hypothetical prote
96	78.5	6.4	475	2 C86863	N-acetyluramoyl-L
97	78.5	6.4	762	2 A34355	cell surface prote
98	78.5	6.4	1959	2 AG1085	hypothetical prote
99	78	6.4	359	2 G82197	RstA1/RstA2 protei
100	78	6.4	376	1 JQ0474	alcohol dehydrogen

ALIGNMENTS

RESULT 1

enterotoxin B precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28179
 R:Couch, J.B.; Soltis, M.T.; Betley, M.J.
 J. Bacteriol. 170, 2954-2960, 1988
 A:Title: Cloning and nucleotide sequence of the type B staphylococcal enterotoxin gene.
 A:Reference number: A28179; MUID:88257005; PMID:3384800
 A:Accession: A28179
 A:Molecule type: DNA
 A:Residues: 1-257 <COU>
 A:Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002
 C:Superfamily: enterotoxin B

Query Match 90.9%; Score 1107; DB 2; Length 257;
 Best Local Similarity 89.7%; Pred. No. 9.7e-88;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 84
 QY 61 HPWNLDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNELT 120
 DB 85 HPWNLDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNELT 144
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTINSENHIDLYLTT 257

RESULT 2

enterotoxin A precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28664; A29566
 R:Berlev, M.J.; Mekalanos, J.J.
 J. Bacteriol. 170, 34-41, 1988
 A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
 A:Reference number: A28664; MUID:88086892; PMID:3335483
 A:Accession: A28664
 A:Molecule type: DNA
 A:Residues: 1-257 <BET>
 A:Cross-references: GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
 A:Experimental source: strain FR1337
 R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
 J. Biol. Chem. 262, 7006-7013, 1987
 A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
 A:Reference number: A29566; MUID:87222293; PMID:3584106
 A:Accession: A29566
 A:Molecule type: protein
 A:Residues: 25-241, 'S', 243-257 <HUA>
 A:Gene: entA
 C:Genetics:
 A:Map position: 6
 C:Superfamily: enterotoxin B

Query Match 77.8%; Score 948; DB 2; Length 257;
 Best Local Similarity 76.4%; Pred. No. 4.6e-74;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 84

DB 25 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 84
 QY 61 HPWNLDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNELT 120
 DB 85 HSWYNDLLVDFDSKDIDVKYGGKVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNELT 144
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTINSENHIDLYLTT 257

RESULT 3

C89984
 enterotoxin p [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701743; PIDN:BA843036.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B

Query Match 75.4%; Score 918; DB 2; Length 260;
 Best Local Similarity 73.0%; Pred. No. 1.8e-71;
 Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELDGALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 87
 QY 61 HPWNLDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNELT 120
 DB 88 HQWYNDLLVLDGSKDTANIYKGGKVDLYGVYGYCTGGTFFKTCACMYGGVTLHDNNELT 147
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 148 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 207
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 208 RGLIEFHSSGSDVGYDLFGAGQGYPTQLRIYRDNTIKSKNMHIDLYLTT 260

RESULT 4

A33953
 enterotoxin D precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
 C:Accession: A33953
 R:Bayles, K.W.; Iandolo, J.J.
 J. Bacteriol. 171, 4799-4806, 1989
 A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
 A:Reference number: A33953; MUID:89359112; PMID:2549000
 A:Accession: A33953
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <ZAB>
 A:Cross-references: GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758691

C:Superfamily: enterotoxin B

Query Match 50.2%; Score 611; DB 2; Length 258;
Best Local Similarity 51.1%; Pred. No. 4.5e-45;
Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;
QY 1 SEKSEINERKDLRKLSELOGTALGNLQKIYYNSKAITSSSEKSDAQFLNTLLFKGFTTG 60
DB 26 NENIDSVKEHLKSKSELSTALNNMKHSYADKNPIIGENKSTGQFLNTLLYKFFTD 85
QY 61 HPWYNLLVLDLSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLT 120
DB 86 LINFEDLLINFNSKENAQHFKNVDVPIRISINCYGGEIDRTACTYGGVTPHSGNKLK 145
QY 121 EKKVZPINIWDKQQTVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
DB 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQ 205
QY 181 RGLIVPHSSEGSVSYDLFDAGQVPTLLRIYRDNNTTSSLSLSLYLY 231
DB 206 RKIEFDSSDGGKSVYDLFDVKGDFPEKQLRIYSONKTLSTELHLDIYLY 256

RESULT 5

H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayaashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701618; PIDN:BA842911.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 34.5%; Score 420.5; DB 2; Length 258;
Best Local Similarity 38.0%; Pred. No. 1.1e-28;
Matches 87; Conservative 50; Mismatches 85; Indels 7; Gaps 4;
QY 6 EINEKDLRKLSELOGTALGNLQKIYYNSKAITSSSEK-SADQFLNTLLFKGFTTGHPWY 64
DB 32 EVDKDLKSKLSDSSKLFNLTSYTDITWQDDESKISTDQLLNTLLKIDISVLKT 91
QY 65 NDLVLDLSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLTEBKK 124
DB 92 SSKLVFEFNSDLANQPKGNHIDYGLYFGNKGVLTEKTSGLYGVTHDGNQDDEBK 151
QY 125 VPINLWDKQQTVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVORGLI 184
DB 152 IGYNFKDGVQEGFV--IKTKAKVTVOELTKVRFKLENLYKLYNKDT--GNLQKCI 207
QY 185 VFHS--SEGTSVSYDLFDAGQVPTLLRIYRDNNTTSSLSLSLYLY 231
DB 208 FFHSHNHQSQSFYDLYNKGSGVGAFFQFYSDNRTVSSSNVHIDVFLY 256

RESULT 6

H89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701623; PIDN:BA842916.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

Query Match 30.6%; Score 372.5; DB 2; Length 260;
Best Local Similarity 38.8%; Pred. No. 1.5e-24;
Matches 93; Conservative 32; Mismatches 92; Indels 23; Gaps 7;
QY 8 NEKD-----LRKSELOGTALGNLQKIYYNS-KAITSSSEKSDAQFLNTLLFKGFTTG 61
DB 29 NEEDPKTESLCKSSVDPIALHNINDYINNRFTEKIVTSIVSTTEKFLDFLLFKSI---- 84
QY 62 PW-----YNDLLVLDLSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLLH 114
DB 85 NWLDGISAEFKDLKVEFSSSAISKEFLGKTVDIYGYVYKAHCHGEHQVDRTACTYGGVTPH 144
QY 115 DNNELTEKKVPIINLWDKQQTVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDS 174
DB 145 ENNKLSBPKNIGVAVYKDNVNVNTFI--VTTDKKVTQAELDIKVRKLNNAVLY--DR 200
QY 175 FGGKVQGLIVFHSSEGSSTVS--YDLFDAGQVPTLLRIYRDNNTTSSLSLSLYLYT 232
DB 201 MTSVDQVGYIKFHSSEHSEKSFYDLYFGNLPDQVLYNKNKTIIDSSDYHIDVLYLT 260

RESULT 7

H89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89991
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701803; PIDN:BA843096.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sel
C:Superfamily: enterotoxin B

Query Match 25.5%; Score 311; DB 2; Length 240;
Best Local Similarity 33.3%; Pred. No. 2.6e-19;
Matches 74; Conservative 36; Mismatches 78; Indels 34; Gaps 6;
QY 24 GNLKQIY----YNNKAITSSSEKSDAQFLNTLLFKGFTTGHPWYN--LLVDLGGSTAATS 78
DB 31 GNLRNFYTKVEYNLKNVKNPSHRLB-----YSYKNDLYAEFDNEYITS 79
QY 79 EYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLTEKKVPIINLWDKQTTV 138
DB 80 DLKGNVDVFGISYKY----GSNSRT--IYGGVTKAENKLDSPRIIPINLIINGKHTV 133
QY 139 PIDKVTSSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKQVORGLIVF 186
DB 134 TTKSVDTKQWVTAQAEIDVLRKYLQDEFNIYGHNDTGKGEYGTSSKFSYSGFDKGSVVF 193

QY 187 HSEGGSTVSDLDFAQQGYPTLLRIYRDNNTTSSLSLSL 228
 Db 194 HMDGNSFSYDLFTYGTGLPESPLKIYKDNKTVDSQFHLDV 235

RESULT 8
 extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (strain N3)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <KUR>
 A:Cross-references: GB:BA000018; PID:gl3701621; PIDN:BAE42914.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sei
 C:Superfamily: enterotoxin B

Query Match 24.3%; Score 296.5; DB 2; Length 242;
 Best Local Similarity 32.4%; Pred. No. 4.7e-17;
 Matches 77; Conservative 39; Mismatches 85; Indels 37; Gaps 10;

QY 8 NEKLRKSELOQ-TALGNLKOIY----YNSKAITSEKSADQFLNTLLFKGFTGHP 62
 Db 17 NIKL---TYAQGDIGVGNLRFYTKHDYIDLKGVTDKLP----IANQLEFS---IG-- 64

QY 63 WYNLLVDLGTAASTSEYSGSDVLYGAYYQACGTPNKTACMGVTLHDNNRLTEE 122
 Db 65 -TNDLISESNWDEISFKGKKLDFIDYNGPC-----KSKYMGATL-SQVYLSA 116

QY 123 KKVPIINWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFG-GK--- 178
 Db 117 RKIPINLVNGKHTISTDKIATNKKLVTAQEIIDVKLRVLOEYNIYCHNVTGKKEYG 176

QY 179 -----VQRLVHSSSEGSTVSDLDFAQQGYPTLLRIYRDNNTTSSLSLSL 228
 Db 177 YKSKFYSGFNNGKVLFLHNLNKSFSYDLFTYGTGLPESPLKIYKDNKTVDSQFHLDV 234

RESULT 9
 S11885
 enterotoxin C3 - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S11885
 R:Howder, C.J.; Hackett, S.P.; Bohach, G.A.
 Mol. Gen. Genet. 220, 329-333, 1990
 A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison of the C3 gene of Staphylococcus aureus and Staphylococcus epidermidis.
 A:Reference number: S11885; MUID:90220508; PMID:2325627
 A:Accession: S11885
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <HOV>
 A:Cross-references: GB:X51661; NID:G46570; PIDN:CA335972.1; PID:G46571
 C:Superfamily: enterotoxin B

Query Match 23.4%; Score 284.5; DB 2; Length 266;
 Best Local Similarity 32.5%; Pred. No. 5.7e-17;
 Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;

QY 11 DLKKSSELOQTALGNLKOIYNNKAITSSP-KSADQFLNTLLFKGFTGHPYNDLLV 69
 Db 37 DLKKSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDRFLAHLDIYNSDKKLKNYDKVKT 93

QY 70 DLGTAATSEYSGSDVLYGAYYQAC-----AGGTENKTACMGVTLHDNNRLTEE 122
 Db 94 ELLNEDLAKYKDEVDVYGSNNYVYVYFSSKDNVKGVTGKTCYGGITKHEGHNFDNG 153

QY 123 --KKVPIINWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVKVQ 180
 Db 154 NLQNLVVRVY-ENKRNITISFE-VQTDKKSVTQAELDIKARNFLINKNLKLYEFNS--SPYE 209

QY 181 RGLIVHSSSEGSTVSDLDFAQQGYPTLLRIYRDNNTTSSLSLSLSLYT 232
 Db 210 TGYIKFIENNGTFTWDMPPAGPKFDQSKYLMNNDKNTVDSKSVKIEVHLTT 263

RESULT 10
 D89969
 enterotoxin SEM [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: D89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: D89969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-239 <KUR>
 A:Cross-references: GB:BA000018; PID:gl3701622; PIDN:BAE42915.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sem
 C:Superfamily: enterotoxin B

Query Match 23.2%; Score 282; DB 2; Length 239;
 Best Local Similarity 29.7%; Pred. No. 8.2e-17;
 Matches 68; Conservative 40; Mismatches 77; Indels 44; Gaps 6;

QY 23 LGNLKQIYVYNSKAIT--SSEKSADQFLNTLLFKGFTGHPWYNDLLVJGSTAATSE- 79
 Db 24 VGVNLNRYGSIPTEDHQISINPENNLHSHQVLF-----SMDNSTVTAAEF 68

QY 80 -----YEGSSVDLYGAYYQACGTPNKTACMGVTLHDNNRLTEEKYPINLWI 131
 Db 69 KNVDDVKFKHADVGVLSYSGYCL-----KNKYIYGGVTL-AGDYLEKRRIPINLWV 122

QY 132 DGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLY-----NSDSFGGKV 179
 Db 123 NGEHOTISTDKVSTNKKLVTAQEIIDVKLRVLOEYNIYGFNDTNKGRNKGSKFSGGF 182

QY 180 QRLIVHSSSEGSTVSDLDFAQQGYPTLLRIYRDNNTTSSLSLSL 228
 Db 183 NAGKILFHLNDGSPSYDLFTGTQQAESFLKIYNDKNTVETEKFLDV 231

RESULT 11
 A60114
 enterotoxin C-2 precursor - Staphylococcus aureus
 N:Alternate names: enterotoxin C-3 precursor
 C:Species: Staphylococcus aureus
 C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
 C:Accession: A60114; A33866
 R:Bohach, G.A.; Schlievert, P.W.
 Infect. Immun. 57, 2249-2252, 1989
 A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
 A:Reference number: A60114; MUID:89277549; PMID:2543637
 A:Accession: A60114
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-266 <BOH>
 A:Accession: B60114

A:Title: Nucleotide sequence of the enterotoxin B gene from *Staphylococcus aureus*.
 A:Reference number: S27360; MUID:86168029; PMID:3957869
 A:Accession: S27360
 A:Molecule type: DNA
 A:Residues: 1-266 <JON>
 A:Cross-references: EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g153000
 A:Experimental source: strain S6
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3518-3525, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
 A:Reference number: A92065; MUID:71007902; PMID:5470821
 A:Accession: A92065
 A:Molecule type: protein
 A:Residues: 28-55, 'NND', '59-68', 'NE', '71', 'FDLIYL', '78-117, 119-127', 'N', '129', 'D', '131-132', 'ENT',
 A:Experimental source: strain S-6
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3511-3517, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
 A:Reference number: A92064; MUID:71007901; PMID:5470820
 A:Contents: annotation; chymotryptic peptides
 R:Huang, I.Y.; Bergdoll, M.S.
 J. Biol. Chem. 245, 3493-3510, 1970
 A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
 A:Reference number: A92063; MUID:71007900; PMID:5470819
 A:Contents: annotation; tryptic peptides
 R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S.
 Biochemistry 4, 1011-1016, 1965
 A:Title: Purification of staphylococcal enterotoxin B.
 A:Reference number: A90548; MUID:66035792; PMID:4953912
 A:Contents: annotation; biological source of protein
 R:Atakhov, V.F.; Kilinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni
 Eur. J. Biochem. 209, 823-828, 1992
 A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B
 A:Reference number: S27240; MUID:93049338; PMID:1425690
 A:Accession: S27240
 A:Molecule type: protein
 A:Residues: 28-42, 128-148 <ALA>
 C:Superfamily: enterotoxin B
 C:Keywords: enterotoxin; extracellular protein; toxin
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-266/Product: enterotoxin B #status experimental <MAT>
 F:120-140/Disulfide bonds: #status experimental

Query Match 22.0%; Score 268.5; DB 1; Length 266;
 Best Local Similarity 31.6%; Pred. No. 1.4e-15;
 Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTG 60
 Db 27 AESQDPKPELHKSKFTG-LNENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDK 84
 Qy 61 HPVNDLLVLDGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKACMYGG 110
 Db 85 LGNYDNRVRFKQNLADKYDKYDVFVGANYTYQCYFSKKTNDINSHQTDKRTKTCMYGG 144
 Qy 111 VTLDNNRLTEEEKVPINLWDGKQTTPIDVKTSKEVTVQELDLQARHYLHGKFLY 170
 Db 145 VTEHNGQLDKYSITVRVFDGK-NLLSPD-VQTNKKSVTAQELDIKARNFINKNL 202
 Qy 171 NSDSFGGKVGQGLVPHSSSEGSTVSYDLFDAQGYPD--TLRIYRDNTTISSTLSISL 228
 Db 203 EFNN--SPYETGYIKFTIENENS-FWIDMMPAPGDKFDQSKYLMYNDNKWDSKDKIEV 259
 Qy 229 YLYT 232
 Db 260 YLTT 263

RESULT 14

ENSAC1

enterotoxin C-1 precursor - *Staphylococcus aureus*C:Species: *Staphylococcus aureus*

C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

C:Accession: S06356; A01816
 R:Bohach, G.A.; Schlievert, P.M.
 Mol. Gen. Genet. 209, 15-20, 1987
 A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to
 A:Reference number: S06356; MUID:88038352; PMID:2823067
 A:Accession: S06356
 A:Molecule type: DNA
 A:Residues: 1-266 <BOH>
 A:Cross-references: EMBL:X05915; NID:946586; PIDN:CAA29260.1; PID:946567
 R:Schmidt, J.J.; Spero, L.
 J. Biol. Chem. 259, 6300-6306, 1983
 A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
 A:Reference number: A01816; MUID:83213327; PMID:6189824
 A:Accession: A01816
 A:Molecule type: protein
 A:Residues: 28-75, 'IL', '78-176', 'N', '178-266 <SCH>
 C:Genetics:
 C:Gene: entC1
 C:Superfamily: enterotoxin B
 C:Keywords: enterotoxin
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
 F:120-137/Disulfide bonds: #status experimental

Query Match 21.6%; Score 263.5; DB 1; Length 266;
 Best Local Similarity 30.6%; Pred. No. 3.7e-15;
 Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;

Qy 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFF 58
 Db 27 AESQDPKPELHKSKFTG-LNENMKVLYDDHVS---ATKVKSVDFLAHDLIYINISD 82
 Qy 59 TCHPWNDLLVLDGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKACMYGGV 111
 Db 83 KKLKNYDKVKTLLNEGLAKKYKDEVVDVYGSVYVNCYFSSKDNVGVKVTGKTCMYGGI 142
 Qy 112 TLHDNNRLTEB--KKVPINLWDGKQTTPIDVKTSKEVTVQELDLQARHYLHGKFL 169
 Db 143 TKHEGNHFDNGNLQNLVIRVY-ENKRTISPE-VQTDKKSVTQAEIDIKARNFINKNL 200
 Qy 170 NSDSFGGKVGQGLVPHSSSEGSTVSYDLFDAQGYPD--TLRIYRDNTTISSTLSIS 227
 Db 201 YEFNS--SPYETGYIKFTIENNGTFWIDMMPAPGDKFDQSKYLMYNDNKTVDSKSVKIE 258
 Qy 228 YLYT 232
 Db 259 YLTT 263

RESULT 15

S18783

exotoxin type A precursor (allele 3) - *Streptococcus pyogenes* phage (strain MGAS158 isolate
 N:Alternate names: scarlet fever toxin
 C:Species: *Streptococcus pyogenes* phage
 A:Variety: strain MGAS158 isolate Nebraska
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
 A:Accession: S18783; S18793; S18801; S18798
 R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded
 A:Reference number: S18782; MUID:92044323; PMID:1940804
 A:Accession: S18783
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEL>
 A:Cross-references: EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290
 A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A:Accession: S18793
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-236 <NEA>
 A:Cross-references: EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID:947314

A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A:Experimental source: strain MGAS624 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795

Query Match 20.6%; Score 251.5; DB 2; Length 236;
Best Local Similarity 31.7%; Pred. No. 3.4e-14;
Matches 72; Conservative 42; Mismatches 102; Indels 11; Gaps 7;
4 SEEINEKLRKSELOQTAL-GNLKQIY--YNSKAITSEKSDAQFLTNTLLFKGFFTG 60
17 SQEVAQPPDPFSQLHSSLVKLNQIYFLYEGDPVTHENVKSVQDLSHDLIYN---VS 73
61 HPWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
74 GNYDKLKTTELKNEMGTFLKKNVDIYGVVEYHYHLCYLCENAKRACIYGGVTHNEGNHL 133
120 TEEKKVPINLWDGKQTTPIDVKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 179
134 EIPKLIIVKVSIDGIQ-SLSFD-IEINKQVTAQSLDYKVRKHLTDNKKQIYNGP--SKY 189
180 QRLIVFHSSEGSTVSYDLFD-DAQGXPDPTLLRIYRDNNTTISSTLSI 226
190 ETGYIKFIPKNESEFWDFPPEFTQSKY----LMYKDNETLDSNTSQI 236

RESULT 17
S18786
N:Altoxin type A precursor (allele 2) - Streptococcus pyogenes phage (strain MGAS250 isolate)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes phage
A:Variety: strain MGAS250 isolate California; strain MGAS251 isolate California; strain N isolate United Kingdom; strain MGAS496 isolate Germany
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18786; S18787; S18788; S18790; S18792; S18795; S18799
R:Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded by the nucleotide sequence of the scarlet fever toxin
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18786
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795

A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316
A:Experimental source: strain MGAS491 isolate United Kingdom unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18801
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61572; NID:g47333; PIDN:CAA43770.1; PID:g47334
A:Experimental source: strain MGAS624 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18798
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A:Experimental source: strain MGAS495 isolate Germany unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18799
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61561; NID:g47297; PIDN:CAA43759.1; PID:g47298
A:Experimental source: strain MGAS250 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18787
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61562; NID:g47299; PIDN:CAA43760.1; PID:g47300
A:Experimental source: strain MGAS251 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18788
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61563; NID:g47301; PIDN:CAA43761.1; PID:g47302
A:Experimental source: strain MGAS256 isolate California unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18790
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61564; NID:g47305; PIDN:CAA43762.1; PID:g47306
A:Experimental source: strain MGAS285 isolate Colorado unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18792
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEO>
A:Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID:g47312
A:Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795

Query Match 20.8%; Score 253.5; DB 2; Length 236;
Best Local Similarity 31.6%; Pred. No. 2.3e-14;
Matches 73; Conservative 45; Mismatches 94; Indels 19; Gaps 10;
4 SBEINEKLRKSELOQTAL-GNLKQIY--YNSKAIT--SSEKSDAQFLTNTLLFKGFFTG 60
17 SQEVAQPPDPFSQLHSSLVKLNQIYFLYEGDPVTHENVKSVQDLSHDLIYN---VS 73
61 HPWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
74 GNYDKLKTTELKNQEMATFLKKNVDIYGVVEYHYHLCYLCENAKRACIYGGVTHNEGNHL 133
120 TEEKKVPINLWDGKQTTPIDVKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 179
134 EIPKLIIVKVSIDGIQ-SLSFD-IEINKQVTAQSLDYKVRKHLTDNKKQIYNGP--SKY 189
180 QRLIVFHSSEGSTVSYDLFD----AQGYPTLLRIYRDNNTTISSTLSI 226
190 ETGYIKFIPKNESEFWDFPPEFTQSKY----LMYKDNETLDSNTSQI 236

RESULT 16
S18789
N:Altoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California)
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
C:Accession: S18789
R:Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encoded by the nucleotide sequence of the scarlet fever toxin
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEZ>
A:Cross-references: EMBL:X61573; NID:g47303; PIDN:CAA43771.1; PID:g47304
A:Experimental source: strain MGAS485 isolate Yugoslavia unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18795

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: EMBL:X61566; NID:947317; PIDN:CAA43764.1; PID:947318
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: EMBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA2
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 20.4%; Score 248.5; DB 2; Length 236;
Best Local Similarity 31.6%; Pred. No. 6.1e-14;
Matches 73; Conservative 44; Mismatches 95; Indels 19; Gaps 10;

QY 4 SEETNEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAOFLTNTLLPKGFFTG 60
DB 17 SQEFAQDPDPQSLHSSLVKNLQNIYFLYEGDPVTHENVKSDVQLSHDLIYN---VS 73

QY 61 HPWYNDLLVDLGPSTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMGYGVTLHNNRL 119
DB 74 GPNYDKLTKELKNQEMATLFPKDNVDIYSEVYHLCVLCENAESACIYGVTHHEGNHL 133

QY 120 TEKKVPINLWDGKQTVPIDKVKTSKKEVTQVQELDLQARHYLHGKGLYNSDSFGGKV 179
DB 134 EIPKKIVKVSIDIGQ-SLSFD-IETNKKMVTQVQELDYKVRKYLTDNKKQYITNGP--SKY 189

QY 180 QRGLIVFHSSEGSTVSVDLFD---AQGVPTDILLRIYRDNNTTISLSLSI 226
DB 190 ETGYIKIPKNKESFWDFPEPEFTQSKY----LMIYKDNELDSNTSQI 236

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N3)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: GB:BA000018; PID:g13701617; PIDN:BA42910.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: seg
C;Superfamily: enterotoxin B

Query Match 19.8%; Score 241; DB 2; Length 258;
Best Local Similarity 28.8%; Pred. No. 3e-13;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINKEKDLRKSELOGTALGNLQIYY---YNSKAITSSKSAOFLTNTLLPKGFFT 59
DB 30 KLDELNKVSDYKNN--KGT-MGNVMNLYTSPVVEGRGVINSR---QFUSHDLIFP--I 79

QY 60 GHPWYNDLLVDLGPSTAATSEYEGSSVDLYGAYGYQCA-----GGTPNKTCAM 107

Db 80 EYKSYNEVKTELENTELANNYKDKKVDIFGVFPYFTCIIPKSEPDINQFEG-----CCM 134

QY 108 YGGVTLH--DNNRLTEKKVPINLWDGKQTVPIDKVKTSKKEVTQVQELDLQARHYLHG 165
Db 135 YGGLTFNSSENER--DKLITVQVTDNRQSLG--FTITTKNNMTIQELDYKARHWTLK 189

QY 166 KFLYNSDSFGGKVQRGLIVFHSSEGSTVSVDLFDAGQGVPTD---LLRIYRDNNTTISST 222
Db 190 EKKLYEFD--GSFESGYIKETERNKNTSFWDLPKXKELVPFPYKFLNIYGDKNKVVDSK 247

QY 223 SLISLSLYLT 232
Db 248 SIKMEVFLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N;Alternate names: scarlet fever toxin; SPE type A (spear)
C;Species: Streptococcus sp.
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A26152
R;Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A;Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staf
A;Reference number: A26152; MUID:86284313; PMID:3526093
A;Accession: A26152
A;Molecule type: DNA
A;Residues: 1-250 <JOH>
C;Superfamily: enterotoxin B
C;Keywords: exotoxin

Query Match 18.1%; Score 220; DB 1; Length 250;
Best Local Similarity 28.9%; Pred. No. 1.9e-11;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;

QY 14 KXSELOGTALGNLQIYY-YNSKAITSE--KSADQFLTNTLLPKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRNLVKTFKIYIFFMVRLTVTHENVKSDVQLSHDLIYN---VSGPNYDKLKE 91

QY 71 LGSTATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMGYGVTLHNNRLTEKKVPINL 129
Db 92 LKNQEMATLFPKDNVDIYSEVYHLCVLCENAESACIYGVTHHEGNHLEIPKIVKV 151

QY 130 WIDGKQT-TVPIDKVKTSKKEVTQVQELDLQARHYLHGKGLYNSDSFGGKVQRGLIVFHS 188
Db 152 SIDGQSLSFDEIQIKNG---NCSRIYTVRKYLTDNKKQYITNGP--SKYETGVKIFIP 205

QY 189 SEGSTVSVDLFD---AQGVPTDILLRIYRDNNTTISLSLSIYLT 232
Db 206 KNKESFWDFPEPEFTQSKY----LMIYKDNELDSNTSQIEVLYLT 249

RESULT 20
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: GB:BA000018; PID:g13701619; PIDN:BA42912.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: yent2

Query Match 15.6%; Score 190; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 3.2e-09;
Matches 46; Conservative 25; Mismatches 54; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHDNNRTEKKV--PINLMT---DGRQTTVPIDKVKTSKEVTQVQLD 157
DB 2 KKTQWYGGVTEHDGNQIDKNNSTONSHNLIKVENERNLSFD-IPTNKNITQAQIDY 60

QY 158 QARYLHCKFGLYNSDSEGGKQVQGLIVFHSSEGSTVSYDLFDAQGQ--YPTLLRIYRD 215
DB 61 KVRNYLLKHNLYBFS--SPYETGYIKFIEGSHSFYDLMPSGKKFYPTKYLIIYND 118

QY 216 NTTISSTLSISLYL 230
DB 119 NKTVESKSNVEVHL 133

RESULT 21
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: A89942
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701400; PIDN:BA842694.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1430

Query Match 14.6%; Score 178; DB 2; Length 157;
Best Local Similarity 31.4%; Pred. No. 4.2e-08;
Matches 37; Conservative 21; Mismatches 59; Indels 2; Gaps 1;

QY 1 SEKSEINEKLRKSELGQTALGNLKOIYYNSKAITSSSEKSADQFLTWLLPKGFTG 60
DB 42 TNSAIEYSDLHKKSFDSKRLSNKQSFNPTQ--LENKNTNDRLLKHDLPHDMFVN 99

QY 61 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYYVOCAGGTENKTCACMYGGVTLHDNNR 118
DB 100 VASKDFKXVERNEALSKKFINKNIDIVAGSYSECHGATNKTCQSYGGVTLSDNNK 157

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-2000
C/Accession: A30509
R;Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: GB:M39514; NID:g153820; PIDN:AAA27017.1; PID:g153821
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 12.8%; Score 155.5; DB 2; Length 235;
Best Local Similarity 24.2%; Pred. No. 6.1e-06;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLTNTLLFKGFTGH-----PW-YNDLLVLDLSTAA-----TSE 79
DB 11 FIITVILISTYTYHQSDSKDISNVKSDLLYAYITPYDYKDCRVNFTTHLIDTQK 70

QY 80 YEGSS-----VDLYGAYYVOCAGGTENKTCACMYGGVTLHDNNRL 119
DB 71 YRGKDYIISSESYEASQKFRDDHVDVFGFLYILNSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDLCARHLHGKFGLYNSDS--FGG 177
DB 126 NH--KULGNLFISGSCQNNLNKILKIDVITFQIDFKIRKYLMDNKKIYDATSPYVSG 183

QY 178 KVQRGLIVFHSSEGSTVSYDLFDA--QGOYPTLLRIYRDNTTISSTLSLS--LSYL 230
DB 184 RTEIG-----TKDGKHEQIDLFDSNEGTRSDIFAK-YKDNRIINMKNFHSDIYL 233

RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: H89941
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701399; PIDN:BA842693.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1429

Query Match 9.4%; Score 115; DB 2; Length 62;
Best Local Similarity 32.1%; Pred. No. 0.0033;
Matches 18; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 176 GKKVQSGGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYL 231
DB 5 GGDIVKGVKYNHDDQCNVEYDFYNLNGEYGEVLEKMYADNKTINRDLHLDIYLF 60

RESULT 24
XCSAS1
toxic shock syndrome toxin-1 precursor - Staphylococcus aureus
N/Alternate names: TSST-1
C:Species: Staphylococcus aureus
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C/Accession: A24606; B24606
R;Blomster-Hautamaa, D.A.; Kreiswirth, B.N.; Kornblum, J.S.; Novick, R.P.; Schlievert, P.
J. Biol. Chem. 261, 15783-15786, 1986
A:Title: The nucleotide and partial amino acid sequence of toxic shock syndrome toxin-1.
A:Reference number: A24606; MUID:87057222; PMID:3782090
A:Accession: A24606
A:Molecule type: DNA
A:Residues: 1-234 <BIO>
A:Cross-references: GB:J02615; NID:g153122; PIDN:AAA26682.1; PID:g153123
A:Accession: B24606
A:Molecule type: protein
A:Residues: 41-106; 199-224 <BIO2>
A:Note: the authors translated the codon ACT for residue 20 as Ile and GGG for residue 15
C:Superfamily: toxic shock syndrome toxin
C:Keywords: toxic shock syndrome; toxin
F;1-40/Domain: signal sequence #status predicted <SIG>
F;41-234/Product: toxin shock syndrome toxin-1 #status experimental <MAT>

Query Match 8.2%; Score 100; DB 1; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.36;

C:Species: Bombyx mori nuclear polyhedrosis virus, BmsNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: EMBL:U33180; NID:G3745835; PIDN:AAC63792.1; PID:G3745945
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase

Query Match 7.9%; Score 96; DB 2; Length 552;
Best Local Similarity 24.9%; Pred. No. 2.5;
Matches 46; Conservative 23; Mismatches 69; Indels 48; Gaps 11;

QY 32 YNSKAITS---SEKSADQFLNTLLFKGFFTHGHPWYNDLLVDLSTAAATSEYSGSVLDLY 88
DB 359 YDKIAVNVYAEAKSLDKIFLMTYDFK-----ANSN---TDLGYQTVTVYAPSNSELY 410
QY 89 GAYYGQC---AGGTPNKT---ACWYG---GVTLHDN-NRLTEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGQVDPNKIIIVGVAMYGRTGVTNTNGYFSGTGNGVPVSGTWEDG--- 467
QY 137 TVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQVQGLVLFVHSSGSTVSY 196
DB 468 -----VVDYROIQDLNNY-----VYTFDS-----AAQASYVFDKSGDLISF 505
QY 197 DLFDA 201
DB 506 DSVDS 510

RESULT 29
D89807
exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700317; PIDN:BA41615.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: set11

Query Match 7.7%; Score 94; DB 2; Length 231;
Best Local Similarity 23.6%; Pred. No. 1.2;
Matches 43; Conservative 27; Mismatches 84; Indels 28; Gaps 6;

QY 2 EKSEINEKDLRKSELQGTALGNLKIY-YNSKAITSSE---KSADQFLNTLLFKGF 57
DB 32 EKQERVQH-----LYDKDLRYYSSESFFSNISGVKNYNGSVNVRNQE 78
QY 58 FTGHFWYNDLLVDLSTAAATSEYSGSVLDLYGAYYGQAGTGNKTAQVGGVTLHDN 117
DB 79 KQHQLF---LJGKDXYKKGLEQNVVVKELI-----DPNGRLSTVGGVTKKNK 128
QY 118 RLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGG 177
DB 129 SSETNTHLFWNK-VYGGNLDASIDSFLNKEEVSLSKELDKIRKQLVKEKYLGRITKYG 187

C:Species: Bombyx mori nuclear polyhedrosis virus, BmsNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: EMBL:U33180; NID:G3745835; PIDN:AAC63792.1; PID:G3745945
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase

Query Match 7.9%; Score 96; DB 2; Length 552;
Best Local Similarity 24.9%; Pred. No. 2.5;
Matches 46; Conservative 23; Mismatches 69; Indels 48; Gaps 11;

QY 32 YNSKAITS---SEKSADQFLNTLLFKGFFTHGHPWYNDLLVDLSTAAATSEYSGSVLDLY 88
DB 359 YDKIAVNVYAEAKSLDKIFLMTYDFK-----ANSN---TDLGYQTVTVYAPSNSELY 410
QY 89 GAYYGQC---AGGTPNKT---ACWYG---GVTLHDN-NRLTEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGQVDPNKIIIVGVAMYGRTGVTNTNGYFSGTGNGVPVSGTWEDG--- 467
QY 137 TVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQVQGLVLFVHSSGSTVSY 196
DB 468 -----VVDYROIQDLNNY-----VYTFDS-----AAQASYVFDKSGDLISF 505
QY 197 DLFDA 201
DB 506 DSVDS 510

RESULT 29
D89807
exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700317; PIDN:BA41615.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: set11

Query Match 7.7%; Score 94; DB 2; Length 231;
Best Local Similarity 23.6%; Pred. No. 1.2;
Matches 43; Conservative 27; Mismatches 84; Indels 28; Gaps 6;

QY 2 EKSEINEKDLRKSELQGTALGNLKIY-YNSKAITSSE---KSADQFLNTLLFKGF 57
DB 32 EKQERVQH-----LYDKDLRYYSSESFFSNISGVKNYNGSVNVRNQE 78
QY 58 FTGHFWYNDLLVDLSTAAATSEYSGSVLDLYGAYYGQAGTGNKTAQVGGVTLHDN 117
DB 79 KQHQLF---LJGKDXYKKGLEQNVVVKELI-----DPNGRLSTVGGVTKKNK 128
QY 118 RLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGG 177
DB 129 SSETNTHLFWNK-VYGGNLDASIDSFLNKEEVSLSKELDKIRKQLVKEKYLGRITKYG 187

QY 178 KV 179
DB 188 KI 189

RESULT 30
JQ0894
P115 protein - Mycoplasma hyorhinis
C:Species: Mycoplasma hyorhinis
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Feb-2001
C:Accession: JQ0894
R:Notarnicola, S.M.; McIntosh, M.A.; Wise, K.S.
Gene 97, 77-85, 1991
A:Title: A Mycoplasma hyorhinis protein with sequence similarities to nucleotide-binding
A:Reference number: JQ0894; MUID:91138990; PMID:1825306
A:Accession: JQ0894
A:Molecule type: DNA
A:Residues: 1-979 <NOT>
A:Cross-references: GB:M34956
A:Note: the authors translated the codon AAA for residue 956 as Leu
C:Comment: This protein is located in the cytoplasm.
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: chromosome segregation protein SMC1
C:Keywords: nucleotide binding; P-loop
F:32-39/Region: nucleotide-binding motif A (P-loop)

Query Match 7.7%; Score 94; DB 2; Length 979;
Best Local Similarity 23.7%; Pred. No. 7.7;
Matches 56; Conservative 41; Mismatches 91; Indels 48; Gaps 10;

QY 17 ELQGTALGNLKOIYYNSKAITSSEKS-----ADQFLT-NTLLFKGFFTHG 61
DB 56 QLRLG---NMDDVIFAGSKTVKPOKAMVKLTFKNEDATEETEQITISRLKRGQGTNE 112
QY 62 PWNDLIV---DLGSTAATSEYSGSVLDLYGAYYGQAGTGNKTAQV---GGVTLHD 115
DB 113 YFYNDQPVRYKDKNLAVESGISKSLAIIISQTISEIAETPEQRKAVIEEAAGSKYK 172
QY 116 NNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEV---TVQELDLQ---ARHYLHGKFLY 170
DB 173 LDKEEAQKLL-----RTNDAIDKLOKAIKELERQVNSLDKQAKAKIYLEKSKALE 224
QY 171 NSDSFGKVGQGLIV---FHSSEGSTVVDLFDAGQGPDTLLRIYRNTTTSST 222
DB 225 S-----VEVGLIVNDLNFNFKLNLTSLLEVEQQRNDLELNITQVSESSISQT 273

RESULT 31
AE1905
outer membrane secretion protein alr0791 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AE1905
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AE1905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-993 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA672748.1; PID:gl7130136; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0791

Query Match 7.5%; Score 91.5; DB 2; Length 993;
Best Local Similarity 26.0%; Pred. No. 13;
Matches 50; Conservative 21; Mismatches 94; Indels 27; Gaps 8;

```

QY 24 GNLKQIYYNSKAITSEKSA-----DOFLNTLLFKGFTGHPWYNLLDLVGSTAAAT--- 77
DB 420 GNLRDYSAFNHTAAPSITSLPDPYETDNFLFLGNTTSAQASSNLQVQLTNRVR 479

QY 78 ----SEYEGSSVDLYGAYGYQ-CAGGTGPKTACMGVTLHDNNRLTEKKV-PINLAI 131
DB 480 FVNADVNGQANTTFRAWCGSNGVAGGTTGVNAVNGNATAFSSNTLTASITVSPINPPI 539

QY 132 DGKQTTVPIDVKVTSKEVTVQVELDQARHYLHGKFLYNSDS-----FGCKVORGII 184
DB 540 QG---TTGLDKLYGTANEDIIN--GNEGNDYLFGRAGNDTLDGEGNDVYFGG---TGND 591

QY 185 VFHSSEGSTVSY 196
DB 592 TLDGEGSDLLY 603

RESULT 32
E64410
DNA-directed DNA polymerase (EC 2.7.7.7) family B, intein containing precursor - Methanococcus
N;Contains: DNA endonuclease (EC 3.1.1.1) PI-I; DNA endonuclease (EC 3.1.1.1) PI-II; DNA
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: E64410
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Werrick, J.M.; Glodek, A.;
; Olson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64410
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1634 <BUL>
A;Cross-references: GB:U67532; GB:L77117; NID:G1591559; PID:G1591563; TIGR:MJ0885; PID:G
C;Genetics:
A;Map position: REV816304-811400
A;Start codon: TTG
C;Function: <DPL>
A;Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at th
C;Function: <EN1>
A;Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phospho
C;Function: <EN2>
A;Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phosph
C;Superfamily: DNA-directed DNA polymerase KOD
C;Keywords: endonuclease; hydrolase; nucleosidyltransferase; protein splicing
F;1-425/795-882/1359-1634/Product: DNA-directed DNA polymerase family B #status predicted
F;1-425/Domain: DNA-directed DNA polymerase family B extein 1 #status predicted <XT1>
F;426-794/Product: DNA endonuclease PI-I (pol B extein 1) #status predicted <MAM2>
F;795-882/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <XT2>
F;883-1358/Product: DNA endonuclease PI-II (pol B extein 2) #status predicted <MAM3>
F;1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <XT3>
F;425-795/Cross-link: peptide (Arg-Ser) #status predicted
F;882-1359/Cross-link: peptide (Arg-Ser) #status predicted

Query Match 7.5%; Score 91; DB 2; Length 1634;
Best Local Similarity 21.6%; Pred. No. 27;
Matches 50; Conservative 36; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELOGTALGNLKOIYYNSKAITSEKSAADQFLNTLLFKGFTGHPWYNLLVDL 71
DB 614 VRKKGTGKAITLGCAGKADYILKIEIL---KNKERYLPAIL-RGPFEGDGYVTVRRAV 669

QY 72 GSTAATSEY-----GSSVDLYGAYGYQACAGGTGPKTACMGVTLHDNNRLTEKKVP 126
DB 670 VVNGQTNVYDKIFIASLLRLGIKVSF-----YYSVEERGGKLRKV 713

QY 127 INLWIDGKQTTVPIDVKVTS-----KCEVTVQVELDQARHYLHGKFLYNSD----- 173
DB 714 IEIFSKG-----DLIKFISILSF-SRRKNLLNIIROKTLKIGDYGFYDLDDVCVS 766

QY 174 --SFGGKV-----ORGLIVFHSSEGS-TVSYDLFLDAQGGYPPDIL 209
DB 767 LESYKGEVYDLTEGRPPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

RESULT 33
CS3312
thymidine phosphorylase (EC 2.4.2.4) - Mycoplasma pirum (strain BER)
C;Species: Mycoplasma pirum
C;Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 23-Dec-2002
C;Accession: CS3312
R;Tham, T.N.; Ferris, S.; Kovacic, R.; Montagnier, L.; Blanchard, A.
J. Bacteriol. 175, 5281-5285, 1993
A;Title: Identification of Mycoplasma pirum genes involved in the salvage pathways for n
A;Reference number: A53310; MUID:93352438; PMID:8349569
A;Accession: CS3312
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <THA>
A;Cross-references: GB:L133289; NID:G401781; PIDN:AAA25432.1; PID:G401784
C;Genetics:
A;Superfamily: thymidine phosphorylase/pyrimidine-nucleoside phosphorylase
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 7.2%; Score 88; DB 1; Length 419;
Best Local Similarity 27.0%; Pred. No. 8.3;
Matches 38; Conservative 22; Mismatches 57; Indels 24; Gaps 7;

QY 47 FLTNLLFKG-FFTHGHPWYNLLDLVGSTAAATSE-----YEGSSVDLYGAYYG 93
DB 57 FLTKAMDSGKIVYFHFPEYKIKILDKHSTGIGIGKVSIALRPILVSPDLGVAKLSGRGLG 116

QY 94 YQACAGTTPNKTCMGVGTTLHDNNRLTEKKV--PINLWIDGK-QTTVPIDVKVTSKKEV 150
DB 117 F--TGGTIDKLE----SINVNTDIDLNKSKILNIAMNFIQVQNDIVPADKLLYAUDRV 170

QY 151 --TVQELDLQARHYLHGKFGFL 169
DB 171 TGTVDLSPLIAASILSKKFL 191

RESULT 34
A53310
phenomone CAD1 binding protein precursor - Enterococcus faecalis plasmid PAD1
N;Alternate names: TraC
C;Species: Enterococcus faecalis
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C;Accession: A53310
R;Tanimoto, K.; An, F.Y.; Clewell, D.B.
J. Bacteriol. 175, 5260-5264, 1993
A;Title: Characterization of the traC determinant of the Enterococcus faecalis hemolysin-
A;Reference number: A53310; MUID:93352433; PMID:8349566
A;Accession: A53310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <TAN>
A;Cross-references: GB:L19532; NID:G388267; PIDN:AAA72024.1; PID:G388269
C;Genetics:
A;Gene: traC
A;Genome: plasmid
C;Superfamily: dipeptide transport protein

Query Match 7.2%; Score 88; DB 2; Length 543;
Best Local Similarity 21.3%; Pred. No. 12;
Matches 46; Conservative 31; Mismatches 61; Indels 78; Gaps 10;

QY 33 NSKAITSEKSAADQFLNTLLFKGFTGTH-----PWYNDLLVDLGSTAATSEY- 80
DB 146 NAKELIAGKQSKSE-----TLAVKS--NGNTIEIELEKPTPIFDLL-----ALTIAYP 192

QY 81 -EGSSVDLYGAYGYQACAGGTGPKTACMGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139

```

Db 193 VQKAIKEYGKDY-----GTSQKSVITNGAFNLTSLGVGTSK-----W-----TIS 235
Qy 140 IDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGORGLIVPHSSEGSTVSVDLF 199
Db 236 KNKEYWDQKESMEKINFQVKEINTGINDY----- 267
Qy 200 DAQQQYDPT-----LLRIYDNTTISSTLSLSLYL 230
Db 268 --DQLDDTPTVGYAKQYKDKKEFTTLMTANTWYL 301
RESULT 35
A71076
hypothetical protein PH0873 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71076
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-788 <KAW>
A:Cross-references: GB:AP000004; NID:G3236131; PIDN:BAA29967.1; PID:d1030910; PID:G32572
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0873
Query Match 7.2%; Score 88; DB 2; Length 788;
Best Local Similarity 23.3%; Pred. No. 19;
Matches 48; Conservative 36; Mismatches 66; Indels 56; Gaps 10;
Qy 5 BEINEKDLRKSELOQTALGNLKIYVNSKATSSSEKSDQFLNTLLPKGFTGHPWY 64
Db 180 BELNEENFRKLEQGG--IKTLLEVALYLYKKYI---DKGENEYFENLKKP----- 225
Qy 65 NDLLVDLGSTAAATSEYSGSSVDLYGAYVYQACGTPNKTACMYGGVTLHDNNRLTEBK 124
Db 226 NELKNDLSYLEASGYKYSQSQIFVALTKG-----FVILSGLTSGKTKIAQEL- 278
Qy 125 VPINLWIDGKOTTPIDKVTSSKEVTVQELDLQA-----RH-----YLHOK----- 166
Db 279 -----GELLDLPL--QVMSASGPNVAKREIKSLQETINRHGFVYGMHPPGKISKIK 328
Qy 167 ----FGLYNS---DSFGKVGORGLIV 185
Db 329 PPFIFWYDSDENDEYKKVPYGIIV 354
RESULT 36
AE1449
hypothetical protein lin0132 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1449
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fahi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A>Title: Comparative genomics of *Listeria* species.
A:Reference number: AE1077; MUID:21537279; PMID:11679669
A:Accession: AE1449
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1946 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95365.1; PID:g16412551; GSPDB:GN00178
A:Experimental source: strain Clip11262

C:Genetics:
A:Gene: lin0132
Query Match 7.2%; Score 87.5; DB 2; Length 1946;
Best Local Similarity 22.0%; Pred. No. 69;
Matches 56; Conservative 30; Mismatches 98; Indels 71; Gaps 12;
Qy 4 SEINEKDLRKSELOQTALGNLKIYV-----YNSKATSSSEKSDQFLNTLL 53
Db 1198 TRNLNADYVRYVTGKPTDSEGNIAGVKFKNIWTKVIAYRGGWISNSETADPF-----S 1252
Qy 54 FK-----GFTGHPWYNDLLVLDLSTAAATSEYSGSSVDLYGAYVYQACAGT-----P 101
Db 1253 FRQEDGSYVAE--LNGRYVDFSSGLVSTEAAGSKIDLYSAQEGVSQVSAITTKALVEP 1310
Qy 102 NKTACMYGGVTLHDNNRLTEKVKPINLWIDGKQTPIDKVTSSKEVTVQ-----ELDIQ 158
Db 1311 NITA--EVSIVYDR-----VKLDVVGEDKDNITTKKONENELF 1347
Qy 159 ARHYLHGKFGLYNSDSFGKVGORGLIVFHSS-----EGTSVSYDLFDAQQYPTL 209
Db 1348 VNAYKEDGSTLVKSVRIDGLPRDIFVTDLSPPKVKVKEG---KYDILLDGEQ--PQN- 1401
Qy 210 LRIYDNTTISSTSL 224
Db 1402 -KVYSETITTEKSL 1415
RESULT 37
T08081
probable myrosinase-binding protein - rape
N:Alternate names: jasmonate inducible protein
C:Species: *Brassica napus* (rape)
C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000
C:Accession: T08081
R:Geshi, N.; Brandt, A.
Planta 204, 295-304, 1998
A>Title: Two jasmonate-inducible myrosinase-binding proteins from *Brassica napus* L. seed
A:Reference number: Z16340; MUID:98192006; PMID:9530873
A:Accession: T08081
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-914 <GES>
A:Cross-references: EMBL:Y11482; NID:e1023100; PIDN:CAA72270.1; PID:e304149
A:Experimental source: cv. Global; isolate a4; seedlings
A>Note: jasmonate inducible
Query Match 7.1%; Score 87; DB 2; Length 914;
Best Local Similarity 20.1%; Pred. No. 28;
Matches 65; Conservative 35; Mismatches 89; Indels 134; Gaps 14;
Qy 2 EKSEINE-----KDLRKSELOQTALGNLKIYV-YS 34
Db 347 EKGEFNDYGFEGVKKITVGADQYSVTYIKIEYKDGKVEIREHGTSGELQEFSDVDFN 406
Qy 35 KATTSSEKSDQFLT--NTLLPKGFTGHPWYNDLLVLDLSTAAATSEY----- 81
Db 407 DSITEVGGYKKNYTYDTLITSLYFTTSKGTSPFLFGINSEKKGTEFEFKDENGKGLIG 466
Qy 82 -----GSSVDLYGAYVYQACG-----TNKTCACMYGGVTLHDNNRLTEE 122
Db 467 LHGRGCGNAIDAGAYPDTGQGGDGVPSKDGPKTDVEFKKGLG-----DKGEFFDD 521
Qy 123 -----KKVPI---NLWIDGKOTTPIDKVTSSKEV-----TVQ 153
Db 522 VGPEGVKKITVGADNLSI---TYIKIEYKDGKVEIREHGTARGKLFESVDYDNDST 577
Qy 154 ELDLQARH-----YLHGKFGLYN-----SDSFGKVGORGLIV 185
Db 578 EVGTYKHNVTYDTLITSLYFTTSKGTSPFLGIDSEKKKGTEFEFKDENGK- ---LIG 633
Qy 186 FHSSEGSTVSYDLFDAQQYPTD 208

Db 634 FHGRGNAI-----DAIGAYFDT 651

RESULT 38

T08102

myosinase-binding protein (clone indmbp2) - rape

C:Species: Brassica napus (rape)

C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-Jul-2000

C:Accession: T08102

R:Taipaleensuu, J.; Eriksson, S.J.; Raek, L.

Eur. J. Biochem. 250, 680-688, 1997

A:Title: The myosinase binding protein from Brassica napus seeds possesses lectin activity

A:Reference number: Z16355; MUID:98121188; PMID:9461290

A:Accession: T08102

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-988 <TAI>

A:Cross-references: EMBL:Y09437; NID:G1711295; PIDN:CAA70587.1; PID:G1711296

A:Experimental source: cv. Hanna; leaves

Query Match 7.1%; Score 87; DB 2; Length 988;

Best Local Similarity 20.5%; Pred. No. 31;

Matches 66; Conservative 35; Mismatches 89; Indels 132; Gaps 15;

QY 2 EKSEELNE-----KDLRKSELOGTALGNLAKIYY-YNS 34

Db 363 EKGEENDVGFEVKKITVGADQSYTYIKIEYKDGKVEIREHGTSGELQEFSDVDPN 422

QY 35 KAITSEKSADQFLT--NTLLFKGFTGHPWYNDLVLGLGTAATSEYE----- 81

Db 423 DSITEVGGTYKHNVTDTLLTSLYFTTSKGFPLFGINSEKKGTEFEFKDENGKGLIG 482

QY 82 -----GSSVDLYGAYGYOCAGG-----TPNKTACK-----YGGVTLHNNRLTSE- 122

Db 483 LHGRGNDAIGAYFDTGSGQGDGVPTKQVLADVPKKGPLGG-----DKGEFFDDV 538

QY 123 -----KKVPT---NLWIDGKQTTVPIDKVKTSKKEY-----TVQEE 154

Db 539 GFEGVKKITVGADNLSI---TVIKIEYKDGKVEVREHGTARGKLFESVDVDPNDSITE 594

QY 155 LDLOQASH-----YLGKGLYN-----SDSPGKVGQGLIVF 186

Db 595 VGQTYKHNVTDTLLTSLYFTTSKGFPLFGIDSEKKGTEFEFKDENGKGR---LIGF 650

QY 187 HSSEGSTSVSYDLFDAQOQYPTD 208

Db 651 HGRGNAI-----DAIGAYFDT 667

RESULT 39

E71403

hypothetical protein - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: columbia

C>Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C:Accession: E71403

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terryn, N.; Giel, vanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans, C.; Chaiwatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A:Reference number: A71400; MUID:98121113; PMID:9461215

A:Accession: E71403

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-722 <BEV>

A:Cross-references: GB:Z244747; PID:e326875; PID:G2244776

C:Genetics:

A:Map position: 4COP9-4G3845

Query Match 7.1%; Score 86.5; DB 2; Length 722;

Best Local Similarity 20.2%; Pred. No. 23;

Matches 47; Conservative 40; Mismatches 79; Indels 67; Gaps 10;

QY 6 EINEKDLRKSELOGTALGNLKOIYYNYSKAITSSSEKSAQDQFLNTLLFKGFTGHPWYN 65

Db 455 KINSEIDGMAEKGKSLGNAQTV---ESETLRVSLPAVD----- 431

QY 66 DLLVDLGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNR---LTE 121

Db 492 SVVYDSNADWSSAANKTGLVDLAG-----NESELMQANVVAEKGKPKDTLSS 539

QY 122 EKKV---PINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHKGFLYNSDSFGGK 178

Db 540 ESSCYASPVSVFEGSDAS---DOIKSSTETSKDLSAQISAE-----SKDEVCRE 586

QY 179 VQRLIVFHSS---EGSTVSYDL---FDAQQYPTDILLRIYRDNTTISSTLSLSI 226

Db 587 SNNGLVEESFNEPNKTEYPISHFGSTGTPDTV-----NTANQISLEI 632

RESULT 40

T30857

glucosyltransferase - Streptococcus salivarius

C:Species: Streptococcus salivarius

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C:Accession: T30857

R:Simpson, C.L.; Giffard, P.M.; Jacques, N.A.

Infect. Immun. 63, 609-621, 1995

A:Title: Streptococcus salivarius ATCC 25975 possesses at least two genes coding for prin

A:Reference number: Z20909; MUID:95122197; PMID:7822030

A:Accession: T30857

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1449 <SIM>

A:Cross-references: EMBL:L35495; NID:G662379; PID:G662379; PIDN:AAC41412.1

C:Genetics:

A:Gene: gtfL

Query Match 7.1%; Score 86.5; DB 2; Length 1449;

Best Local Similarity 25.0%; Pred. No. 57;

Matches 46; Conservative 26; Mismatches 75; Indels 37; Gaps 9;

QY 23 LGNLKQIYYNYSKAITSSSEKSAQDQFLNTL-----LFGKFTGHPWY- 64

Db 245 LSNQKE-YRFDKNGGIGS---SADSTNTNTVNGDKNAFYGTDDKDIELVDGYFTANTWYR 301

QY 65 -NDLLVDLGSTAAITSEYE-----GSSVDLYGAYGYOCAGGT-PNKTACMYGGVTLH 114

Db 302 PKELKDGKWTASTENDKRPLLTVWMPSKAIQASLYNMYKKEQGLGNTQYTSFSSQTM 361

QY 115 DNNRLTEKKVPINLWIDGK---QTTVPIDKVKTSKEVTVQELDLQARHLYHKGFLY 170

Db 362 DQAALEVKQKIEERAREGNTDMLRTIK-NFVKTPQGNWSTSE-NLDNNDHLQGGALLY 419

QY 171 NSDS 174

Db 420 NNDS 423

RESULT 41

T38720

chromodomain helicase hrp3 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002

C:Accession: T38720

R:Gentiles, S.; Churcher, C.M.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z21797

A:Accession: T38720

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1388 <GEN>

A;Cross-references: EMBL:Z99167; PIDN: CAB16277.1; GSPDB:GN00066; SPDB:SPAC3G6.01
A;Experimental source: strain 972h-; cosmid c3G6
C;Genetics:

A;Gene: SPDB:SPAC3G6.01

A;Map position: 1

A;Introns: 64/3

C;Superfamily: chromodomain helicase CHD1; chromobox homology

Query Match 7.1%; Score 86; DB 2; Length 1398;
Best Local Similarity 25.1%; Pred. No. 60;
Matches 45; Conservative 27; Mismatches 69; Indels 38; Gaps 10;

Qy 35 KAITSSEKSAQDLTNT-----LTFKGF-----FTGHPWYNDLLVLCGSTAATSEYE 81

Db 1047 KAVSAAEKDLSDQSNKSSRKALLIFKGVYNIAETLVORLNDLDI-LYDAMPTSGYS 1105

Qy 82 GSSVDLY-GAYGYQCAGGTNNKTCMYGGVTLH-----DNNRLTEKKVPINLWI 131

Db 1106 NFQIPMHVRSVHGWSQWG-FREDSMLLSGICKEGFGAWLEIRDDPELKMCKIFLE--- 1161

Qy 132 DGKQT--TVPIDKVTSSKEVTVOELDQARHYL-----HGKGLYNSD--SFGGKVQ 180

Db 1162 DTQTDNSVPDKENKEKKVPSAVHLVRRGYLLSALREHHQNFQIKSSPAISTNGTKQ 1220

RESULT 42

AH0340

putative autotransporter protein yapC [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C;Accession: AH0340

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

ii, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0340

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-638 <KUB>

A;Cross-references: GB:AL590842; PIDN: CAC93031.1; PID: g15980769; GSPDB:GN00175

C;Genetics:

A;Gene: yapC

Query Match 7.0%; Score 85.5; DB 2; Length 638;
Best Local Similarity 21.1%; Pred. No. 24;
Matches 43; Conservative 20; Mismatches 70; Indels 71; Gaps 6;

Qy 68 LVDLG--STAATSEYSSVDLYGAYGYQCAGGTNNKTCMYGGVT----- 112

Db 299 VVDLVGYQGLYSQBSNGSTDWYLATSTEELPGTTPNVTAPMLSSAQGVNLMAAPRHI 358

Qy 113 -----LHNNRLTEKKVPINLWIDGKQTTVPIDKV 143

Db 359 LNAELSTLRQGEKKADEGTGVWARYLTDLSKNSKNIAFNKVLUSGME--IGADK- 415

Qy 144 KTSKEVTVOELDQARHYLHGKFLGYNDSFGGKVQRGLIVFHSSEGSTVSY-----D 197

Db 416 -----QGLGNLNLGAFSTYSSSDVKST-----HDANGDIRSYGGGLYLT 457

Qy 198 LFDAQGYPDLLRIYRDNTRISS 221

Db 458 YLDQSGFYDVTVLKANRPNKMNKT 481

RESULT 43

T30552

glucosyltransferase N - Streptococcus salivarius (fragment)

C;Species: Streptococcus salivarius

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C;Accession: T30552

R;Jaffe, R.I.

submitted to the EMBL Data Library, February 1998
A;Description: Streptococcus salivarius V1477 gcfn.

A;Reference number: Z20854

A;Accession: T30552

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1449 <JAP>

A;Cross-references: EMBL:AF049609; NID:g2935545; PID:g2935546; PIDN:AAC05156.1

C;Genetics:

A;Gene: gtfN

Query Match 7.0%; Score 85.5; DB 2; Length 1449;
Best Local Similarity 25.0%; Pred. No. 70;
Matches 46; Conservative 26; Mismatches 75; Indels 37; Gaps 9;

Qy 23 LGNLKQIYYNKAITSSEKSAQDLTNTL-----LFGGFTGHPWY- 64

Db 245 LSNQKE-YRFDKNGSGFS--SADSTNTNTVANGDKNAFYGTTDKDIELVDGFIANTWYR 301

Qy 65 -NDLLVDLGSTAATSEYE-----GSSVDLYGAYGYQCAGGT-PNKTCMYGGVTLH 114

Db 302 PREILKDGKEWTASTENDKEPLLTVMWPSKAICASLYNMYKEQGLGTNTQYTSFSSQIOM 361

Qy 115 DNNRLTEKKVPINLWIDGK---QTVPIDKVTSSKEVTVOELDQARHYLHGKFLGY 170

Db 362 DQAALEVQKRIEGRAREGNTDMLRTTIK-NFVKTPQGWNSTSE-NLDNNDHLQGGALLY 419

Qy 171 NSDS 174

Db 420 NND5 423

RESULT 44

AG1749

glycosidase homolog lin2540 [imported] - Listeria innocua (strain Clp11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C;Accession: AG1749

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AG1749

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1090 <GLA>

A;Cross-references: GB:AL592022; PIDN: CAC97767.1; PID: g16415062; GSPDB:GN00178

A;Experimental source: strain Clp11262

C;Genetics:

A;Gene: lin2540

Query Match 7.0%; Score 85; DB 2; Length 1090;
Best Local Similarity 21.8%; Pred. No. 53;
Matches 64; Conservative 35; Mismatches 100; Indels 98; Gaps 15;

Qy 8 NEXDLKKSELOGTALGNLK-----QIYYNKAITSSEKSAQDLTN 50

Db 400 NEWD--RESDV-STALSNAKENEIPATGFVLEQWSDEEYIWNDAITYAKNGEFPAYD 456

Qy 51 TLLFKGFFTGHPWYNOLLVDLGSTAA-----TSEYESSVDL-YGAYGYQCAGG 99

Db 457 DFTFNGKWTNPKAMVDVSHDAGMNIWLQVPLKDDNTVYQRDNDDEYMSQGSADGG 516

Qy 100 T--PNKTACMY---GGVTLHDNNRLTEKKVPINLWIDGKQ---TVPIDKVTSSKEVT 151

Db 517 TGAPYRVPASQWFGNGILLDFTN-----KDAVNWTSOREVYLLTVDGIDGFKDGGEMV 570

Qy 152 -----VOELDQARHYLHG-----KFLGYNSS-- 172

Dd

QY

Dd

RESULT 45
S23771

A:outer membrane porin protein OprD precursor PA0958 [imported] - Pseudomonas aeruginosa C:NAlternate names: pore-forming protein; protein D2
C:Species: Pseudomonas aeruginosa
C>Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text_change 15-Jun-2001
C:Accession: S23771, S61560; S25008; E83527
R:Ionoyama, H.; Yoshihara, E.; Nakae, T.
A:title: Nucleotide sequence of the protein D2 gene of Pseudomonas aeruginosa.
A:Reference number: S23771; PMID:93037310; PMID:1339257
A:Accession: S23771
A:Molecule type: DNA
A:Residues: 1-443 <YON>
A:Cross-references: EMBL:X63152; NID:g45370; PIDN:CAA44855.1; PID:g45371
A:Accession: S61560
A:Molecule type: protein
A:Residues: 24-34 <YOW>
R:Huang, H.; Siehnell, R.J.; Bellido, F.; Rawling, E.; Hancock, R.E.W.
submitted to the EMBL Data Library, July 1992
A>Description: Analysis of two gene regions involved in the expression of the impenem-sensitizing mechanism of Pseudomonas aeruginosa.
A:Reference number: S23859
A:Accession: S25008
A:Molecule type: DNA
A:Residues: 1-443 <HUA>
A:Cross-references: EMBL:Z14065; NID:g45372; PIDN:CAA78448.1; PID:g45373
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Lorian, V.; Tenenbaum, B.C.; White, O.; Holtzapple, K.T.; Smith, T.F.; Olson, M.V.; Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
adman, S.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A:title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A:Reference number: A82950; UID:20437337; PMID:10984043
A:Accession: E83527
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <STO>
A:Cross-references: GB:AEO04529; GB:AEO04091; NID:g9946851; PIDN:AAG04347.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
C:Gene: oprD; PA0958
C:Superfamily: Pseudomonas aeruginosa outer membrane porin PA0958
C:Keywords: porin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-443/Product: protein D2 #status experimental <MAT>

Query Match 6.9%; Score 84.5; DB 2; Length 443;
Best Local Similarity 23.2%; Pred.No.18;
Matches 60; Conservative 30; Mismatches 98; Indels 71; Gaps 14;

QY 15 KGELQQTALGNTKQIIYYNSKAITSSEKSADOFLLTLFKGGFTTGHWPYNLDLVLGST 74
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
34 KGFIEDSSDLLLRNYFNFRDKSGSGSDVD-----WTQGFLTTY-----ESGTF 78
QY 75 AAATSEVEGSVDLYGAYGYQCACGGTPNKTA----CMYGCVTLHDNNRLTEEKVYPIN- 128
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
79 QGT---VGFGVAIFG-YLGLK-LDGTSCKTGCLNVMDNGPKRDDYSRAGAIVKRISK 133
QY 129 ----LWTDGRQTTPVIDKVTKSK-----KEVTVOQLDLQAHHYLHGK----- 166
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
134 TWLKMGEE-MQPAPVPFAAGSRLEPQTATGFOQSSEPEGLDEAGHFTEGEPTVKRS 192
QY 167 ---FFGIY-----NSDSFGKGVRGLIIVHSSEGSTVSVDLFDAQQGYPDTHIRYDNLT 217
Db : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
193 GELYATPATGETAKSAFDIGRR-----YAITDNLASJLAEGLEDVIHQY-----YLNLSNY 242
QY 218 TI---SSTSISISLYLYTT 233

89806

Db 193 GHRRLGYGELPGRDRSHLHSLWGGT-----WGGIEGFTSSLYAELQ-----NVW---- 239

Qy 134 KQTTPIDKVKTSKKEVTQVELD-----LQARHLYHGKFGLYNSDSFGGKVGRLIVPHS 188

Db 240 KQYADV-----YTVIEDNWSLNPAGAHYK-----TVDSGDSLLGRIDNNTVSLHF 287

Qy 189 SEG---STVSYDLFDAQGGYPTLLR-----IYRDNT 217

Db 288 AVGYRQHTVAVLKQVNGNTPFYINQGDIFLDNS 323

RESULT 51

A64556

toxin-like outer membrane protein HP0289 - Helicobacter pylori (strain 26695)

C:Species: Helicobacter pylori

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999

C:Accession: A64556

R:Tomb, J.F.; White, O.; Kervlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 386, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; MUID:9739467; PMID:9252185

A:Accession: A64556

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: GB:AE000547; GB:AE000511; NID:G2313377; PIDN:AAD07355.1; PID:G231338

A:Residues: 1-2893 <TOM>

Query Match 6.8%; Score 83; DB 2; Length 2893;

Best Local Similarity 20.3%; Pred. No. 2.8e+02;

Matches 49; Conservative 32; Mismatches 61; Indels 92; Gaps 12;

Qy 16 SELOGTALGNLKIYYNYSKAITSS-----EKSADQFLTWTLFKGFTGHPWYN 65

Db 2258 SKIKGSA--NIKNLVYNAFOANLITISQAVLEKNA-SFTVNNLNIQGAFFNN--- 2310

Qy 66 DLLVLDLGSATSEYB-----GSSVDLYGAYGVQCAGGTPNKTACMYGGVTLHDNNR 118

Db 2311 -----ATQKIEVLNVLVNASLSTGIYGVGALNNSGA-----IHFN--- 2351

Qy 119 LTEKKVPINLWDGKQTTVPIDKVKTSKKEVTQVELDQARHLYHGKFGLYNSDSFGGK 178

Db 2352 -----LENTQTPTPL-----IQAB-----GIINLNT--- 2372

Qy 179 VQRLIVFHSSEGSTVSYDLFDAQGGYPTLLRIVRDNTTISTLSLSLYIT 232

Db 2373 TQPFMVNNSMANNTYTLKLS-SRYD-----YNIIPNSLQSYLNIYT 2416

RESULT 52

F64187

p-aminobenzoate synthase component I homolog - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999

C:Accession: F64187

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervlavage, P.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: F64187

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-328 <TIG>

A:Cross-references: GB:U32797; GB:L42023; NID:G1574095; PIDN:AC22834.1; PID:G1574097; T

Query Match 6.8%; Score 82.5; DB 2; Length 328;

Best Local Similarity 27.3%; Pred. No. 18;

Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;

Qy 136 TTVPIDKVKTSKKEVT---VQELDQARHLYHGKFGLYNSDSFGGKVGRLI-----V 185

Db 237 TLLPAGSISGAPKKTQIIQAEKQKRGYYTGIFGFDGKTLQSAVAIRFISQVDEKEY 296

Qy 186 FHSSEGSTVSYDLFDAQGGYPTLLRIY 213

Db 297 FHSGGGITH---SNAQDEYEELLEKRY 321

RESULT 53

S39663

aminopeptidase homolog ywad - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 07-Oct-1994 #sequence_revision 24-Feb-1995 #text_change 15-Oct-1999

C:Accession: S39663; S16427; D70050

R:Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, N.A.; Rapoport, G.; Danchin, A.

Mol. Microbiol. 10, 371-384, 1993

A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region for A:Reference number: S39655; MUID:95020537; PMID:7934828

A:Accession: S39663

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-455 <GLA>

A:Cross-references: EMBL:X73124; NID:G413923; PIDN:CAAS1564.1; PID:G413932

R:Glaser, P.; Kunst, F.; Debarbouille, M.; Vertes, A.; Danchin, A.; Dedonder, R. DNA Seq. 1, 251-261, 1991

A:Title: A gene encoding a tyrosine tRNA synthetase is located near sacS in Bacillus subtilis

A:Reference number: S16421; MUID:92216127; PMID:1806041

A:Accession: S16427

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-68 <GL2>

A:Cross-references: EMBL:X52480; NID:G40236; PIDN:CAA36725.1; PID:G40243

R:Kunst, F.; Ogawara, K.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruchsi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emmerson, P.T.; Etian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallercach, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, J.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: D70050

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-455 <KUN>

A:Cross-references: GB:Z99123; GB:AL009126; NID:G2636240; PIDN:CAB15973.1; PID:e1186346;

A:Experimental source: strain 168

C:Genetics:

A:Gene: ywad

Query Match 6.8%; Score 82.5; DB 2; Length 455;

Best Local Similarity 22.0%; Pred. No. 28;

Matches 41; Conservative 25; Mismatches 67; Indels 53; Gaps 6;

Qy 1 SEKSEINEXDLRKKSELOQTALGNLKIYYNYSKAITSSKADOF-----LTNTLLFK 55

Db 53 SQISEALGPR-----IAGTAEKKSALLIASSMRKLDVKVQFNTPDRLEGLTSSA 105

Qy 56 GFTTGHFWYNDLVLGSLTAATSEYSGSSVDLYGAYGVQCAGGTPNKTACMYGGVTLHD 115

Db 106 G-----RDILLQAASGSAPTEQGLTAPLNYAGLYQ-----KDFADAKGKIALIS 152

Qy 116 NNRLT-----EKKVPINLWDGKQTTVPIDKVK-----TSK 147

Qy	188	SSEGSTVSY	196
		: :: ::	
Dd	549	TSDGSTMYS	557
 RESULT 55			
B91025			
NADH dehydrogenase I chain			
C:Species: Escherichia coli			
C>Date: 18-Jul-2001 #sequen			
C:Accession: B91025			
R:Hayashi, T.; Makino, K.;			
gasawara, N.; Yasunaga, T.;			
DNA Res. 8, 11-22, 2001			
A:Title: Complete genome se			
A:Reference number: A99629;			
A:Accession: B91025			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-600 <HAY>			
A:Cross-references: GB:BA000			
A:Experimental source: stra			
C:Genetics:			
A:Gene: ECgsl70			
C:Superfamily: Escherichia			
 Query Match			
Best Local Similarity	2		
Matches	51;	Conservati	
Qy	26	LKQIYYNNSKAITP	
	:	:	:
Dd	380	LREFLDWFPEKRLA	
Qy	85	VDLYGA--YGYQYQ	
	:	:	:
Dd	436	FDFRKARPYSGYGE	
Qy	132	DGKQTTPIDKVUKV	
	:	:	:
Dd	496	DHPLTTPP-----	
Qy	188	SSEGSTVSY	196
	:	:	:
Dd	549	TSDGSTMYS	557
 RESULT 56			
C95869			
NADH dehydrogenase I chain			
C:Species: Escherichia coli			
C>Date: 16-Feb-2001 #sequen			
C:Accession: C95869			
R:Perna, N.T.; Plunkett III			
iller, L.; Grotbeck, E.J.;			
Nature 409, 529-533, 2001			
A:Title: Genome sequence of			
A:Reference number: A95480;			
A:Accession: C95869			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-600 <STO>			
A:Cross-references: GB:AEO00			
A:Experimental source: stra			
C:Genetics:			
A:Gene: nuoc			
C:Superfamily: Escherichia			
 Query Match			
Best Local Similarity	2		
Matches	51;	Conservati	

```

F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-466/Product: dep protein #status predicted <MAI>

Query Match          6.7%; Score 82; DB 2; Length 466;
Best Local Similarity 23.2%; Pred. No. 31;
Matches 48; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY  29 IYYNSKAITSSEKSADQFLNTLL-----FKGFFTGHPWYNDLLDLGSGTAATS--EY 80
DB 125 IYFNGEPIETGETUIQDRLARTLKKIQEKAQFEG-----GVARAISTAKISLEDI 179

QY  81 EGGSSVD----LYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQT 136
DB 180 KGKYKEVRKPKNGTMYGDVVTAPP-----PFGSVTLQLQMLKLAKEKEV----YKDV DHT 230

QY  137 TVPIDKVTXSKKEVTVQELDQARHYLHGKGLYNSDSFGKVGORGLIVFHFSGSGTSVSY 196
DB 231 ATYNGKME-----EISRIAYQDRKNIGDPNYVMNDPKWVSDKYISTMKNGDALSS- 283

QY  197 DLFDAGQGYPTLLRIYRDNTHSTTS 223
DB 284 ---EAEHSESTHFVIIDRDGTWVSSTN 307

RESULT 59
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C;Species: Haemophilus influenzae
A;Variety: strain SB29
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S70908; S73321
R;Locomote: S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: S70908
A;Molecule type: DNA

```

A;Residues: 1-631 <LOW>
A;Cross-references: EMBL:U15055
A;Experimental source: strain SB29, clone DS-1090-3-2
R;Locomore, S.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73321
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250,'L',252-349,'RTDATN',357-631 <LOW>
A;Cross-references: EMBL:U15055; NID:G1223948; PIDN:AAQ43931.1; PID:G1223949
A;Experimental source: strain SB29, clone DS-1090-3-2
C;Genetics:
A;Gene: *cbp2*
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an
F;1-17/Domain: signal sequence #status predicted <SIG>

```

Query Match      6.7%; Score 82; DB 2; Length 631;
Best Local Similarity 19.9%; Pred. NO. 47;
Matches 54; Conservative 27; Mismatches 62; Indels 128; Gaps 12;

      14 KXSEIQQGTALG-----NLKQIYYNSKAITSSSEKSADQLTNTLFLKG 56
      QY   : : : : : : : : : : : : : : : : : : : : : : : : : :
      190 QYSLFGSFGAFGAYNRRRS AISIEDINLENNLK-----EFTVNFGTKK- 237
      DB   : : : : : : : : : : : : : : : : : : : : : : : : : :
      57 FFTGHPWNDL-----LVDLGTAATSEYEG-----SSVDL 87
      QY   : : : : : : : : : : : : : : : : : : : : : : : : : :
      238 -LTGKLYNEBETNNNKLQKRKHELYDIDADLYSNRFRGKVPTQKDSQHEPFTSEGL 296
      DB   : : : : : : : : : : : : : : : : : : : : : : : : : :
      88 YGAYYGYOCAGGTPNKTACMTGGVTLHDNNRL-----TEKKVPINLWDGKQTT 137
      QY   : : : : : : : : : : : : : : : : : : : : : : : : : :
      297 EGGFYG-----PNGEE- LGGKFLAGDNRVFGVFSABEETKKDKLURETLIDGKLIT 347
      DB   : : : : : : : : : : : : : : : : : : : : : : : : : :
      138 VFIDK-----VKTSKKEVTVQELD-----LQARHYL 163
      QY   : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 348 PKTKTDAKTAANAKTDEKNTTKDIPSGADYLLINDYVPVLPPEBNTNDFITSRHHK 407

QY 164 HG-----KFLGYNDSFGGK 178

Db 408 VGDKTYKVEACCKNLSYKFGWYEDPLNGE 438

RESULT 60

T33730

Hypothetical protein - Zymomonas mobilis

C:Species: Zymomonas mobilis

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2003

C:Accession: T33730

R:Lee, J.S.; Jin, S.J.; Kang, H.L.; Kang, H.S.

Submitted to the EMBL Data Library, August 1998

A:Description: Sequence analysis of 67E10 cosmid clone of Zymomonas mobilis ZM4.

A:Reference number: T33732

A:Accession: T33730

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-644 <LE>

A:Cross-references: EMBL:AF086791; NID:G3820589; PIDN:AACT70368.1

C:Superfamily: glycyl monoaminopeptidase

Query Match 6.7%; Score 82; DB 2; Length 644;

Best Local Similarity 20.8%; Pred. No. 48;

Matches 60; Conservative 27; Mismatches 76; Indels 126; Gaps 12;

QY 51 TLLFKGFTGH-----PWYND-----LLVDLGSTAAATSEY 80

Db 77 TLLYEWLPFGHSGPIEKLAGLIVTANNQVDPQSDVVDYAPHLDIPAGVTEITAY 136

QY 81 -----EGSSVDLYGAY-----GYQCA----- 97

Db 137 QVLSFTSQRIQSTPEWNLQWNTLALYAGYETROIQPTVYPTGWSALEIS 196

QY 98 -----GGTPN-----CMYGGVTLHNNRLTEERKVPINLWDGKQITVP 139

Db 197 GITPDGQTPNVQYKTTDFDITLDSPPVMAGRYTRTE-----TLAPGRLNLIADKPEDVMW 252

QY 140 IDKVTSTKEVTQELDQ-ARHYLHGKFLGYNDSFG-----KVQGLIVFHSS 189

Db 253 TDQNLNAHQTLQTAQVLYGQHYSHYDPLLALSEKGLGLEHHQSSDEGADYFSKW 312

QY 190 EGSTVSVDLDAQ-----GQV-----PDTLLRIYRDN 217

Db 313 DKSAGVGRLLAHEYNHNSWNGKVRPADLWTPDYKTPMDSLLWVYEGOT 361

RESULT 61

D82568

Conserved hypothetical protein XF2349 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: D82568

R:Anonymous, D.

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82568

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-745 <SIM>

A:Cross-references: GB:AE004045; GB:AE003849; NID:G9107517; PIDN:AAF85148.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neco, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, P.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2349

Query Match 6.7%; Score 82; DB 2; Length 745;

Best Local Similarity 22.3%; Pred. No. 58;

Matches 44; Conservative 37; Mismatches 86; Indels 30; Gaps 10;

QY 14 KSELOQTALGNLQKQIYYNNSKAITSEKAD--QFLTNTLLFKGF----FTCHPPYNDL 67

Db 113 KALSADGSIAGGYQYIRIHESSSANLEKASNGKFLANDGVSATFIPVWSDGSWENEV 172

QY 68 LVDLG--STAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHNNRLTEKKV 125

Db 173 KLELGILESOVVALSGDGKTI--YGF-----STHLVPIIWSGSHWKDKHLDVPKE- 224

QY 126 PINLWIDGKQTTVPID-KVK---TSKEVTQELDQAR-----HYLHGKFLGYNDSFGG 177

Db 225 ---YYDAEVRALSTDGKVGAGYISSKNITRIGILECKSRNDTKNFTHA--FIWSGDGFGI 278

QY 178 KVQGLIVFHSSSEGSTV 194

Db 279 KTDGLTLNNSSEGAEV 295

RESULT 62

H72204

Pullulanase - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Jun-2003

C:Accession: H72204

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.

Nature 399, 323-329, 1999

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: H72204

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-843 <ARN>

A:Cross-references: GB:AE001821; GB:AE000512; NID:G4982421; PIDN:AAD36907.1; PID:G498242

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TMI845

C:Superfamily: pullulanase type debranching enzyme

Query Match 6.7%; Score 82; DB 2; Length 843;

Best Local Similarity 28.3%; Pred. No. 68;

Matches 32; Conservative 15; Mismatches 36; Indels 30; Gaps 6;

QY 4 SEEINRDLRKSGEL--QG-----TALGNLQIYYNNSK--AITSEKSGADQFLTNTLLF 54

Db 186 SESLKEEDLRKDVLEIEGYKPARVIMMEILDYDDYDGLGAVYSPEKT-----IF 236

QY 55 KGFTTGHFWNDLLVDLGS-----TAAATSEYEGSSV-----DLGAYGYQ 95

Db 237 RVMSPSVKMKVKLLFKNGEDTEPYQVYNNMEYKNGVWEAVEGDLGVFLYQ 289

RESULT 63

C90595

Hypothetical protein MYPU_6670 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C:Accession: C90595

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, P.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21287165; PMID:11353084
A:Accession: C90395

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-888 <KUR>
A:Cross-references: GB:AL445566; PID:g14090082; PIDN:CAC13840.1; GSPDB:GN00153
A:Experimental source: strain UAB CT1P
C:Genetics:
A:Gene: MYP1 6670
A:Genetic code: SGC3
C:Superfamily: isoleucine-tRNA ligase

Query Match 6.7%; Score 82; DB 2; Length 888;
Best Local Similarity 23.9%; Pred. No. 73;
Matches 56; Conservative 25; Mismatches 89; Indels 64; Gaps 11;

QY 41 EKADQFLNTLFGKFTGHPWYNLLDLGTAATSEYEGSSV--DIY----- 88
DB 501 EKSVDELLPEYKKNK-WTKETIMDVWFDGSGTSIGVEIEGVSPFDLYLEIGIDYRGW 559
QY 89 -----GAYGVQ----- -CAGTTPNKTACMYGGVTLHDNNRLTEKKVPI-NL 129
DB 560 FNSIINSVAYWGQSPYRLLSHGFLVDGKGNKSKOLGNV--DPQEIIOKYGADILRL 617

QY 130 WIDQ-----KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSF 175
DB 618 WVANCEYADVSVSESIKQTVENYKIRN-----IKFLGNLQDYHDKNL----- 666

QY 176 GKGVRGLIVFHSGSEGTSTVYDFDAGQYPP--DTLLRYRDNNTTISSTLSIS 227
DB 667 --KLE-GIHELINERLKKVFDILOAYNDYDFNDVKTTLNPLTDLSSFLYSIS 717

RESULT 64
C89808

exotoxin 15 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C:Accession: C89808

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89808

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <KUR>

A:Cross-references: GB:BA000018; PID:g13700324; PIDN:BAB41622.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: set15
C:Superfamily: toxic shock syndrome toxin

Query Match 6.7%; Score 81.5; DB 2; Length 227;
Best Local Similarity 21.0%; Pred. No. 13;
Matches 46; Conservative 40; Mismatches 90; Indels 43; Gaps 8;

QY 10 KDLRKKSELOGTALGNLQKIYYNSKAITSSSEKSAQFLNTLLFKGFTGHPWYNLLIV 69
DB 41 QDLSEYKGGFELTNVTGKYGNKVTFFDINSQIDVTLTG-----NEKL- 85

QY 70 DLGTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVPI-NL 129
DB 86 -----TVKDDDEVSNVDVFFVRGSDKSAITTS-----IGGIT-KTNGQHKDVTQNNVL 134

QY 130 WID--GKQTT-VPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVGORGLIV 185
DB 135 SVKSTGCHTSTVTSSEYISYKEISLKELDFKLKRLDKHDLKTEPKDSKIR----- 189

QY 186 FHSSEGSTSVYDLFDAGQYPPDTLLRYRDNNTTISSTLS 224

DB 190 ITMKNGGYTFEL-----NKKLQPHRMGDIIDSRNI 220

RESULT 65
AH1903

hypothetical protein all0778 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AH1903

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, R.; Kaneko, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH1903

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-374 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA872735.1; PID:g17130123; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0778

Query Match 6.7%; Score 81.5; DB 2; Length 374;
Best Local Similarity 21.4%; Pred. No. 26;
Matches 49; Conservative 35; Mismatches 88; Indels 57; Gaps 10;

QY 9 EKDLRKKSELOGTALGNLQKIYYNSKAITSSSEKSAQFLNTLLFKGFTGHPWYNLL 68
DB 54 QKMAKTELEQGISLPELNSGYASLNKLQNGENVQLTIANSI-----WVQ-- 101

QY 69 VDLGTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVPI-N 128
DB 102 -----DVSRLPDPFVQTTDFYQA-----KVNLDQFQNTAVN--TIN 136

QY 129 LWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVGORGLIVFHS 188
DB 137 SWVQ-ENTGKIDKIVDNIE--FNQALFLINAIYFNGKW---SNAP-DKSQTPQTFYT 188

QY 189 SEGSTSVYDLFDAGQYPPDTLLRYRDNNTTISSTLS-----SISLYLY 231
DB 189 ASGQKQHPMMSQTGEYR-----YETPQFQSVSLPYGQDGKVSLYIF 231

RESULT 66
A90267

proteinase related protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C:Accession: A90267

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-4
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90267

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1269 <KUR>

A:Cross-references: GB:AE006641; NID:g13814328; PIDN:AAK41392.1; GSPDB:GN00155
C:Genetics:
A:Gene: SS01141

Query Match 6.7%; Score 81.5; DB 2; Length 1269;
Best Local Similarity 23.7%; Pred. No. 1.3e+02;
Matches 50; Conservative 27; Mismatches 85; Indels 49; Gaps 10;

QY 33 NSKAITSEKSAQFLNTLLFKG---FFTGHFWYNLLVDLGTAATSEYEGSSVDLYG 89

Db 1032 NVKILNVSGNLLDPLTNVIVNSVKILNGN---ISNVIRNSTVLIMQSNANNITLY- 1087

Qy 90 AYYGYCCAGGTPNKTACMYGVTWLDHNNRLTEEEKVPIINLWIDGKQTVTPIDKVKTSKKE 149

Db 1088 -----NSTLYAIGG-SINGLN-VYNSKWPINHIQGLYPELPSISINLPSKN 1133

Qy 150 VT-----VQELDLQARHLYGKFGLYNSDSFGKQVQGLIVFHSSEGSTVSVDLFD 200

Db 1134 VTGTVNVTNVVIGEDVSRINYVING--NLINSFTTNGT-----HIVINTQNY---- 1179

Qy 201 AQQQVFDLTLRIYRDNNTTISSTLSISLYLY 231

Db 1180 PDGGYNLTAVTAIQSDGLSSNSS-----YLY 1205

RESULT 67

T29999

hypothetical protein ZC8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T29999

R:Latreille, P.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid ZC8.

A:Reference number: Z20719

A:Accession: T29999

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-228 <LAT>

A:Cross-references: EMBL:U64862; PIDN:AA52624.1; GSPDB:GN00028; CESP:ZC8.4

A:Experimental source: strain Bristol N2; clone ZC8

C:Genetics:

A:Gene: CESP:ZC8.4

A:Map position: X

A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/

Query Match 6.7%; Score 81.5; DB 2; Length 2288;

Best Local Similarity 17.8%; Pred. NO. 2.8e+02;

Matches 51; Conservative 44; Mismatches 103; Indels 89; Gaps 8;

Qy 8 NEXDLRKSELOQTALGN-----LKQIYYNSKATTSSEKADQFLNTLPLKGFPGHP 62

Db 93 NVEQOREVSEMM-AALQNKVHEYKRGHAELEGRVWGAARNMLDPTSNVIMFDNYDQNT 151

Qy 63 WYNLLVLDGSTA-----ATSEYEGSSVDLYGAYGYCCAGGT 100

Db 152 YITHNVELWSPARGKRETIILGGGAPGLTTVNVHAGAGYSGSVAGYGG--GVQAMVGD 209

Qy 101 PNKTACMYG-----GVTLHDNN----- 117

Db 210 PNANYEMARLDEERRRDEVRMQWENRQKSLSEDLNRLREFERYANDSKDKTF 269

Qy 118 -----RLTEKKVPINLWIDGKQTVTPIDKVKTSKKEVTVQELDLQARHLYHGKFG 168

Db 270 INRERLAQYLSDEQKMLDLWTELQVRKQFSDLKTH-----TEEDLKQKAEFTAIRN 325

Qy 169 LYN-----SDSPGKVGRLIVFHSSEGSTVSVDLFDACQYPTLLRI 212

Db 326 VNNISRNAAFSAGAGDGLGLYLEDGDDVNRITNNYKVFETIKRM 372

RESULT 68

A1161

flagellar hook protein FlgB homolog lmo0697 [imported] - Listeria monocytogenes (strain

C:Species: Listeria monocytogenes

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: A1161

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: A1161

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC98775.1; PID:gl6410086; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0697

Query Match 6.7%; Score 81; DB 2; Length 411;

Best Local Similarity 20.4%; Pred. NO. 32;

Matches 43; Conservative 32; Mismatches 64; Indels 72; Gaps 9;

Qy 72 GSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGVTWLDHNNRLTEEK----- 123

Db 82 GSPTSTGRNKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVSDNNYLTQQGKYVMGYA 139

Qy 124 -----KVPINLWIDGKQTVTPIDKVKTSKKEVTVQELDLQARH 161

Db 140 TDKNGVNLNGNLQPIQIPLNSALPGBATKNGSLSGNIPLD---WGKDTISSELSVY--- 193

Qy 162 YLHGKFGLYNSDSFGG--KVQGLIVFHSSEGSTVSVDL-----FDA 201

Db 194 -----DNAGGKHLQVNMKAATPDASGNVSVEYEQMDGKALTPPVVTGTLNLYNA 242

Qy 202 QGOY--PDTLLRIYRDNNTTISSTLSISLYL 230

Db 243 QGELTNPDAKNI-QINSIVNGKQVNMGLNL 272

RESULT 69

A11520

flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain Clip11;

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: A11520

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Krett, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: A11520

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC95937.1; PID:gl6413157; GSPDB:GN00178

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin0705

Query Match 6.7%; Score 81; DB 2; Length 411;

Best Local Similarity 20.4%; Pred. NO. 32;

Matches 43; Conservative 32; Mismatches 64; Indels 72; Gaps 9;

Qy 72 GSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGVTWLDHNNRLTEEK----- 123

Db 82 GSPTSTGRNKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVSDNNYLTQQGKYVMGYA 139

Qy 124 -----KVPINLWIDGKQTVTPIDKVKTSKKEVTVQELDLQARH 161

Db 140 TDKNGVNLNGNLQPIQIPLNSALPGBATKNGSLSGNIPLD---WGKDTISSELSVY--- 193

Qy 162 YLHGKFGLYNSDSFGG--KVQGLIVFHSSEGSTVSVDL-----FDA 201

Db 194 -----DNAGGKHLQVNMKAATPDASGNVSVEYEQMDGKALTPPVVTGTLNLYNA 242

Qy 202 QGOY--PDTLLRIYRDNNTTISSTLSISLYL 230

Db 243 QGELTNPDAKNI-QINSTVNGKQVNMGLNL 272

RESULT 70
T15410
hypothetical protein C04F6.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 26-May-2000
C:Accession: T15410
R:Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C04F6.
A:Reference number: Z18346
A:Accession: T15410
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-611 <NHA>
A:Cross-references: EMBL:U42835; NID:g1125760; PID:g1125764; PIDN:AAA83588.1; CESP:C04F6
C:Genetics:
A:Gene: CESP:C04F6.4
A:Introns: 25/1; 184/3; 349/1; 514/3; 577/1
C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 6.7%; Score 81; DB 2; Length 611;
Best Local Similarity 18.7%; Pred. No. 55;
Matches 53; Conservative 46; Mismatches 78; Indels 106; Gaps 12;

QY 23 LGNEKQIYYNSKAITSSSEKADQFLNTLLPKGFTGH--PW-----YNDLLVDLGST 74
DB 313 LGSIDQVRYGHNKAITALSSAD-----GKTLFSADAEHINSWDISTGISNRVFDVHAT 368
QY 75 AATSEYEGSSVDLYGAY-----GYQAGGTENK-----TA 105
DB 369 MITGIKTSKGLFTVSWDHLKVPAGSGVDSSKAVANKLSSQPLGLAVSADGDIIVA 428
QY 106 CMYGGVTLHNNRLTEKKVPIN-----LWIDGQTTVPIDKV---KTSKK 148
DB 429 ACYKHAIYSHGKLTE---VPISYNSCCVALSNDKQFVAVGGQDSKVHVYKLSGASVSEV 485
QY 149 EVTVQELDL-----QAR---HYLHGKFLYNSDSFGSKVQGLIVFHS 188
DB 486 KTIHFAEITSVAFSNGAFLVATQDSKVIPISVANNEFAHTNSW-----TFHT 536
QY 189 SEGTSVYDLFDAGQGPPTLLRIYRDNTTISTSLISLYLY 231
DB 537 AKVACVWS-----PDNVRLATGSLDNSVIVW 563

RESULT 71
T28421
probable DNA-directed RNA polymerase (EC 2.7.7.6) - Pichia kluyveri mitochondrion linear
N:Alternate names: RNA polymerase
C:Species: Mitochondrion Pichia kluyveri
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T28421
R:Nosek, J.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20485
A:Accession: T28421
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-992 <NOS>
A:Cross-references: EMBL:Y11606; PIDN:CAA72339.1
A:Experimental source: strain CBS 7907
C:Genetics:
A:Genome: Mitochondrion linear plasmid
C:Superfamily: phage T7 DNA-directed RNA polymerase
C:Keywords: mitochondrion; nucleotidyltransferase; transcription

Query Match 6.7%; Score 81; DB 2; Length 992;
Best Local Similarity 24.5%; Pred. No. 16+02;
Matches 37; Conservative 28; Mismatches 62; Indels 24; Gaps 8;

QY 4 SEEINEKDLRKKSELOGTALGNLKOIYYNSKAITSSSEKADQFLNTLLPKGFFTGHPW 63
DB 598 SKDMSPRDF--YTFIKDSVLDNKKDM---NMNPNNSVERTLEMGLETRQMW-KTMVWIMPY 651
QY 64 YNDLLVDLGSTAAITSEYEGSSVDLYGAYGYQ-----CAGGTPNKATACMGVGTLDHNN 117
DB 652 -----NAGVTTMT-KYLEDLSLVNMGYYTADKDLVCCCKSGSEKDSCHY-YKSLLENN 703
QY 118 RLTEKKVP-----INLWIDGQTTVPIDKVK 144
DB 704 ARSPESKVPENNLNMTLTSKYSKSLCKCK 734

RESULT 72
AF1489
cell wall-associated protein precursor wapA (B. subtilis) homolog lin0454 [imported] - Lj
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1489
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kref, J.; Kuhn, M.; Kunz, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1489
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2167 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95686.1; PID:g16412895; GSPDB:GN00178
A:Experimental source: strain Clp11362
C:Genetics:
A:Gene: lin0454

Query Match 6.7%; Score 81; DB 2; Length 2167;
Best Local Similarity 21.7%; Pred. No. 2.9e+02;
Matches 41; Conservative 23; Mismatches 81; Indels 44; Gaps 8;

QY 32 YNSKAITSSSEKADQFLNTLLPKGFTGHPWYNDLLVDLGSTAAITSEYEGSSVDLYGAY 91
DB 1432 WNSAVVVKTKPVKMLKVTMPFRNGLTGKAWFDDVRVEGVLTKEVDAS-----GNY 1486
QY 92 Y--GYQAGGTGPNKATACMGVTLHNNRLTEKKVPINLWIDGQTTVP----- 140
DB 1487 VTASYDEGRKISFTYDIYGNKTSE-----TDEKGNKTKLTYDADNALIDTKLANGTSA 1541
QY 141 ----DKVTSKKEVTVOELDQARVHLGKF--GLYNSDSFGKVGQGLIVFHSSSGSTV 194
DB 1542 KYDDNNGNITTEKVTAS-----GKTKQNKIYEYD-----VDNKITAFDTALNRTI 1585
QY 195 SYDLFDAGQ 203
DB 1586 KYE-YDAAG 1593

RESULT 73
S25997
gene atpA intron 1 protein - liverwort (Marchantia polymorpha) mitochondrion
C:Species: Mitochondrion Marchantia polymorpha
C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 19-Jan-2001
C:Accession: S25997
R:Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; Kane, J.; Mol. Biol. 223, 1-7, 1992
A:Title: Gene organization deduced from the complete sequence of liverwort Marchantia po
A:Reference number: S25941; MUID:92114051; PMID:1731062
A:Accession: S25997
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1395 <ODA>
A:Cross-references: EMBL:M68929; NID:g786182; PIDN:AA09444.1; PID:g786230
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992

C;Genetics:

A;Genome: mitochondrion
C;Superfamily: gene atpA intron protein; H+-transporting ATP synthase alpha chain homol
C;Keywords: mitochondrion; nucleotide binding; P-loop
F:1-329/Region: atpA exon 1 encoded
F:170-177/Region: nucleotide-binding motif A (P-loop)
F:331-1395/Region: atpA intron encoded

Query Match 6.6%; Score 80.5; DB 2; Length 1395;

Best Local Similarity 18.9%; Pred. No. 1.8e+02;
Matches 42; Conservative 41; Mismatches 92; Indels 47; Gaps 10;

Qy 29 IYNNKAITSSKADQFLNTLLFKGFTGHWPYNDLLVDLSTAAATSEYEGSSVDLY 88

Db 300 VFYLSRLLEAAKMSDQ-----TGAGSLTALP-----VIECAPTGRSMIQTWVGGEVA 348

Qy 89 GAYGYQCAGGTGPKNTACWYGVTLHNNRLTEKKVP-INL--WIDGKQTT----- 137

Db 349 GRYQTTRSPKQDSARRIGRADLHGKVPINPSSGFVNLVQWVNAASKYDESSGYK 408

Qy 138 -VPIDKVKTSKEVT-----VOELDQARHYLHGKFLYNSDSFGKVKVQRLIV 185

Db 409 HIPVPIHSGSAHLTRQGLLRPSGVVTEGD-KPKAYALGTRN-YSKDSFQPLTEGV-- 464

Qy 186 FHSSEGSTVSVDLPDA-----QGQYPTDLLRIYRDNTTI 219

Db 465 -HTNEGTTGTFELTGLNRWVKVTKGYEDIFPSLIAREDNLI 505

RESULT 74

A55426

Gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis

N;Alternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R

C;Species: Porphyromonas gingivalis

C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999

C;Accession: A55426; D53113

R;Payloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, P

J. Biol. Chem. 270, 1007-1010, 1995

A;Title: Molecular cloning and structural characterization of the Arg-gingipain proteina

A;Reference number: A55426; MUID:95138080; PMID:7836351

A;Accession: A55426

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1704 <PAV>

A;Cross-references: GB:U15282; NID:9557067; PIDN:AAA69539.1; PID:G557068

R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J.

J. Biol. Chem. 269, 406-411, 1994

A;Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolac

A;Reference number: A53113; MUID:94103245; PMID:8276827

A;Accession: D53113

A;Status: preliminary

A;Molecule type: protein

A;Residues: 228-249 <PIK>

A;Experimental source: H66

A;Note: sequence extracted from NCBI backbone (NCBIP:141694)

C;Keywords: cysteine proteinase; hydrolase

Query Match 6.6%; Score 80.5; DB 2; Length 1704;

Best Local Similarity 22.4%; Pred. No. 2.3e+02;

Matches 61; Conservative 33; Mismatches 107; Indels 71; Gaps 12;

Qy 5 BEINKDLRKKSELOQTALGNLQIYYNNKAITSSKAD-QFLTNLLFKGFTGHWP 63

Db 1075 EPIITAKGVSPAIRIGTQWRQ-----KTVDLPAGTKYVAFRHFSQDPMF 1121

Qy 64 YNDL-----LVLDLSTAAATSEY-----EGSSVDLYGAYGYQCA----- 97

Db 1122 YIDLDEVEIKANGKRAEDTETPESSTHGEAFABWTTIDADGGQGLCLSSGQLDLTAH 1181

Qy 98 GGTGPKNTACWYGVTLHNNRL-----TEKKV-----PINLWIDGKQTTVPIDKVKTSK 148

Db 1182 GGTNVVAFSFWNGMALNPENYLSKDVTCATKYKYIYVNDGFGDHYAVMISKITG 1241

Search completed: August 12, 2004, 13:33:09

Job time : 11.3708 secs

Qy 149 ETVQVQ-ELDQARHYLHGKFLYNSDSFGKVKQ-----RGLIVFHSSEGSTV 194

Db 1242 DFTVVFEETPNCINKGARFGL-STEANGAKQSPQSWIERTVDLPAGTKYVAFRHYNCSDL 1300

Qy 195 SYDLPD-----AQQYP-----DTLLRIYRDNTTI 219

Db 1301 NYILLDDIOFTWGGSPPTDYTYTVYRDGTGI 1332

RESULT 75

G82875

hypothetical protein UU558 [imported] - Ureaplasma urealyticum

C;Species: Ureaplasma urealyticum

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: G82875

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: the complete sequence of Ureaplasma urealyticum: Alternate views of a mini

A;Reference number: A82870

A;Accession: G82875

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1883 <GLA>

A;Cross-references: GB:AE002154; GB:AF222894; NID:G6899557; PIDN:AAF30971.1; GSPDB:GN001;

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: UU558

A;Genetic code: SGC3

Query Match 6.6%; Score 80.5; DB 2; Length 1883;

Best Local Similarity 22.4%; Pred. No. 2.6e+02;

Matches 49; Conservative 29; Mismatches 76; Indels 65; Gaps 10;

Qy 11 DLKKSELOQTALGNLQIYYNNKAITSSKADQFLTNLLFKGFTGHWPYNDLLVD 70

Db 814 DIKPSRLKA-----EYFYNDQ--NSQEQKNDNFKFGSVIEK----- 849

Qy 71 LGSTATSEYEGSSVDLYGAYGYQCAGTGNK-----TACWYGVTLHNNRLTEKKV 125

Db 850 -----PGLSKYDGLIKD-----GMGPIPKFKDGRIVY---KLHKKKH--PYK 890

Qy 126 PINLWIDGKQTTVPID-----KVKTSKKEVTVOEL-----DLQARHYLHGKF---G 168

Db 891 DIEILIKTKNTPVIDLSTCLKSDGTINRKLNEKVKREIQDSINSLIVKNYNGWDENG 950

Qy 169 LYNDSFGGKVGRLIVFHSSEGSTVSVDLFDAGQGYPD 207

Db 951 NFDTSMFNLKTYPDHPMFTSNEKRKWAERITDAMFKYPD 989

Search completed: August 12, 2004, 13:33:09

Job time : 11.3708 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:22:49 ; Search time 5.11863 Seconds
(without alignments)
2370.233 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEKDLRKSEBQ.....RDNTTISTSLISLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	90.9	257	1	ETXE STAAU
2	948	77.8	257	1	ETXA STAAW
3	611	50.2	258	1	ETXD STAAU
4	308	25.3	241	1	ETXH STAAW
5	284.5	23.4	266	1	ETC1 STAAW
6	277.5	22.8	266	1	ETC2 STAAU
7	269.5	22.1	251	1	SPEA STRPY
8	268.5	22.0	266	1	ETXB STAAU
9	263.5	21.6	266	1	ETC1 STAAU
10	241	19.8	258	1	ETXG STAAW
11	185	15.2	236	1	SPBG STRPY
12	183.5	15.1	234	1	SPEG STRPY
13	148.5	12.2	235	1	SPEC STRPY
14	100	8.2	234	1	TSTT STAAU
15	95.5	7.8	150	1	R19E THEVO
16	93	7.6	979	1	P115 MYCHR
17	91	7.5	1634	1	DPOL NETUA
18	90	7.4	447	1	LEC PARPC
19	88.5	7.3	150	1	R19E THEAC
20	88	7.2	419	1	TYPH MYCPI
21	86	7.1	1388	1	HRP3 SCHPO
22	84.5	6.9	443	1	PORD SEAE
23	84	6.9	1050	1	ITA5 XENLA
24	83.5	6.9	282	1	PRTA ASPNG
25	83	6.8	612	1	DNAX STRMU
26	82.5	6.8	308	1	TX30 CAEEL
27	82.5	6.8	314	1	RPOA LACPL
28	82.5	6.8	328	1	YB7D HAEIN
29	82.5	6.8	455	1	YWAD BACSU
30	82.5	6.8	600	1	NUCD ECOLI
31	82	6.7	607	1	DNAX STRPY
32	82	6.7	843	1	PURA THEMA
33	82	6.7	3718	1	LMA5 MOUSE

34	81	6.7	607	1	DNAX STRP3
35	81	6.7	609	1	DNAX STRA3
36	81	6.7	611	1	WDRI CAEEL
37	80.5	6.6	943	1	UNRA STRMU
38	80	6.6	345	1	PURA METJA
39	80	6.6	411	1	PGK METTH
40	80	6.6	1151	1	ITAI HUMAN
41	79.5	6.5	324	1	YE64 PASMU
42	79.5	6.5	637	1	VE1 HPV35
43	79.5	6.5	692	1	Y650 METJA
44	79	6.5	551	1	CHIT NPVAC
45	79	6.5	862	1	SLA2 BACAA
46	79	6.5	3695	1	LMA5 HUMAN
47	78.5	6.4	396	1	YJRI YEAST
48	78.5	6.4	413	1	SP74 YEAST
49	78.5	6.4	509	1	CLS1 BACAA
50	78.5	6.4	762	1	SLAP ACEKI
51	78	6.4	376	1	ADHI ORYSA
52	78	6.4	607	1	DNAX STRPN
53	78	6.4	607	1	DNAX STRR6
54	78	6.4	683	1	BGH3 RABIT
55	78	6.4	1157	1	XYNA THESA
56	78	6.4	1592	1	GTF2 STRDO
57	78	6.4	1914	1	RLF HUMAN
58	77.5	6.4	254	1	Y663 HAEIN
59	77.5	6.4	985	1	Y786 CORGL
60	77.5	6.4	1419	1	MDR PLAFF
61	77.5	6.4	2352	1	MOKC SCHPO
62	77	6.3	351	1	FEN AERPE
63	77	6.3	704	1	MSN2 YEAST
64	77	6.3	1597	1	GTF1 STRDO
65	76.5	6.3	284	1	YPV2 METTF
66	76.5	6.3	428	1	YQPI CAEEL
67	76.5	6.3	600	1	NUCD SALTY
68	76.5	6.3	635	1	ETFL YABAM
69	76.5	6.3	1689	1	RPAL SCHPO
70	76.5	6.3	2971	1	YCX9 CHLRE
71	76	6.2	247	1	PCNA HALMA
72	76	6.2	449	1	G6PI STRTR
73	76	6.2	509	1	YF08 MICPN
74	76	6.2	670	1	PBP STAAU
75	76	6.2	704	1	NEUL HUMAN
76	76	6.2	1165	1	PEX6 PICPA
77	76	6.2	1902	1	P2P LACPA
78	75.5	6.2	420	1	ALA5 HUMAN
79	75.5	6.2	457	1	GALS KUULA
80	75.5	6.2	814	1	SYL STAEF
81	75	6.2	316	1	MIAA TREPA
82	75	6.2	343	1	FEN PYRHO
83	75	6.2	349	1	PEN SULSO
84	75	6.2	445	1	SLP2 DROME
85	75	6.2	455	1	EPIC STAEF
86	75	6.2	479	1	CBSP SULSO
87	75	6.2	506	1	SYE BIFLO
88	75	6.2	596	1	TRX1 DROME
89	75	6.2	695	1	CICA PAEPP
90	75	6.2	808	1	DHG GLUOC
91	74.5	6.1	171	1	LACB STAEF
92	74.5	6.1	654	1	MCPC BACSU
93	74.5	6.1	676	1	HS70 BRELC
94	74.5	6.1	1887	1	FAS2 YEAST
95	74	6.1	380	1	ADH WALDO
96	74	6.1	406	1	G6PI CAMJE
97	74	6.1	449	1	G6PI STRA3
98	74	6.1	485	1	HOXA BRAJA
99	74	6.1	504	1	FLIC SALEN
100	74	6.1	507	1	FLGX BACSU

ALIGNMENTS

RESULT 1

```

ETXE STAAU          STANDARD;          PRT;    257 AA.
ID  ETXE STAAU          STANDARD;          PRT;    257 AA.
AC  P1293;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Enterotoxin type E precursor (SEE).
GN  ENTE.
OS  Staphylococcus aureus.
OX  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCBI_TaxID=1280;
RN  [1]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC  STRAIN=MJB265;
RX  MEDLINE=88257005; PubMed=3384800;
RA  Couch J.L., Soltis M.T., Betley M.J.;
RT  "Cloning and nucleotide sequence of the type E staphylococcal
RL  enterotoxin gens.";
RL  J. Bacteriol. 170:2954-2960(1988).
RN  [2]
RP  3D-STRUCTURE MODELING.
RX  MEDLINE=96022987; PubMed=7552730;
RX  Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT  "Residues defining V beta specificity in staphylococcal
RL  enterotoxins.";
RL  Nat. Struct. Biol. 2:680-686(1995).
CC  -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC  staphylococcal food poisoning syndrome. The illness characterized
CC  by high fever, hypotension, diarrhea, shock, and in some cases
CC  death.
CC  -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC  for the toxin interaction with MHC class II (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC  family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
CC  EMBL: M21319; AAA26617.1; --
CC  PIR: A28179; A28179.
CC  PDB: 1SEE; 1S-OCT-95.
CC  InterPro: IPR008992; Bact_endotox.
CC  InterPro: IPR006177; Bactr_tox.
CC  InterPro: IPR006123; Staph/Strep_toxin.
CC  InterPro: IPR006126; Staph/Strep_tox.
CC  InterPro: IPR006173; Staph_tox_OB.
CC  Pfam: PF02876; Staph_Strep_tox_C; 1.
CC  Pfam: PF01123; Staph_Strep_toxin; 1.
CC  PRINTS: PR00279; BACTR_TOXIN.
CC  PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC  PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW  Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW  3D-structure.
FT  SIGNAL          1 27
FT  CHAIN          28 257  ENTEROTOXIN TYPE E.
FT  METAL          211 211  ZINC (BY SIMILARITY).
FT  METAL          249 249  ZINC (BY SIMILARITY).
FT  METAL          251 251  ZINC (BY SIMILARITY).
FT  METAL          33 35  ZINC (BY SIMILARITY).
FT  HELIX          39 41
FT  STRAND         42 42
FT  TURN          46 47
FT  HELIX          48 51
FT  STRAND         52 54
FT  STRAND         59 64
FT  TURN          66 67
FT  STRAND         69 69

```

Query Match 90.9%; Score 1107; DB 1; Length 257;

Best Local Similarity 89.7%; Pred. No. 1.6e-89;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQDLTNTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQDLTNTLLFKGFFTG 84

QY 61 HPWNLDLVDLGSAAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDNNRLT 120

DB 85 HPWNLDLVDLGSAAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDNNRLT 144

QY 121 BEKVPINLMDGKQTTVPIDKVKTSKEVTQVQLDQARHLYHGKFLYNSDSFGSKVQ 180

DB 145 BEKVPINLMDGKQTTVPIDKVKTSKEVTQVQLDQARHLYHGKFLYNSDSFGSKVQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISSTLSLSLYLYTT 233

DB 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISSTLSLSLYLYTT 257

RESULT 2

ETXA STAAW

ID ETXA STAAW STANDARD; PRT; 257 AA.

AC F13163;

DT 01-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type A precursor (SEA).

GN ENTA OR MW1899.

OS Staphylococcus aureus (strain MW2), and

OS Staphylococcus aureus.

OX Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=196620; 1280;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MW2;

RX MEDLINE=22040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,

RA Yamamoto K., Hiramatsu K.

RT "Genome and virulence determinants of high virulence community-

RT acquired MRSA.";

RL Lancet 359:1819-1827(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PR1337.
 RA MEDLINE=89086892; PubMed=3335483;
 RX Bielew M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
 RL J. Bacteriol. 170:34-41(1988).
 RN [3]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=97222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
 RT Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RL "Crystal structure of the superantigen staphylococcal enterotoxin
 type A.";
 RN EMBO J. 14:3292-3301(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
 RA Abrahmsen L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding.";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [7]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 CC staphylococcal food poisoning syndrome. The illness characterized
 CC by high fever, hypotension, diarrhea, shock, and in some cases
 CC death.
 CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF004828; BAB95754.1; -;
 DR EMBL; M18970; AAA26681.1; -;
 DR PIR; A28664; A28664.
 DR PDB; 1BSF; 11-JUL-96.
 DR PDB; 1SXT; 19-NOV-97.
 DR PDB; 1DYO; 21-FEB-02.
 DR PDB; 114G; 21-MAR-01.

DR PDB; 114H; 21-MAR-01.
 DR PDB; 1LOS; 18-DEC-02.
 DR PDB; 1SEA; 15-OCT-95.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRL_TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 3).
 FT HELIX 28 31
 FT TURN 32 33
 FT HELIX 39 41
 FT TURN 44 45
 FT HELIX 46 55
 FT TURN 56 56
 FT STRAND 59 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 79 80
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 116
 FT TURN 118 119
 FT TURN 125 126
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 149
 FT STRAND 151 155
 FT TURN 156 157
 FT STRAND 158 160
 FT HELIX 164 166
 FT STRAND 167 171
 FT STRAND 173 175
 FT HELIX 176 191
 FT TURN 193 194
 FT HELIX 197 199
 FT TURN 200 200
 FT STRAND 205 212
 FT STRAND 218 221
 FT TURN 222 223
 FT HELIX 230 233
 FT HELIX 234 237
 FT TURN 238 239
 FT STRAND 242 244
 FT STRAND 248 255
 SQ SEQUENCE 257 AA; ADEBFSBCALF14577 CRC64;
 Query Match 77.8%; Score 948; DB 1; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-75;
 Matches 179; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTC 60
 DB 25 SEKSEINEKDLRKSELQGTALGNLKOIYYNEKAKTENKESHDFLOHTLLFKGFFTD 84
 QY 61 HPWYNLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 120

Db 85 HSWYNDLLVDFDSKIDVYKGRKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 180

Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSISLYTT 233

Db 205 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSISLYTT 257

RESULT 3

ETXD STAAU STANDARD; PRT; 258 AA.

AC P20723;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type D precursor (SED).

GN ENTD.

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89359112; PubMed=2549000;

RA Bayles K.W., Iandolo J.J.;

RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.;"

RL J. Bacteriol. 171:4799-4806(1989).

RN [2]

RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RC STRAIN=ATCC 23235;

RX MEDLINE=97157473; PubMed=9003758;

RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W.,

RA Dohlsten M.;

RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization.;"

RL EMBO J. 15:6832-6840(1996).

CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication by high fever, hypotension, diarrhea, shock, and in some cases death.

CC -1- SUBUNIT: Homodimer; zinc-dependent.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; M28521; AAB06195.1; -

DR PIR; A33953; A33953.

DR HSSP; P13163; LSXT.

DR InterPro; IPR006952; Bact_endotox.

DR InterPro; IPR006177; Bctrl_tox.

DR InterPro; IPR006123; Staph_Strep_toxin.

DR InterPro; IPR006126; Staph/Strep_tox.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF02876; Staph_Strep_tox_C7_1.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR PRINTS; PR00275; BACTETOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen; Zinc.

FT SIGNAL 1 25

FT CHAIN 26 258 ENTEROTOXIN TYPE D.

FT METAL 212 212 ZINC.

FT METAL 250 250 ZINC.

FT METAL 252 252 ZINC.

FT VARIANT 114 114 P->A (IN STRAIN ATCC 23235).

SQ SEQUENCE 258 AA; 29746 MW; 47766A28D42597FD CRC64;

Query Match 50.2%; Score 611; DB 1; Length 258;

Best Local Similarity 51.1%; Pred.No.3.6e-46;

Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

QY 1 SEKSEENEDLRKKSLOQTALCNLKIYYVNSKAITSEKSDADQFLNTLLFKGFTG 60

Db 26 NENIDSVKRELHKKSLSSTALNNMKGVSADKNPIGENKSTGDFLENTLYKFFTD 85

QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 86 LINFEDLLINFNSKEMAQHFKNVDVPIRYISVYGVGIBDRTACTYGGVTPHEGKCLK 145

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 180

Db 146 ERKIPINLWINGVQKEVSIDKVTDKKNVTVOELDLQARHYLQKDLKLYNDTLGGKI 205

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSISLYLY 231

Db 206 RGKIEFDSGSKSVSYDLFVKGDFPKQLRIYSDNKNLSTELHLDIYLY 256

RESULT 4

ETXH STAAU STANDARD; PRT; 241 AA.

AC Q53585;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type H precursor (SEH).

GN ENTH OR SEH OR MW0051.

OS Staphylococcus aureus (strain MW2), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.

OX NCBI_TaxID=196620, 1280;

RN [1]

RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.

RC STRAIN=D4508;

RX MEDLINE=95053699; PubMed=7964453;

RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,

RA Fischetti V.A., Zabriskie J.B.;

RT "Characterization and biological properties of a new staphylococcal exotoxin.;"

RL J. Exp. Med. 180:1675-1683(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MW2;

RX MEDLINE=22040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,

RA Yamamoto K., Hiramatsu K.;

RT "Genome and virulence determinants of high virulence community-acquired MRSA.;"

RL Lancet 359:1819-1827(2002).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).

RX MEDLINE=20444256; PubMed=10986116;

RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,

RA Atonsson P., Svensson L.A.;

RT "The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TCR molecules.;"

RL J. Mol. Biol. 302:527-537(2000).

CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.

CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.

CC -1- SUBCELLULAR LOCATION: Secreted.

```

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U11702; AAA19777.1; -.
DR EMBL; AF004822; BAB93916.1; -.
DR PDB; 1ENF; 10-JAN-01.
DR PDB; 1EWC; 10-JAN-01.
DR PDB; 1F77; 10-JAN-01.
DR PDB; 1HXV; 27-JUN-01.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
FT SIGNAL 1 24
FT CHAIN 25 241 ENTEROTOXIN TYPE H.
FT METAL 230 230 ZINC.
FT METAL 232 232 ZINC.
FT DISULFID 106 116
SQ SEQUENCE 241 AA; 27858 MW; 70F77985977616CE CRC64;

Query Match 25.3%; Score 108; DB 1; Length 241;
Best Local Similarity 33.9%; Pred. No. 9.7e-20;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

Qy 10 KDLRRKSELOGTALGNLKKQIYYNSKAITSESADQLNTLLFKGFTGHWPYNDLV 69
Db 25 EDLHDKSELTLALAN--AYQYNHPFKENIKSDEISGERKDLFRN--QGDSG-NDLRV 79

Qy 70 DLGSTATSEGEVSVDLYGAYVQACGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 80 KFATADLAQKFNKNDVIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVI GANV 138

Qy 130 WIDGQOTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGSKVGORGLIVFESS 189
Db 139 WVDGQKTEEL--ITFNKNQVTLQELDIKIRKLSDKKIYKDS---EISKGLIEFDMK 193

Qy 190 EGSTVSYDLFDAQQYPTLLRIYRDNNTTISSTLS-ISLYLYT 232
Db 194 TPRDYSFDIYDLKGENDYEIDKIVEDNKTLSDDISHDVNLVT 237

RESULT 5
ETC3_STAAM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN ETC3 OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;

```

```

RX MEDLINE=21311192; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.",
RT Lancet 357:1225-1240 (2001).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=90220508; PubMed=2325627;
RX Hovde C.J., Hackett S.P., Bohach G.A.;
RA "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins.",
RT Mol. Gen. Genet. 220:329-333 (1990).
RL [3]
RN X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malchioldi E.L., Li H., Yeern X., Stauffacher C.V.,
RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen.",
RT Nature 384:188-192 (1996).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP003364; BAB58171.1; -.
DR EMBL; AP003135; BAB43097.1; -.
DR EMBL; X51661; CAA35972.1; -.
DR PIR; S11885; S11885.
DR PDB; 1JCK; 12-NOV-97.
DR PDB; 1KLU; 02-AUG-02.
DR PDB; 1KLU; 14-AUG-02.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006136; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
KW Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137
SQ SEQUENCE 266 AA; 30671 MW; 5ED9A32D11FFCA59 CRC64;

Query Match 23.4%; Score 284.5; DB 1; Length 266;
Best Local Similarity 32.5%; Pred. No. 1.2e-17;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;

Qy 11 DLRRKSELOGTALGNLKKQIYYNSKAITSES-KSADQLNTLLFKGFTGHWPYNDLV 69
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;

```

Db 37 DLHKSSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDKKLKNYDKVKT 93
 Qy 70 DLGSTAATSEYSGSSVDLYGAYGYOC-----AGGTPNKTAQMYGGVTLHDNNRLTEE 122
 Db 94 ELLNEDLAKYKDBVVDVYGSNNYVNCYFSSKDNVGVTKGTCMYGGITKHEGNHFDNG 153
 Qy 123 --KKVPINLWIDGKQTVTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
 Db 154 NLQNLVRVY-ENKRTISFE-VQTKKSVTAQELDIKARNFINKNLYEFNS--SPYE 209
 Qy 181 RGLIVHSSEGSVSVYDLFDAQQYPD--TLRIYRDNTTISTSLISLYLT 232
 Db 210 TGYIKFIENNGNFWYDMPPAPGDKFDQSKYLMWYNDKTVDSKVKIEVHLT. 263

RESULT 6
 ETC2 STAAU STANDARD; PRT; 266 AA.
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ETC2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins."
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity."
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 staphylococcal food poisoning syndrome. The illness characterized
 by high fever, hypotension, diarrhea, shock, and in some cases
 death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 family.
 CC PIR; A60114;
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1CQV; 19-SEP-01.
 DR PDB; 1I4P; 19-SEP-01.
 DR PDB; 1I4Q; 19-SEP-01.
 DR PDB; 1I4R; 19-SEP-01.

PDB; 1I4X; 19-SEP-01.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph_tox_08.
 DR Pfam; PF02876; Staph_Strep_tox_C7; 1.
 DR Pfam; PF01123; Staph_Strep_coxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 27 ENTEROTOXIN TYPE C-2.
 FT CHAIN 28 266
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 44 44
 FT TURN 48 48
 FT STRAND 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT STRAND 73 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FBL8536FAC08 CRC64;
 Query Match 22.8%; Score 277.5; DB 1; Length 266;
 Best Local Similarity 31.1%; Pred. No. 5.1e-17;
 Matches 76; Conservative 47; Mismatches 102; Indels 19; Gaps 9;
 Qy 1 SEKSEENKDLKKKSELOQTALGNLKOIYYNKAITSSE-KSADQFLTNLLFKGFFT 59
 Db 27 AESQPDTPDELHKSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDK 83
 Qy 60 GHPWYNDLLVDLGSTAATSEYSGSSVDLYGAYGYOC-----AGGTPNKTAQMYGGVT 112
 Db 84 KLNVDKVKTELLNEDLAKYKDBVVDVYGSNNYVNCYFSSKDNVGVTKGTCMYGGIT 143
 Qy 113 LHDNNRLTEE--KKVPINLWIDGKQTVTPIDKVKTSKEVTVOELDLQARHYLHGKFLY 170

Db 144 KHEGNHFDNGNLQNLVIRV-ENKRNITSEB-VQTDKSKVTAQELDIKARNFLINKKNLY 201

Qy 171 NSDSFGKQVQGLIVFHSSEGSTSVYDLFDAGQYDP--TLRIYRNTWISSTLSISL 228

Db 202 EFNS--SPYETGYKFIENNGNTFWYDMPAGDKFDQSKYLMYNDKNTVDSKSVKIEV 259

Qy 229 YLYT 232

Db 260 HLTT 263

RESULT 7

SPEA STRPY STANDARD; PRT; 251 AA.

AC P08055;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (SPE A).

DE SPEA OR SPYM18 0393.

GN Streptococcus pyogenes, and

OS Streptococcus pyogenes (serotype M18).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314, 186103;

RN [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=86166804; PubMed=3514452;

RA Weeks C.R., Ferricelli J.J.;

RT "Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.";

RL Infect. Immun. 52:144-150(1986).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=86284313; PubMed=3526093;

RA Johnson L.P., L'Italian J.J., Schlievert P.M.;

RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B.";

RT Mol. Gen. Genet. 203:354-356(1986).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=MGAS8232 / Serotype M18;

RA MEDLINE=21927593; PubMed=11917108;

RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;

RA "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).

RN [4]

RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).

RA MEDLINE=99094887; PubMed=9878045;

RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B., O'Brien S.M., Tranter H.S., Acharya K.R.;

RT "Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell receptors.";

RT EMBO J. 18:9-21(1999).

CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever.

CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta chain.

CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; U40453; AAC48868.1; -

DR EMBL; X03929; CAA27568.1; -

DR EMBL; AB009982; AAL97141.1; -

DR PIR; A26152; A26152.

DR PDB; 1B12; 24-NOV-99.

DR PDB; 1FNU; 17-NOV-00.

DR PDB; 1FNV; 17-NOV-00.

DR PDB; 1FNW; 17-NOV-00.

DR PDB; 1HAS; 03-APR-02.

DR PDB; 1LOX; 03-APR-02.

DR InterPro; IPR008982; Bact_endotox.

DR InterPro; IPR006177; Bactrl_tox.

DR InterPro; IPR006123; Staph_Strep_toxin.

DR InterPro; IPR006126; Staph_Strep_tox.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF02876; Staph_Strep_tox_C1.

DR Pfam; PF01223; Staph_Strep_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW Toxin; Signal; 3D-structure; Complete proteome.

FT SIGNAL 1 30 EXOTOXIN TYPE A.

FT CHAIN 31 251

FT DISULFID 117 128

FT CONFLICT 6 6 K -> E (IN REF. 2).

FT CONFLICT 17 18 VT -> MK (IN REF. 2).

FT CONFLICT 25 35 SOEVFAQDDP -> LPKGICSTRPK (IN REF. 2).

FT CONFLICT 40 40 H -> Q (IN REF. 2).

FT CONFLICT 43 43 S -> N (IN REF. 2).

FT CONFLICT 47 59 NQNTLYFLYEGDP -> TEKIYFFMRVTL (IN REF. 2).

FT CONFLICT 129 129 I -> L (IN REF. 2).

FT CONFLICT 165 178 TNKQWTAQELDYK -> QIKNGCSRSYPT (IN REF. 2).

FT HELIX 36 38

FT HELIX 42 44

FT TURN 48 48

FT HELIX 49 56

FT STRAND 60 66

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 78

FT STRAND 82 82

FT TURN 83 84

FT STRAND 85 85

FT STRAND 87 91

FT HELIX 95 101

FT TURN 102 103

FT STRAND 105 110

FT STRAND 113 113

FT TURN 115 116

FT STRAND 126 130

FT STRAND 133 135

FT TURN 137 138

FT STRAND 140 153

FT TURN 154 155

FT STRAND 156 167

FT STRAND 169 171

FT HELIX 172 187

FT STRAND 199 205

FT STRAND 212 215

FT HELIX 224 227

FT STRAND 228 231

FT TURN 232 233

FT STRAND 236 238

FT TURN 239 241


```

relatedness to other pyrogenic toxins. ";
[2] Mot. Gen. Genet. 209:15-20(1987).
SEQUENCE OF 28-266.
MEDLINE=83213327; PubMed=6189824;
Schmidt J. J., Spero L.;
"The complete amino acid sequence of staphylococcal enterotoxin C1.";
J. Biol. Chem. 258:6300-6306(1983).
-!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcement/
or send an email to license@isb-sib.ch).
-----
EMBL; X05815; CRA92260.1; -.
PIR; S06356; ENSAC1.
HSSP; P34071; ISE2.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR06177; Bct_1_tox.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006126; Staph/Strep_tox.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF02876; Staph_Strep_tox_C; 1.
Pfam; PF01123; Staph_Strep_toxin; 1.
PRINTS; PR00279; BACTELTOXIN.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Enterotoxin; Toxin; Signal; Superantigen.
KW SIGNAL
FT 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFD 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
FT SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;
Query Match 21.6%; Score 263.5; DB 1; Length 266;
Best Local Similarity 30.6%; Pred. No.8.5e-16;
Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;
QY 1 SEKSEENEDIKPKSELQGTALGNLKOYV--VYNSKAITSSEKSAQOFLNTLLPKGFF 58
DB 27 AESQDPTPELHKASKFTG-LMNNKVLVDHYYS---ATKVSVDKFLAHLDIYISD 82
QY 59 TGHWPYNDLVLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACTMYGGV 111
DB 83 KKLKNYDKVKTELLNGLAKKYKDEVDVYGSNYVNCVFSSKNVGVKVGKTCMYGGI 142
QY 112 TLHNNRLTEE--KKVPINLWIDGKQTTPVDKVKTSKKEVTVOELDQARHYLHGKFL 169
DB 143 TKHSGNHFNDGNLQNVLLIRYV-ENKNTISFE-VQTDKSKSVTAQELDIKAFNFKNNL 200
QY 170 YNSDSFGKVGQRLGILVFHSSSEGSTVSVDLDAQGYPD--TLRLRYDNTTISSTLSIS 227
DB 201 YEFNS--SPVETGYIKFENNGNTPFYDMWPAFGKFFQSKYLMYNDNKTVDKSVKIE 258
QY 228 LYLVT 232
DB 259 VHLT 263
RESULT 10
ETXG STAAH STANDARD; PRT; 258 AA.
ID ETXG STAAH
OC O85382;

```

QY	3	KSEINEKDLRRKSELGCTALGNKQLIYY---YNSKAITSSKSAOQFLTNLLFGGFTT 59
DB	30	KLDELINKSVSDYKNN--KGT-MGNVMNLYTSPVPEGRGVINSR---QFLSHDLIFP---I 79
QY	60	GHPWYNDLLVDLGSATSTSEYEGSSVDLYGAYGYOCA-----GGTPNKATCM 104
DB	80	EYKSNVEKTELENTVELANNYKDKVDIFGVPFYTCIIIPKSEPDINQPPG-----CCM 134
QY	108	YGVTLH--DNNRITEKKVPINLWIDGKOTTPIWDIKVTKTSKKEVTVOELDQARHYLHG 165
DB	135	YGLGLTFSSENER--DKLITVQVTIDNRQSLG--FTTTNKNMVTIQELDYKARHWLTK 189
QY	166	REGLVNSDSFGKVQRGGLIIVPHSSEGSTVSYDLFDAGQGYPDT---LLRTYRDNTTIST 222
DB	190	EKLTYEFD--GSAPESGVIKTEKNITSFWDLFPFKELVFPVYKFLNIYGDNKVDK 247
QY	223	SLISISLYLT 232
DB	248	SIKMEVFLNT 257
RESULT 11		
SPEH_STRPY		
ID	SPEH_STRPY	STANDARD; PRT; 236 AA.
AC	Q9X5C8;	
DT	16-OCT-2001	(Rel. 40, Created)
DT	16-OCT-2001	(Rel. 40, Last sequence update)
DT	10-OCT-2003	(Rel. 42, Last annotation update)
DE	Exotoxin type H precursor (SPE H).	
GN	SPEH OR SPY1008.	
OS	Streptococcus pyogenes.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI_TaxID=1314;	
RL	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=M15;	
RC	MEDLINE=993093428; PubMed=9874566;	
RT	Prof T. Moffatt S.L., Berkahn C.J., Fraser J.D.;	
RT	"Identification and characterization of novel superantigens from	
RT	Streptococcus pyogenes";	
RL	J. Exp. Med. 189:189-192(1999).	
RL	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=SF370 / ATCC 700294 / Serotype M1;	
RC	MEDLINE=21192684; PubMed=11296296;	
RA	Ferretti J.J., McShan W.M., Ajdic D.J., Savić D.J., Savić G., Lyon K.,	
RA	Prineaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,	
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,	
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;	
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.;"	
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).	
CC	!- SUBUNIT: Mitogenic for human peripheral blood lymphocytes.	
CC	!- FUNCTION: Binds to major histocompatibility complex class II beta	
CC	chain.	
CC	!- SUBCELLULAR LOCATION: Secreted.	
CC	!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin	
CC	family.	

This SWISS-PROT entry is copyright. It is produced through a collaboration		
between the Swiss Institute of Bioinformatics and the EMBL Outstation		
the European Bioinformatics Institute. There are no restrictions on its		
use by non-profit institutions as long as its content is in no way		
modified and this statement is not removed. Usage by and for commercia		
entities requires a license agreement (see http://www.isb-sib.ch/announcement		
or send an email to license@isb-sib.ch).		

CC	EMBL; AF124500; AAD30989.1; -	
DR	EMBL; AE006546; AAK33907.1; -	
DR	PDB; 1ET9; 24-MAY-00.	
DR	PDB; 1EU4; 24-MAY-00.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR006123; Staph/Strep_toxin.	

```
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strp_tox_C; 1.
DR Pfam: PF01123; Staph_Strp_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; Complete proteome; 3D-structure.
KW SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 236 EXOTOXIN TYPE H.
FT CHAIN 33 236 EXOTOXIN TYPE H.
SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 15.2%; Score 185; DB 1; Length 236;
Best Local Similarity 26.7%; Pred. No. 5.3e-09;
Matches 56; Conservative 46; Mismatches 84; Indels 24; Gaps 9;

Qy 25 NLKQIYVNSKAI-TSSEKADQFLNTLLFKGFTGHPWYN-----DLLVDLGSSTAATSE 79
Db 42 NLESYKXHSNLIBADSIKNSPDIVTSHML-----KYSVKDKNLSVFFKDWISQE 92
Qy 80 YEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHNNRLTEEEKKVPINLWIDGKQTTVP 139
Db 93 FKXKEVDIYALSAQEVCE--CPGRXYEARFGGITLTNSEK--KEIKVPVNVWDSKQ--P 146
Qy 140 IDKVKTSKKEVTVQELDLQARHYLHGKFLGNSDFGKVGKQVGLIVFHSSEGSTVSYDL- 198
Db 147 PMFITVNRKPKVTAGEDIKVRKLLIKYDIYNNRE--QKYSKGTVTLLDLSGDKDIVFDLY 204
Qy 199 FDAQGVPTLLRIYRDNTTISSTLSLSISL 228
Db 205 YFGNGDP-NSMLKYSNNERIDSTQFHVQV 233

RESULT 12
SPEC STRPY STANDARD; PRT; 234 AA.
AC Q9X5G7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type G precursor (SPE G).
GN SPEC OR SPY0212.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=99093428; PubMed=9874556;
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes."
RL J. Exp. Med. 189:89-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF124499; RAD30988.1; -.
CC EMBL; AE006489; AAK33303.1; -.
CC HSSP; PI3380; 1AN8.
CC InterPro: IPR008992; Bact_endotox.
CC InterPro: IPR006177; Bctrl_tox.
CC InterPro: IPR006123; Staph/Strep_toxin.
CC InterPro: IPR006126; Staph/Strep_tox.
CC InterPro: IPR006173; Staph_tox_OB.
CC Pfam; PF02876; Staph_Strp_tox_C; 1.
CC Pfam; PF01123; Staph_Strp_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC Toxin; Signal; Complete proteome.
KW SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
FT CHAIN 25 234 EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 15.1%; Score 183.5; DB 1; Length 234;
Best Local Similarity 27.6%; Pred. No. 7e-09;
Matches 56; Conservative 37; Mismatches 81; Indels 29; Gaps 7;

Qy 33 NSKAITSSKSDAQFLNTLLFKGFTGHPWYNLLVDLGSSTAATSEYEGSSVDLYGAYY 92
Db 57 NSIHINTKQRSECL-----YVDSIVSLGIT--DQFIKDKVDVFLPY 99
Qy 93 GYQCAGGTPNKATCMYGGVTLHNNRLTEEEKKVPINLWIDGKQTTVPIDKVKTSKEVTV 152
Db 100 NF-----SPYVDNTYGGIVKHSNQGKSLQFVGI-LNQDGKETVLPSEAVIKKKQFTL 153
Qy 153 QELDLQARHYLHGKFLGNSDFGKVGKQVGLIVFHSSEGSTVSYDLFDAQGV--PDTLL 210
Db 154 QEFDPKIRKFLMEKYNIDSES---RYTSGSLFLATKSKHYEVDLFNKDDLKLSRDSFF 210
Qy 211 RIYRDNTTISSTLS-LSLYLT 232
Db 211 KRYKDKNFNSEISHFDIYLT 233

RESULT 13
SPEC STRPY STANDARD; PRT; 235 AA.
AC PI3380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=88314303; PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C."
RL Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=92363541; PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Molecular population genetic evidence of horizontal spread of two
RT alleles of the pyrogenic exotoxin C gene (speC) among pathogenic
RT clones of Streptococcus pyogenes."
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
```

SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RA "Complete genome sequence of an M1 strain of *Streptococcus*
 RT *pyogenes*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
 RX MEDLINE=97397352; PubMed=9253413;
 RA Rousset A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
 RT "Crystal structure of the streptococcal superantigen SPE-C:
 RT dimerization and zinc binding suggest a novel mode of interaction
 RT with MHC class II molecules.";
 RL Nat. Struct. Biol. 4:635-643(1997).
 CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
 CC fever, have been associated with streptococcal toxic shock-like
 CC disease and may play a role in the early events of rheumatic
 CC fever.
 CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M35514; AAA27017.1; ALT_SEQ.
 DR EMBL; M97156; AAB59091.1; -.
 DR EMBL; M97157; AAB59092.1; -.
 DR EMBL; AE006523; AK33664.1; -.
 DR EIR; A30509; A30509.
 DR EIR; A44799; A44799.
 DR PDB; 1AN8; 29-APR-98.
 DR PDB; 1KTK; 07-JUN-02.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 3D-structure; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 235 EXOTOXIN TYPE C.
 FT CONFLICT 53 53 N -> D (IN REF. 1).
 FT HELIX 33 44
 FT STRAND 49 59
 FT STRAND 63 67
 FT HELIX 69 72
 FT TURN 74 75
 FT STRAND 77 81
 FT HELIX 84 87
 FT TURN 88 89
 FT TURN 92 93
 FT STRAND 95 100
 FT TURN 108 109
 FT STRAND 110 114
 FT STRAND 117 119
 FT STRAND 127 128
 FT STRAND 131 135

FT TURN 136 137
 FT STRAND 141 142
 FT TURN 144 145
 FT STRAND 148 149
 FT STRAND 153 155
 FT HELIX 156 171
 FT TURN 173 174
 FT TURN 176 177
 FT STRAND 182 189
 FT TURN 190 191
 FT STRAND 194 198
 FT TURN 204 205
 FT HELIX 208 212
 FT STRAND 213 217
 FT STRAND 220 222
 FT HELIX 223 225
 FT STRAND 226 235
 SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
 Query Match 12.2%; Score 148.5; DB 1; Length 235;
 Best Local Similarity 23.8%; Pred. No. 8.1e-06;
 Matches 58; Conservative 39; Mismatches 85; Indels 45; Gaps 11;
 QY 34 SKAITSEKSADQFLNTLLFKGFFTGHPW-VNDLLVDLGSTAA-----TSEYEGSS---- 84
 DB 22 SPIIKSDSKDISNVKSDLLYA--YITPVDYKNCRVNFTTHTLNDITQYRGKDYIS 79
 QY 85 -----VDLYGAYGYQCAGTPTKACMYGGVTLDHNRLEKKVPIN 128
 DB 80 SEMSEYASQKFKEDHVDVDFGLFYILNHTG-----EYTGITPAQNNKVNH--KLLGN 132
 QY 129 LWIDGQTTVPIDKVTSKVETVQELDLQARHLGKFGLYNSDS--FGGKVQORGLIVF 186
 DB 133 LFTSGSQQLNNKILKIDKIVTFQIDFKIKYLMNDYKIYDATSPYVSGRIEIG---- 188
 QY 187 HSSEGSTVSVDLFDA--QGQYPTLLRIYRDNNTTISTSLIS-LSLYL 230
 DB 189 -TXDGGHEQIDLFDSFNEGTRSDIFAK-YKDNRIINMKNFHFDIYL 233
 RESULT 14
 TSST STAAU STANDARD; PRT; 234 AA.
 AC P06886;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Toxic shock syndrome toxin-1 precursor (TSSST-1).
 GN TST.
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=87057222; PubMed=3782090;
 RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
 RA Schlievert P.M.;
 RT "The nucleotide and partial amino acid sequence of toxic shock
 RL J. Biol. Chem. 261:15783-15786(1986).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94150598; PubMed=8107781;
 RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
 RA Brehm R.D., Tranter H.S.;
 RT "Structural basis of superantigen action inferred from crystal
 RT structure of toxic-shock syndrome toxin-1.";
 RL Nature 367:94-97(1994).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94092653; PubMed=8268150;
 RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlivert P.M.,
 RA Ohlendorf D.H.;

RT "Structure of toxic shock syndrome toxin 1.":
RL Biochemistry 32:13761-13766(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
RX MEDLINE=96319751; PubMed=8759320;
RA Papageorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RA Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RT 2.07-A resolution.";
RL J. Mol. Biol. 260:553-569(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=97337442; PubMed=9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dingas M.W., Cook W.J., Schlvert P.M., Ohlendorf D.H.;
RT "Refined structures of three crystal forms of toxic shock syndrome
RT toxin-1 and of a tetramer with reduced activity.";
RL Protein Sci. 6:1220-1227(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE=98254504; PubMed=9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlvert P.M., Ohlendorf D.H.;
RT "Structures of five mutants of toxic shock syndrome toxin-1 with
RT reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
RN [7]
CC -!- FUNCTION: Responsible for the symptoms of toxic shock syndrome.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J02615; AAA26682.1; --
DR PIR: A24606; XCSAS1.
DR PDB: 2TSS; 24-DEC-97.
DR PDB: 3TSS; 24-DEC-97.
DR PDB: 4TSS; 24-DEC-97.
DR PDB: 5TSS; 24-DEC-97.
DR PDB: 1QIL; 12-AUG-97.
DR PDB: 2QIL; 12-AUG-97.
DR PDB: 1AW7; 18-NOV-98.
DR PDB: 1TS2; 16-DEC-98.
DR PDB: 1TS3; 16-DEC-98.
DR PDB: 1TS4; 16-DEC-98.
DR PDB: 1TS5; 16-DEC-98.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph_exotoxin.
DR InterPro: IPR006173; Staph_tox OB.
DR InterPro: IPR006125; Staph_toxin.
DR Pfam: PF02876; Staph_Strep_tox C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR01800; STAPHSTREP_TOXIN.
DR PRINTS: PR01501; TOXICSHOCK_TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Superantigen; Signal; 3D-structure.
FT SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
FT HELIX 46 54
FT STRAND 58 69
FT TURN 70 71
FT STRAND 72 76
FT TURN 78 79
FT STRAND 82 86

FT TURN 91
FT TURN 98
FT STRAND 101 108
FT STRAND 113 114
FT TURN 116 117
FT STRAND 120 125
FT STRAND 128 129
FT STRAND 133 138
FT STRAND 142 146
FT TURN 147 148
FT STRAND 149 151
FT STRAND 159 161
FT STRAND 163 164
FT HELIX 166 181
FT TURN 183 185
FT TURN 187 188
FT STRAND 192 198
FT TURN 199 200
FT STRAND 203 207
FT TURN 208 209
FT HELIX 214 216
FT STRAND 221 222
FT HELIX 223 225
FT STRAND 226 234
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;

Query Match 8.2%; Score 100; DB 1; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.14;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

QY 25 NLKQI---YYNSKAITSE-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
DB 45 NIKLLDWYSSSDFTNSEVLDSLSGMRINKTGDGI-SLIIFPS-----EYSPAFK 98
QY 69 ---VILGSTAAITSEGGSSVDLYGAYGYQCAGGTPNTACMYGGVTLHNNRLTEKKV 125
DB 99 GKVKDL-NTRTKKSGHTS---EGTVHFQISGVT-----NTEKLTPIEL 140
QY 126 ENLWIDGKQTVDPDKVTSKVTQQLDLQARHYLHGKFLY-NSPSFGG--KVQSG 182
DB 141 PLKVKVHGKDSPLKYGP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDXTGYSWKIT-- 197
QY 183 LIVFHSSEGSTVSIDL 198
DB 198 -----MNDGSTVQSDL 208

RESULT 15
R19E THEVO STANDARD; PRT; 150 AA.
ID R19E THEVO
AC Q97CU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19E.
GN RPS19E OR TV0007 OR TVG0008143.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasma;
CC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=1121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshita T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: AP000591; BAB59149.1; -
 DR InterPro: IPR001286; Ribosomal_S19E.
 DR Pfam: PF01090; Ribosomal_S19E; 1.
 DR ProDom: PD003854; Ribosomal_S19E; 1.
 DR PROSITE: PS00628; RIBOSOMAL_S19E; FALSE NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 150 AA; 17063 MW; FD5881CF684EB415 CRC64;

Query Match 7.8%; Score 95.5; DB 1; Length 150;
 Best Local Similarity 29.3%; Pred. No. 0.2;
 Matches 23; Conservative 17; Mismatches 37; Indels 1; Gaps 1;

QY 116 NNRLETEKKVPINLWDGKQTTVPIDKVTSKSEVTVQELDLQARHYLHGKFLYN-SDS 174
 DB 17 SGKLEKKIKENWVKYKTSKSEKPLQDDWIVYRAAAMRLKLYINGLIGISMSE 76
 QY 175 FGKVGORGLIVFHSSEGS 192
 DB 77 YGKVGDRGSKRYHAASGS 94

RESULT 16
 ID P115_MYCHR STANDARD; PRT; 979 AA.
 AC P41508;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P115 protein.
 OS Mycoplasma hyorhinis.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2100;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91138990; PubMed=1825306;
 RA Notarnicola S.M., McIntosh M.A., Wise K.S.;
 RT "A Mycoplasma hyorhinis protein with sequence similarities to
 RT nucleotide-binding enzymes."
 RL Gene 97:77-85(1991).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- DOMAIN: Consists of two putative central coiled-coil regions
 CC flanked by putative globular regions at the N- and C-termini.
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. SIMILAR TO OTHER MYCOPLASMA
 CC P115.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: M34956; AAA25423.1; -
 DR PIR: JQ0894; JQ0894.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR005289; GTP-binding_dom.
 DR InterPro: IPR003405; SMC C.
 DR InterPro: IPR003395; SMC N.
 DR Pfam: PF02483; SMC C; 1.
 DR Pfam: PF02463; SMC N; 1.
 DR TIGRfam: TIGR00650; MG442; 2.
 KW ATP-binding; Coiled coil.
 DR NP_BIND 32 39 ATP (POTENTIAL).
 FT DOMAIN 169 224 COILED COIL (POTENTIAL).
 FT DOMAIN 231 400 COILED COIL (POTENTIAL).
 FT

FT DOMAIN 569 821 COILED COIL (POTENTIAL).
 FT DOMAIN 884 912 ALA/ASP-RICH (DA-BOX).
 SQ SEQUENCE 979 AA; 110566 MW; 30D51C56B56280F4 CRC64;
 Query Match 7.6%; Score 93; DB 1; Length 979;
 Best Local Similarity 23.3%; Pred. No. 3.3;
 Matches 55; Conservative 41; Mismatches 92; Indels 48; Gaps 9;

QY 17 ELQGTALGNLQKQIVYNSKAITSSKSADQ-----FLTNLLPKGFPTGH 61
 DB 56 QLRLG---NMDDVIFAGSKVKQEKAMVKLTFNEDAETKQITISRLLRGGGTNE 112
 QY 62 PWNDDLIV---DLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCAMY---GGVTLHD 115
 DB 113 YFYNDQPVRYKDIKNLAVESGISKSLAITSQGTISEIAEATPEQKAVIEAAGTSKYK 172
 QY 116 NNRLETEKKVPINLWDGKQTTVPIDKVTSKSEVTVQELDLQ---ARHYLHGKFLY 170
 DB 173 LDKEEAQKKL-----ITNDAILQQAIEKLERQVNSLDKQAKKIYLEKSKALE 224
 QY 171 NSDSFGSKVQORGLIV---FHSSEGSTVSVDLFDQAQQVPTLLRIYRNTTISST 222
 DB 225 S-----VEVGLIVNDLNFNEKLNNTLSLLEVBQQRNDLELNLTQTVYESSISQT 273

RESULT 17
 ID DPOL_METJA STANDARD; PRT; 1634 AA.
 AC Q58255;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
 DE intein].
 DN POL OR Mj0885.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Keriavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.F., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).
 CC -1- PFM: This protein undergoes a protein self splicing that involves
 CC a post-translational excision of the intervening region (intein)
 CC followed by peptide ligation (Potential).
 CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U67532; AAB98889.1; -
 DR HSSP: P56689; ITGO.
 DR TIGR: Mj0885; -
 DR InterPro: IPR006172; DNA_pol_B.
 DR


```

RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513 (2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AL445063; CAC11198.1; -
DR InterPro; IPR001266; Ribosomal_S19E.
DR Pfam; PF01090; Ribosomal_S19e; 1.
DR ProDom; PD003854; Ribosomal_S19e; 1.
DR PROSITE; PS00628; RIBOSOMAL_S19E; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 150 AA; 17109 MW; F3215035CE0DC22C CRC64;

Query Match 7.3%; Score 88.5; DB 1; Length 150;
Best Local Similarity 26.9%; Pred. No. 0.81;
Matches 21; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 116 NNPLTEKKVPINLWDGQTTVPIDKVTSEKVTQVQLDQARHYLHKGGLYN-SDS 174
DB 17 SEKLSEKIAEPDWSKYKVTGISREKSPVNDWIYVRAAAMLRKLYINGILGRMSSE 76
QY 175 FGKVGQGLIVFHSRGS 192
DB 77 YGKVDGRGSKRYHAAQS 94

RESULT 20
TYPH_MYCPI
ID TYPH_MYCPI STANDARD; PRT; 419 AA.
AC P47717;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thymidine phosphorylase (EC 2.4.2.4) (TdrPase).
DE DECO.
OS Mycoplasma pium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2122;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BER;
RX MEDLINE=93352438; PubMed=8349569;
RA Tham T.N., Ferris S., Kovacic R., Montagnier L., Blanchard A.;
RT "Identification of Mycoplasma pium genes involved in the salvage
RT pathways for nucleosides."
RL J. Bacteriol. 175:5281-5285 (1993).
CC -!- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
CC OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
CC COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
CC OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
CC ribose 1-phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the thymidine/pyrimidine-nucleoside
CC phosphorylase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/

```

```

CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L13289; AAA25432.1; -
DR PIR; C53312; C53312.
DR HSSP; P77836; 1BRW.
DR InterPro; IPR000312; Glyco trans 3.
DR Pfam; PF02885; Glycos transf 3N; 1.
DR PIRSF; PIRSF000478; Thymid phosphis; 1.
DR ProDom; PD001864; Glyco trans 3; 1.
DR ProDom; PD005916; Thymid phosphis; 1.
DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 419 AA; 47278 MW; C1620F2EF33929E3 CRC64;

Query Match 7.2%; Score 88; DB 1; Length 419;
Best Local Similarity 27.0%; Pred. No. 3.2;
Matches 38; Conservative 22; Mismatches 57; Indels 24; Gaps 7;

QY 47 FLTNLLFKG-FTGHPWYNDLLVGLGTAATSE-----YEGSSVDLYGAYG 93
DB 57 FLTKAMIDSGKIYKHFPEYKKILIDKHSTGIGKVSIALRPIVLSFDLGVAKLSRGLG 116
QY 94 YQACAGTPTNKTACMYGGVTLHNNRITTEKKV--PINLWDGK-QTTVPIDKVKTSKEY 150
DB 117 F--TGGTIDKLE---SINVTIDLKNKKILNIANMFVGTNDIVPADKLYALRDV 170
QY 151 --TVQELDLQARHYLHKGGL 169
DB 171 TGTVDLSPLIAASILSKKFAL 191

RESULT 21
HRP3_SCHPO
ID_HRP3_SCHPO STANDARD; PRT; 1388 AA.
AC Q14139;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chromodomain helicase hrp3.
GN HRP3 OR SPAC3G6.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hounsbury T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McJann J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkhardt G., Aert R., Robben J., Grymprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Bozzym K., Langer I., Beck A., Lehtach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,

```

RA Cezutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2].
RP GENE NAME, FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=22122317; PubMed=12127990;
RA Yoo E.J., Jang Y.K., Lee M.A., Ejerling P., Kim J.B., Ekwall K.,
RA Seong R.H., Park S.D.;
RT "Hrp3, a chromodomain helicase/ATPase DNA binding protein, is required
RL for heterochromatin silencing in fission yeast.";
RL Biochem Biophys. Res. Commun. 295:970-974(2002).
CC -!- FUNCTION: Involved in heterochromatin silencing. Required for
CC transcriptional repression at the silence loci of mat3, where it
CC has a direct role as a chromatin remodeling factor.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
CC -!- SIMILARITY: Contains 2 chromo domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z99167; CAB16277.1; -
CC PIR; T38720; T38720.
CC GeneDB SPombe; SPAC3G6.01; -
CC InterPro; IPR000953; Chromo.
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR001650; Helicase_C.
CC InterPro; IPR000330; SNF2_N.
CC Pfam; PF00385; chromo; 2.
CC Pfam; PF00271; helicase_C; 1.
CC Pfam; PF00176; SNF2_N; 1.
CC SMART; SM00298; CHROMO; 2.
CC SMART; SM00487; DEXDC; 1.
CC SMART; SM00490; HELICC; 1.
CC PROSITE; PS00598; CHROMO 1; 1.
CC PROSITE; PS00013; CHROMO 2; 2.
CC PROSITE; PS00690; DEAD ATP HELICASE; FALSE NEG.
CC Transcription regulation; Hydrolase; Helicase; Repressor;
CC Nuclear protein; ATP-binding; DNA-binding; Repeat.
CC Domain 169 175 POLY-GLU.
CC DOMAIN 191 260 CHROMO 1.
CC DOMAIN 288 349 CHROMO 2.
CC NP_BIND 400 407 ATP (POTENTIAL).
CC SITE 508 511 DEAD BOX.
CC DOMAIN 947 950 POLY-GLU.
CC SEQUENCE 1388 AA; 159377 MW; F7B431084BD29F8D CRC64;

Query Match 7.1%; Score 86; DB 1; Length 1388;
Best Local Similarity 25.1%; Pred. No. 21;
Matches 45; Conservative 27; Mismatches 69; Indels 38; Gaps 10;

QY 35 KAITSSERSAQDFLNT-----LTFKGF-----FTGHWPYNDLLVGLGTAATSEYE 81
DB 1047 KAVSAEKLNDQNNKSSKALLITFKGVNNAETLVORLNDLDI-LYDAMPTSGYS 1105

QY 82 GSSVDLY-GAYGYQACGTPNKTCMYGVTLH-----DNNRLTEKKVPINLWI 131
DB 1106 NFQIPMVRSHVGSQWG-PREDSMLLSGICKGFGAWLEIRDDPELKMCKIFLE--- 1161

QY 132 DGKQT--TVPIDKYTSKKEVTQVQLDQARHYL-----HGKGLYNSD--SFGGKVQ 180
DB 1162 DTQTDNSVPKDKENKCKVPSAVHLVRGEGYLLSALREHFQNGIKSSPAISNTKIQ 1220

RESULT 22
PORD_PSEAE STANDARD; PRT; 443 AA.
ID FORD_PSEAE

AC P32722;
AC 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Porin D precursor (EC 3.4.21.-) (Outer membrane protein D2)
DE (Imipenem/basic amino acid-specific outer membrane pore).
DE OFRD OR PA0596.
GN Pseudomonas aeruginosa.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OC NCBI TaxID=287;
OC [1]_TaxID=287;
RN SEQUENCE FROM N.A.
RP MEDLINE=93037310; PubMed=1339257;
RX Yoneyama H., Yoshihara E., Nakae T.;
RA "Nucleotide sequence of the protein D2 gene of Pseudomonas
RT aeruginosa.";
RL Antimicrob. Agents Chemother. 36:1791-1793(1992).
RN [2].
RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-40.
RC STRAIN=ATCC 15692 / PAO1 / H103;
RX MEDLINE=93051258; PubMed=1427017;
RA Huang H., Siehnell R.J., Bellido F., Rawling E., Hancock R.E.W.;
RT "Analysis of two gene regions involved in the expression of the
RT imipenem-specific, outer membrane porin protein OprD of Pseudomonas
RT aeruginosa.";
RL FEMS Microbiol. Lett. 76:267-273(1992).
RN [3].
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [4].
RP SEQUENCE OF 24-48.
RX MEDLINE=94282208; PubMed=8012497;
RA Michea-Hamzehpour M., Sanchez J.-C., Epp S.F., Paquet N., Hughes G.J.,
RA Hochstrasser D.F., Pechere J.-C.;
RT "Two-dimensional polyacrylamide gel electrophoresis isolation and
RT microsequencing of Pseudomonas aeruginosa proteins.";
RL Enzyme Protein 47:1-8(1993).
RN [5].
RP CHARACTERIZATION.
RX MEDLINE=90368779; PubMed=2118530;
RA Trias J., Nikaido H.;
RT "Protein D2 channel of the Pseudomonas aeruginosa outer membrane has
RT a binding site for basic amino acids and peptides.";
RL J. Biol. Chem. 265:15680-15684(1990).
RN [6].
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=97000016; PubMed=8843159;
RA Yoshihara E., Gotoh N., Nishino T., Nakae T.;
RT "Protein D2 porin of the Pseudomonas aeruginosa outer membrane bears
RT the protease activity.";
RL FEBS Lett. 394:1179-1182(1996).
RN [7].
RP MUTAGENESIS OF HIS-179; ASP-231; SER-319 AND HIS-390, AND ACTIVE
RP SITES.
RX MEDLINE=98300298; PubMed=9636669;
RA Yoshihara E., Yoneyama H., Ono T., Nakae T.;
RT "Identification of the catalytic triad of the protein D2 protease in
RT Pseudomonas aeruginosa.";
RL Biochem. Biophys. Res. Commun. 247:142-145(1998).
CC -!- FUNCTION: Porin with a specificity for basic amino acids. Also
CC possesses serine protease activity.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

CC -|- SIMILARITY: Belongs to peptidase family 843.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X63152; CAA44855.1; -;
 CC EMBL; Z14065; CAA78448.1; -;
 CC EMBL; AE004529; AAG04347.1; -;
 CC PIR; S23771; S23771.
 CC MEROPS; S43.001; -;
 CC GO; GO:0045203; C: integral to external outer membrane (sensu . . .); IDA.
 CC GO; GO:0015288; F: porin activity; IDA.
 CC GO; GO:0008236; F: serine-type peptidase activity; IDA.
 CC GO; GO:0015802; P: basic amino acid transport; IDA.
 CC InterPro; IPR005318; Peptidase_S43.
 CC Pfam; PF03573; OprD; 1.
 CC Hydrolase; Serine protease; Transport; Outer membrane; Transmembrane;
 KW Porin; Signal; Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 443 PORIN D.
 FT ACT_SITE 179 179
 FT ACT_SITE 231 231
 FT ACT_SITE 319 319
 FT MUTAGEN 179 179
 FT MUTAGEN 231 231
 FT MUTAGEN 319 319
 FT MUTAGEN 390 390
 FT MUTAGEN 443 443
 FT CONFLICT 44 44 L -> Y (IN REF. 2).
 FT SEQUENCE 443 AA; 48360 MW; E083FFE074DCB64 CRC64;
 Query Match 6.9%; Score 84.5; DB 1; Length 443;
 Best Local Similarity 23.2%; Pred. No. 6.9;
 Matches 60; Conservative 30; Mismatches 98; Indels 71; Gaps 14;
 QY 15 KSLQGTALGNLQIYYVNSKAITSEKSDQFLTNLLFKGFFTGHPWYNDLLVGLST 74
 Db 34 KGIEDSSLDLLRNYYFRDCKSGGDRVD-----WTQGLFTY-----ESGFT 78
 QY 75 AATSEYEGSSVDLYGAYGYQCAGGTPNKTA-----CMYGGVTLHDNNRLTBEKVPIN- 128
 Db 79 QGT---VGFVDVAFG-YLGLK-LDGTSDTGTGNLPVNDGKPRDDYSRAGGAVKVRISK 133
 QY 129 ---LWIDGKQTTVPIDKVTSK-----KEVTVOELDLQARHYLHGK----- 166
 Db 134 TMLKWGE-WQPTAPVFAAGSRLFPQTATGFLQSSPEGLDLEAGHFTGKEPTTVKSR 192
 QY 167 ---FGLY-----NSDSFGKQVRGLIVFHSSEGSTVSVDLFDACQGPDTLLRIYRNT 217
 Db 193 GELYATYAGETAKSADFIGR-----YAITDNLASLYGAELEDIYRQY-----YLSNYS 242
 QY 218 TI---SSTSLISLYLYTT 233
 Db 243 TIPLASDQSLGDFNIYRT 261
 RESULT 23
 ITAS_XENLA STANDARD; PRT; 1050 AA.
 AC Q06274;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integrin alpha-5 precursor (Fibronectin receptor alpha subunit)
 DE (Integrin alpha-F) (VLA-5).
 OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=95344994; PubMed=7619730;
 RA Jocs T.O.; Whittaker C.A.; Meng F.; Desimone D.W.; Gnau V.;
 RA Hausen P.;
 RA "Integrin alpha 5 during early development of Xenopus laevis.";
 RT Mech. Dev. 50:187-199(1995).
 RL [2]
 RN SEQUENCE OF 318-393 FROM N.A.
 RP MEDLINE=94008528; PubMed=8404528;
 RX Whittaker C.A.; Desimone D.W.;
 RA "Integrin alpha subunit mRNAs are differentially expressed in early
 RT Xenopus embryos.";
 RL Development 117:1239-1249(1993).
 CC -|- FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN.
 CC IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
 CC -|- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
 CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
 CC DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -|- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12683; AAA99668.1; -;
 CC EMBL; L10191; AAA16249.1; -;
 CC PIR; I51527; I51527.
 CC HSP; P06756; IJUV2.
 CC InterPro; IPR000413; Integrin_alpha.
 CC Pfam; PF01839; FG-GAP; 4.
 CC Pfam; PF00357; Integrin_A; 1.
 CC SMART; SM00191; Integrin_A; 5.
 CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 KW Signal; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 1050 INTEGRIN ALPHA-5.
 FT CHAIN 33 932 INTEGRIN ALPHA-5 HEAVY CHAIN (POTENTIAL).
 FT CHAIN 933 1050 INTEGRIN ALPHA-5 LIGHT CHAIN (POTENTIAL).
 FT DOMAIN 33 996 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 997 1022 POTENTIAL.
 FT DOMAIN 1023 1050 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 48 110 FG-GAP 1.
 FT REPEAT 120 188 FG-GAP 2.
 FT REPEAT 189 246 FG-GAP 3.
 FT REPEAT 259 312 FG-GAP 4.
 FT REPEAT 313 373 FG-GAP 5.
 FT REPEAT 379 438 FG-GAP 6.
 FT REPEAT 442 494 FG-GAP 7.
 FT CA_BIND 324 332 POTENTIAL.
 FT CA_BIND 390 398 POTENTIAL.
 FT CA_BIND 454 462 POTENTIAL.
 FT SITE 1025 1029 GPFKR MOTIF.
 FT DISULFID 90 99 BY SIMILARITY.
 FT DISULFID 145 166 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 502 513 BY SIMILARITY.
 FT DISULFID 519 575 BY SIMILARITY.
 FT DISULFID 636 642 BY SIMILARITY.
 FT DISULFID 708 721 BY SIMILARITY.
 FT DISULFID 862 910 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 917 922 BY SIMILARITY.

```

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 714 714 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 861 861 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 1050 AA; 115961 MW; 10ED961535B8D918 CRC64;

Query Match 6.9%; Score 84; DB 1; Length 1050;
Best Local Similarity 21.9%; Pred. No. 22;
Matches 60; Conservative 38; Mismatches 94; Indels 82; Gaps 14;

QY 12 LRKSEIQ-GTALGNLKOIYYNKAITS-SEKADQFLNTLLFKGFTGHPWYNDLIV 69
DB 242 LEYKQMTQROAASYSDDSYFGYVAVGEFSEDATEDFV-----GVPKGNITYGYVTI 295
QY 70 DLGSTAATSEYEGSSVDLYGAYVQVACAGTPNKTA---CMYGGVTLHD---NNRLTEEK 123
DB 296 -LNGTDLRLSYNFGEQM-ASYFGYSVATDLNSDGLDILLGAPLPMWRTHDGRVQEVG 353
QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTYVQELDLQARHYLHGKFG-----LYNSDS---- 174
DB 354 RVVVVLQGDHMESTPHL--ILTMEE-----YGRFGSSIASLGDLDDQDGFN 397
QY 175 -----FGGKQVQGLI-VFHSSEGSTVSYDLFDAQOQ-----SSTLSIS 227
DB 398 DIATGAPGGAQAGVAFIFNGQGVGVDSKPSQVLOGGSSQOQSPFFGLSTRGCHLDG 457
QY 205 --YPTLLRIYRDNNTTI-----SSTLSIS 227
DB 458 NGYPDLIYVAGVDTLLVYRGRPIIHASASLSIS 491

RESULT 24
PRTA ASPNG STANDARD; PRT; 282 AA.
AC P24665;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE Aspergillopepsin II precursor (EC 3.4.23.19) (Acid protease A)
DE (Protease A).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Var. Macrosporus;
RA MEDLINE=92011747; PubMed=1918060;
RA Inoue H., Kimura T., Makabe O., Takahashi K.;
RT "The gene and deduced protein sequences of the zymogen of Aspergillus
RT niger acid proteinase A.";
RL J. Biol. Chem. 266:19484-19489 (1991).
RN [2]
RP SEQUENCE OF 60-98 AND 110-282.
RC STRAIN=Var. Macrosporus;
RA MEDLINE=92011746; PubMed=1918059;
RA Takahashi K., Inoue H., Sakai K., Kohama T., Kitahara S.,
RA Takashima K., Tanji M., Athauda S.B.P., Takahashi T., Akanuma H.,
RA Mamiya G., Yamasaki M.;
RT "The primary structure of Aspergillus niger acid proteinase A.";
RL J. Biol. Chem. 266:19480-19483 (1991).
RN [1]
RP CATALYTIC ACTIVITY: Preferential cleavage in A chain of insulin:

```

```

CC 3-Asn-Gln-4, 13-Gly-Ala-14, and 26-Tyr-Thr-27.
CC -! SUBUNIT: Heterodimer of two noncovalently bound light and heavy
CC chains.
CC -! SIMILARITY: Belongs to peptidase family A4.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M68871; AAA32687.1; -.
CC DR 21R; A41025; A41025.
CC DR MEROPS; A04.002; -.
CC DR InterPro; IPR000250; Peptidase_A4.
CC DR Pfam; PF01828; Peptidase_A4; 1.
CC DR PRINTS; PR00977; SCYTLDEPTASE.
CC DR ProDom; PD018627; AspartylproteaseA4; 1.
CC KW Hydrolase; Aspartyl protease; Zymogen; Signal;
CC KW Pyroliidone carboxylic acid. POTENTIAL.
CC FT SIGNAL 1 18
CC FT PROPEP 19 59 ASPERGILLOPEPSIN II LIGHT CHAIN.
CC FT CHAIN 60 98
CC FT PROPEP 99 109 ASPERGILLOPEPSIN II HEAVY CHAIN.
CC FT CHAIN 110 282
CC FT MOD_RES 110 110 PYRROLIDONE CARBOXYLIC ACID.
CC FT DISULFID 115 139
CC FT DISULFID 127 210
CC SQ SEQUENCE 282 AA; 29887 MW; 4EA727F9AE33F72A CRC64;

Query Match 6.9%; Score 83.5; DB 1; Length 282;
Best Local Similarity 19.2%; Pred. No. 4.8;
Matches 52; Conservative 34; Mismatches 102; Indels 83; Gaps 10;

QY 13 RKSEIQGTALGNLKOIYYNKAITSSEKADQFLNTLLFKGFTGHPWYNDLIVDLG 72
DB 28 RKEARAAGKRHSNPPYIPGSDKEILKNGTNEEYSSN-----WAGAVLIGDG 75
QY 73 STAATSEYEGSSVDL-----YGAVYGY-----QCAG-----GTPNKTCMYGG 110
DB 76 YTKVTGFTVPSVSAGSSGSGYGGYGNKRNQSEECASAWVGIDGDTCTETAILQGT 135
QY 111 VTLHNNRLTEKKVPEINLWI-----DGKQTTVPIDKVKTSKEVTYVQEV 154
DB 136 VDF-----CYEDQTSYDAWYEPDYAYDFSDITISEGDSIKVTVEATSKSGSATVEN 190
QY 155 LDL--CARHYLHGKF-----GLYNSDSFGKVGKQGLIVHSSB-----GSTV 194
DB 191 LTGQSVTHTFSGNVEGDLCEETNAEWIVDFSGDSLVAFAFDGSGVFTFNABATSGGIV 250
QY 195 SYDLFDAQOQYPTLLRIYRDNNTTISSTLS 225
DB 251 -----GPSDATVMDIEQDGSVLTETSVS 273

RESULT 25
DNAX STRMU STANDARD; PRT; 612 AA.
AC O06942;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaX (Heat shock protein 70) (Heat shock 70 kDa
DE protein) (HSP70).
GN DNAX OR SMU.82.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.

```


Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Mc Kenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.P., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;

"Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";

Science 269:496-512(1995).

- !- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE COMPONENT I.

-----CC

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

-----CC

EMBL; U12797; AAC22834.1; -

PIR; F64187; F64187.

TIGR; H11170; -

InterPro; IPR005801; Anth synth chor.

Pfam; PF00425; chorismate_bind_1.

PRINTS; PR00085; ANTSNTHASEI.

ProDom; PD000779; Anth synth_chor; 1.

Hypothetical protein; Anth_complete proteome.

SW SK SEQUENCE 328 AA; 37734 MW; 1C02BCD0088957B0 CRC64;

-----CC

Query Match 6.8%; Score 82.5; DB 1; Length 328;

Best Local Similarity 27.3%; Pred. No. 7; 1;

Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;

QY 136 TTPIDKVKTSKEVT--VQELDQARHYLHGKGLYNSDFGKVKQRLI-----V 185

Db 237 TLLPAGSISGAPKEKTKTQIIQAQEKQRCGYTCIGIFDGKTLQSAVAIRFISQVDEKFY 296

QY 186 FHSSEGSTVSYDLFDAQGYPTLLRIY 213

Db 297 FHSGGITIH---SNAQDYEELLEKVV 321

RESULT 29

YVAD BACSU STANDARD; PRT; 455 AA.

AC P25152;

ID YVAD BACSU

AD P25152;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical peptidase yvad precursor (EC 3.4.11.-).

GN YVAD OR IPA-8R OR BSU38470.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC MEDLINE=95020537; PubMed=7934828;

RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,

RA Hullo M.F., Ionescu M., Dubochinsky B., Marcelino L., Mosser I.,

RA Prescan E., Santana M., Schneider E., Schweizer J., Vertes A.,

RA Rapoport G., Panchin A.;

RA "Bacillus subtilis genome project: cloning and sequencing of the 97

RL kb region from 325 degrees to 333 degrees.";

RL Mol. Microbiol. 10:371-384 (1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=168;

RC MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.C., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Eriington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Hollappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kunita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipatt R., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256 (1997).
 RN [3]
 RP SEQUENCE OF 1-68 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=92216127; PubMed=1806041;
 RA Glaser P., Kunst F., Debarbouille M., Vertes A., Danchin A.,
 RA Dedonder R.,
 RT "A gene encoding a tyrosine tRNA synthetase is located near sacs in
 RT Bacillus subtilis.";
 RL DNA Seq. 1:251-261 (1991).
 CC -1- SIMILARITY: Belongs to peptidase family M28B.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X73124; CAAS1564.1; -
 DR EMBL; Z99123; CAB15873.1; -
 DR EMBL; X52480; CAAS36725.1; -
 DR PIR; S39663; S39663.
 DR MEROPS; M28.U0P5; -
 DR Subtilisin; BG10554; ywaD.
 DR InterPro; IPR003137; PA.
 DR InterPro; IPR007484; Peptidase_M28.
 DR Pfam; PF04225; PA; 1.
 DR Pfam; PF04369; Peptidase M28; 1.
 KW Hypothetical protein; Hydrolase; Amino peptidase; Metalloprotease;
 KW Zinc; Signal; Complete proteome.
 FT SIGNAL 31 31
 FT CHAIN 32 455 HYPOTHETICAL PEPTIDASE YWAD.
 SQ SEQUENCE 455 AA; 49450 MW; 89E6A6EEB0CE18 CRC64;
 Query Match 6.8%; Score 82.5; DB 1; Length 455;
 Best Local Similarity 22.0%; Pred. No. 11;
 Matches 41; Conservative 25; Mismatches 67; Indels 53; Gaps 6;
 QY 1 SEKSEFINKDKRKSELOGTALGNLKIYYNYSKAITSEKSAQDF-----LNTLTLFK 55
 Db 53 SQLSEAIQPR-----IAGTAAEKKSALLIASNRKILKLDVKVQRFNIPDRLEGLTSSA 105

QY 56 GFTTGHFWYNDLIVDGLSTAASTSEYSGSSVDLYGAYGYOCAGGTNKTACMYGVTLLHD 115
 Db 106 G-----RDILQAASGAPTEEQGLTAPLYNAGLGYO-----KDFADAKGKIALIS 152
 QY 116 NNRLT-----EKKVPINLMDGKQTTVPIDKVK-----TSK 147
 Db 153 RGLTYTYEKAARAEAKAVIYNKESLVPMTNLSGNKVGIPVVGKEDGEALTOQ 212
 QY 148 KEVTQV 153
 Db 213 KEATLK 218
 RESULT 30
 NUCD ECOLI
 ID NUCD ECOLI STANDARD; PRT; 600 AA.
 AC P33599; P33600; P78089; P78309;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-quinone oxidoreductase chain C/D (EC 1.6.99.5) (NADH
 DE dehydrogenase I, chain C/D) (NDH-1, chain C/D) (NUO3/NUO4).
 GN NUO3 OR NUO4 OR NUO3 OR NUO4 OR B2286.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / AN387;
 RX MEDLINE=93389724; PubMed=7690854;
 RA Weidner U., Geier S., Ptock A., Friedrich T., Leif H., Weiss H.;
 RT "The gene locus of the proton-translocating NADH: ubiquinone
 RT oxidoreductase in Escherichia coli. Organization of the 14 genes and
 RT relationship between the derived proteins and subunits of
 RT mitochondrial complex I.";
 RL J. Mol. Biol. 233:109-122 (1993).
 RN [2]
 RP REVISIONS
 RC STRAIN=K12 / AN387;
 RA Weidner U.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1230-1244 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97349980; PubMed=9205837;
 RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itch T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT analysis of its sequence features.";
 RL DNA Res. 4:91-113 (1997).
 RN [5]
 RP SEQUENCE OF 179-600 FROM N.A.
 RX MEDLINE=94209210; PubMed=8157582;
 RA Pruss B.M., Nels J.M., Park C., Wolfe A.J.;
 RT "Mutations in NADH:ubiquinone oxidoreductase of Escherichia coli
 RT affect growth on mixed amino acids.";
 RL J. Bacteriol. 176:2143-2150 (1994).

CC and skin. Expressed in many tissues in embryonic day 11.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI, IV and G are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -!- SIMILARITY: Contains 2 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 2 laminin IV domains.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ293593; CAB99255.1; -
CC EMBL; U37501; AAC53430.1; -
CC PIR; T10053; T10053.
CC HSSP; P02468; 1TLE.
CC MGD; MGI:105382; Lama5.
CC GO; GO:0005684; C:basement membrane; IDA.
CC GO; GO:0005178; F:integrin binding; IDA.
CC GO; GO:0030324; P:lung development; IMP.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00053; laminin_B; 1.
CC Pfam; PF00054; laminin_G; 2.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC ProDom; PD003031; Laminin_B; 1.
CC SMART; SM00180; EGF_Lam; 20.
CC SMART; SM00281; LamB; 1.
CC SMART; SM00282; LamG; 5.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 19.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01248; LAMININ TYPE EGF; 19.
CC PROSITE; PS50025; Lam_G DOMAIN; 5.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 40
FT CHAIN 41 3718 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 305 363 LAMININ EGF-LIKE 1.
FT DOMAIN 364 433 LAMININ EGF-LIKE 2.
FT DOMAIN 434 479 LAMININ EGF-LIKE 3.
FT DOMAIN 500 546 LAMININ EGF-LIKE 4.
FT DOMAIN 547 592 LAMININ EGF-LIKE 5.
FT DOMAIN 593 637 LAMININ EGF-LIKE 6.
FT DOMAIN 638 682 LAMININ EGF-LIKE 7.
FT DOMAIN 683 728 LAMININ EGF-LIKE 8.
FT DOMAIN 729 781 LAMININ EGF-LIKE 9.
FT DOMAIN 782 833 LAMININ EGF-LIKE 10.
FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 856 1442 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12.
FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13.
FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14.
FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15.
FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1643 1831 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1832 1864 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1865 1914 LAMININ EGF-LIKE 17.
FT DOMAIN 1915 1970 LAMININ EGF-LIKE 18.

FT DOMAIN 1971 2024 LAMININ EGF-LIKE 19.
FT DOMAIN 2025 2071 LAMININ EGF-LIKE 20.
FT DOMAIN 2072 2188 LAMININ EGF-LIKE 21.
FT DOMAIN 2119 2169 LAMININ EGF-LIKE 22.
FT DOMAIN 2169 2735 DOMAIN II AND I.
FT DOMAIN 2736 2933 LAMININ G-LIKE 1.
FT DOMAIN 2947 3119 LAMININ G-LIKE 2.
FT DOMAIN 3128 3296 LAMININ G-LIKE 3.
FT DOMAIN 3337 3511 LAMININ G-LIKE 4.
FT DOMAIN 3518 3689 LAMININ G-LIKE 5.
FT DOMAIN 2205 2257 COILED COIL (POTENTIAL).
FT DOMAIN 2330 2464 COILED COIL (POTENTIAL).
FT DOMAIN 2604 2621 COILED COIL (POTENTIAL).
FT DOMAIN 2639 2705 COILED COIL (POTENTIAL).
FT SITE 1723 1725 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1839 1841 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 305 314 BY SIMILARITY.
FT DISULFID 307 327 BY SIMILARITY.
FT DISULFID 329 338 BY SIMILARITY.
FT DISULFID 341 361 BY SIMILARITY.
FT DISULFID 364 373 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 401 410 BY SIMILARITY.
FT DISULFID 413 431 BY SIMILARITY.
FT DISULFID 434 445 BY SIMILARITY.
FT DISULFID 436 452 BY SIMILARITY.
FT DISULFID 454 463 BY SIMILARITY.
FT DISULFID 466 476 BY SIMILARITY.
FT DISULFID 500 512 BY SIMILARITY.
FT DISULFID 502 521 BY SIMILARITY.
FT DISULFID 523 532 BY SIMILARITY.
FT DISULFID 535 544 BY SIMILARITY.
FT DISULFID 547 559 BY SIMILARITY.
FT DISULFID 549 566 BY SIMILARITY.
FT DISULFID 568 577 BY SIMILARITY.
FT DISULFID 580 590 BY SIMILARITY.
FT DISULFID 593 605 BY SIMILARITY.
FT DISULFID 595 611 BY SIMILARITY.
FT DISULFID 613 622 BY SIMILARITY.
FT DISULFID 625 635 BY SIMILARITY.
FT DISULFID 638 650 BY SIMILARITY.
FT DISULFID 640 656 BY SIMILARITY.
FT DISULFID 658 667 BY SIMILARITY.
FT DISULFID 670 680 BY SIMILARITY.
FT DISULFID 683 695 BY SIMILARITY.
FT DISULFID 685 702 BY SIMILARITY.
FT DISULFID 704 713 BY SIMILARITY.
FT DISULFID 716 726 BY SIMILARITY.
FT DISULFID 1443 1455 BY SIMILARITY.
FT DISULFID 1445 1482 BY SIMILARITY.
FT DISULFID 1464 1473 BY SIMILARITY.
FT DISULFID 1476 1486 BY SIMILARITY.
FT DISULFID 1533 1548 BY SIMILARITY.
FT DISULFID 1535 1555 BY SIMILARITY.
FT DISULFID 1557 1566 BY SIMILARITY.
FT DISULFID 1569 1579 BY SIMILARITY.
FT DISULFID 1582 1594 BY SIMILARITY.
FT DISULFID 1584 1601 BY SIMILARITY.
FT DISULFID 1603 1612 BY SIMILARITY.
FT DISULFID 1615 1630 BY SIMILARITY.
FT DISULFID 1865 1874 BY SIMILARITY.
FT DISULFID 1867 1881 BY SIMILARITY.
FT DISULFID 1884 1893 BY SIMILARITY.
FT DISULFID 1896 1912 BY SIMILARITY.
FT DISULFID 1915 1930 BY SIMILARITY.
FT DISULFID 1917 1939 BY SIMILARITY.
FT DISULFID 1941 1950 BY SIMILARITY.
FT DISULFID 1953 1968 BY SIMILARITY.
FT DISULFID 1971 1986 BY SIMILARITY.
FT DISULFID 1973 1993 BY SIMILARITY.
FT DISULFID 1996 2005 BY SIMILARITY.
FT DISULFID 2008 2022 BY SIMILARITY.
FT DISULFID 2072 2083 BY SIMILARITY.

RA Radune D., Fedorova N.B., Scanlan D., Khouiri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.B., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.,
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Rioux C.R., Martin D., Hamel J., Brodeur B.R.;
RT "Heat shock protein HSP70 and amino terminus of DnaJ of Streptococcus
RT agalactiae";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL766843; CAD45741.1; -;
DR EMBL; AE014196; AAM95005.1; -;
DR EMBL; U72719; AAB39219.1; -;
DR HSSP; P04475; LDG4.
DR SagalList; gbs0096; -;
DR TIGR; SAG0097; -;
DR HAVAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR Chaperone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
KW MOD_RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 173 173
SQ SEQUENCE 609 AA; 64980 MW; 298D8ADCC9D31E0C CRC64;

Query Match 6.7%; Score 81; DB 1; Length 609;
Best Local Similarity 27.0%; Pred. No. 21;
Matches 37; Conservative 19; Mismatches 63; Indels 18; Gaps 5;

Qy 69 VDLGST-AATSEYEGSSVDLYGAYGQCAGGTPTKTCMYGGVTLHDNNRLTEBEKVPI 127
Db 7 IDLGTNSAVALEGTESKIITANPEGNRT---TPSVVSFKNGEIIIVGDAKRAQVTPNPT 63

Qy 128 NLWDGKQTTVPIDKVTSKTEVTVOELDLQARHYLHGKFLGNSDSFGGKVGRLIVFH 187
Db 64 VISIKSKMGT--SEKVSANGKEYTPQEISAMILQYLKG---YAEDYLGEKVERAVI--- 114

Qy 188 SSEGSTVSVDLYDAQGQ 204
Db 115 -----TVPAYFNDAQRQ 126

RESULT 36
WDRI CAEEL STANDARD; PRT; 611 AA.
AC Q11176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Actin interacting protein 1 (AIP1) (Uncoordinated protein 78).
GN UNC-78 OR C04F6.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=21157410; PubMed=11257131;
RA Ono S.;
RT "The Caenorhabditis elegans unc-78 gene encodes a homologue of
RT actin-interacting protein 1 required for organized assembly of muscle
RT actin filaments";
RL J. Cell Biol. 152:1313-1320(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nhan M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Induces disassembly of actin filaments in conjunction
CC with ADP/cofilin family proteins. Regulator of actin organization
CC in myofibrils.
CC -!- SIMILARITY: Belongs to the WD-repeat AIP1 family.
CC -!- SIMILARITY: Contains 9 WD repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF324437; AAK11613.1; -;
DR EMBL; U42835; AAB3588.1; -;
DR PIR; T15410; T15410.
DR WormPep; C04F6.4; CE03924.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 9.
DR PRINTS; PR00320; GPROTEINBREP.
DR ProDom; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 10.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00682; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Actin-binding; Cytoskeleton; Repeat; WD repeat.
FT REPEAT 57 96
FT REPEAT 145 185 WD 1.
FT REPEAT 188 227 WD 3.
FT REPEAT 237 276 WD 4.
FT REPEAT 322 361 WD 5.
FT REPEAT 446 485 WD 6.
FT REPEAT 489 528 WD 7.
FT REPEAT 534 573 WD 8.
FT REPEAT 579 610 WD 9.
SQ SEQUENCE 611 AA; 65323 MW; 821452C661B5D27A CRC64;

Query Match 6.7%; Score 81; DB 1; Length 611;
Best Local Similarity 18.7%; Pred. No. 21;
Matches 53; Conservative 46; Mismatches 78; Indels 106; Gaps 12;

Qy 23 LGNLKOIYYNSKAITTSSEKSDAQFLTNLTLLFKGPFTGH--PW-----YNDLLVLDLST 74
Db 313 LGSIDQVRYCHNKAITALSSAD----GKTLFSADAEGHINSWDSTGISNRVFPDVHAT 368

Qy 75 AATSEYEGSSVDLYGAYG-----GYQCAGGTPTK-----TA 105
Db 369 MITGIKTTSGDLFTVSWDDHLKVPAGSGVDSSKAVANKLSQPLGLAVSADGDIAVA 428

Qy 106 CMYGGVTLHDNNRLTEBEKVPI-----LWIDGKQTTVPIDKV---KTSKK 148
Db 429 ACYKHAIYSHGKLT-----VPISYNSCVVALSNDKQFVAVGGQDSKVHYKLUSGASVSV 485

Qy 149 EVTVQVELDL-----QAR-----HYLHGKFLGNSDSFGGKVGRLIVFHS 188
Db 486 KTIIVHAEITSVAFSNNGAFLVATDQSRKVIPIVSVANNFELAHNSW-----TFHT 536

OY 189 SEGSTVSYDLFDAQGOVPTDRLRIYEDNTTISSTISISLYLY 231
 DB 537 AKVACVSW- - - - -PDNVLATGSLDNSVIVW 563

RESULT 37

UVRU_STRMU STANDARD; PRT; 943 AA.
 AC P72481;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A).
 GN UVRU OR SMU.1851.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;
 RX MEDLINE=22295063; PubMed=12397186;
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
 Carson M.B., Primeaux C., Tian K., Kenton S., Jia H., Lin S., Qian Y.,
 Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
 pathogen."; Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
 RL [2]
 RP SEQUENCE OF 469-604 FROM N.A.

RC STRAIN=GS-5;
 RA Peruzzi F., Pigott P.J., Daneo-Moore L.;
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
 processing of DNA lesions. UvrA is an ATPase and a DNA-binding
 protein. A damage recognition complex composed of 2 UvrA and 2
 UvrB subunits scans DNA for abnormalities. When the presence of a
 lesion has been verified by UvrB, the UvrA molecules dissociate
 (By similarity).
 CC -!- SUBUNIT: Forms a heterotetramer with UvrB during the search for
 lesions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the ABC transporter family. UvrA subfamily.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AEC15012; AAN59473.1; -;
 CC EMBL; U75479; AAB41197.1; -;
 CC HAMAP; MF 0205; -; 1.
 CC InterPro; IPR003439; ABC transporter.
 CC InterPro; IPR004602; UvrA.
 CC Pfam; PF00005; ABC_tran; 1.
 CC ProDom; PD000006; ABC transporter; 1.
 CC TIGRFAMs; TIGR00630; UvrA; 1.
 CC PROSITE; PS00211; ABC TRANSPORTER 2; 1.
 CC PROSITE; PS00893; ABC TRANSPORTER 2; 1.
 CC SOS response; Excision nuclease; DNA repair; DNA recombination;
 CC DNA excision; ATP-binding; DNA-binding; Repeat; Zinc; Metal-binding;
 CC Zinc-finger; Complete proteome.
 FT NP_BIND 32 39 ATP (POTENTIAL).
 FT ZN_FING 251 278 C4-TYPE.
 FT NP_BIND 641 648 ATP (POTENTIAL).
 FT ZN_FING 740 766 C4-TYPE.
 SQ SEQUENCE 943 AA; 104118 MW; 8DB3B8F588B86212 CRC64;

Query Match

6.6%; Score 80.5; DB 1; Length 943;

Best Local Similarity 26.7%; Pred. No. 39;
 Matches 47; Conservative 21; Mismatches 61; Indels 47; Gaps 8;
 OY 21 TALG-NLKQIYY- - - - -NSKAITSEKSAQFLNTLLPKGFFTHPYNDL 67
 DB 501 TQIGSNLSGLVYLDEPSIGLHQDNDRLISSLKMRD--LGNTLIWVERHEDTMAADW 558
 OY 68 LVDLGSTAATSEYEGSSVDLYGAYGVQCAGGTPNKTACMYGVGTLDHNNRLTEEEKVPI 127
 DB 559 LVDVGPCA- - - - -GALGGEIVASGTTPROVAKNKISIT---GOYLSGKKIP- 601
 OY 128 NLWIDGQTTVPIDKVKTSKEVTVO---ELDQARH--YLHKGFLGYNDSDFGK 178
 DB 602 - - - - -VPLDRRKSGRFEIKGAENNLQINVKFPLKFTIAVTGVSQSGK 647

RESULT 38

PURA_METUA STANDARD; PRT; 345 AA.
 AC Q57981;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
 DE (AdSS) (AMPase).
 GN PURA OR MJ0561.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8689087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 Kertlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii"; Science 273:1058-1073 (1996).
 RL [1]
 CC -!- FUNCTION: Plays an important role in the de novo pathway of purine
 nucleotide biosynthesis.
 CC -!- CATALYTIC ACTIVITY: GTP + IMP + L-aspartate = GDP + phosphate +
 adenylosuccinate.
 CC -!- COFACTOR: Binds 1 magnesium ion per subunit (By similarity).
 CC -!- PATHWAY: AMP biosynthesis; first committed step.
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the adenylosuccinate synthetase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U67505; AAB98554.1; -;
 CC EMBL; A64370; A64370.
 CC HSP; P12283; IADE.
 CC TIGR; M00561; -;
 CC HAMAP; MF 00011; -; 1.
 CC InterPro; IPR001114; Asucc synthetase.
 CC Pfam; PF00709; Adenylsucc synt; 1.
 CC ProDom; PD001188; Asucc synthetase; 1.
 CC TIGRFAMs; TIGR00184; PURA; 1.
 CC PROSITE; PS01286; ADENYLOSUCIN_SYN_1; 1.

DR PROSITE; PS00513; ADENYLOSUCIN SYN 2; FALSE NEG.
KW Purine biosynthesis; Ligase; GTP-binding; Metal-binding; Magnesium;
Complete proteome.
FT NP_BIND 18 24 GTP (POTENTIAL).
FT ACT_SITE 144 144 BY SIMILARITY.
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 48 48 MAGNESIUM (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
SQ SEQUENCE 345 AA; 37820 MW; 9974D8C30D1DEE72 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 345;
Best Local Similarity 22.6%; Pred. No. 13;
Matches 44; Conservative 33; Mismatches 60; Indels 58; Gaps 11;

QY 4 SEENIEK-DLRKSELOQTALGNLKOIYYNSKAITSEKSADOFINT-----51
DB 166 SEEYNALDRGENVLIEGTQ-GTLISLYGYPTVTSKDTASSFAADVIGPTKVDEVI 224
QY 52 LLFKGFFT---GHPWYNDLLDLGTAATSEYEGSSVDLYG-----AYGYQCAGG 99
DB 225 VVKTFTRVCGAGFPFEMSL-----EAESLGIVEYGVTVGRRRRVGYDFELA-- 274
QY 100 TPNKTACMYGVT-----LHNNRLTEKKVPINLWIDGKQTTVPIDKV 143
DB 275 ---RKACRLNGATQIALTGIDKYDCEGVTEYNKLSKAKEFINK-IE-EVTGVPVTII 329
QY 144 KTSKKEVTQELDLQ 158
DB 330 STGPE--WHQTIDLR 342

RESULT 39
ID_PGK_METTH STANDARD; PRT; 411 AA.
AC 027121;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR WH1042.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzaden R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155 (1997).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
phospho-D-glycerol phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcements/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AB000876; AAB85538.1; --
DR PIR; B69006; B69006.
DR HSSP; P36204; 1VPE.
DR HAMAP; MF_00145; -; 1.
DR InterPro; IPR001576; PGK.
DR Pfam; PF00162; PGK; 1.
DR PRINTS; PR00477; PHGLYCKINASE.
DR PROSITE; PS00111; PGLYCERATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Complete proteome.
SQ SEQUENCE 411 AA; 44997 MW; E82D9737C6F74F76 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 411;
Best Local Similarity 22.5%; Pred. No. 16;
Matches 47; Conservative 35; Mismatches 75; Indels 52; Gaps 11;

QY 7 INEKLKSELOQTALGNLKO--IYYNSKAITSS-----EKSADQLTNTLLPK 55
DB 184 VMERELR---TLQG-ALENVERPCVVVLGSGVKDDSIWMKNVLENGSADLVLTGLVAN 239
QY 56 GFTGHPWYNDLLDLGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLDH 115
DB 240 IFLAG-----CGVIGKV-----NMDIKS-RGY-----CDFIKVAKKL 272
QY 116 NNRLTEKKVPINLMI--DGKQTTVPIDKVTSK-KEVTQBELDQARH-----YLRG 165
DB 273 KKRFFERIVVPDVAVCRDGRVDPVKIPNHPIDQIGMETIKLYARRIREARTLFANG 332
QY 166 KFGLYNSDSFGCKVQGLIVFHSSEGSTV 194
DB 333 PAGVFENPDFSTGTEDILNAISSEGFISI 361

RESULT 40
ID_ITAL_HUMAN STANDARD; PRT; 1151 AA.
AC P56199;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a).
GN ITGA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155124; PubMed=8428973;
RA Briesewitz R., Epstein M.R., Marcantonio E.E.;
RT "Expression of native and truncated forms of the human integrin alpha
1 subunit."
RL J. Biol. Chem. 268:2989-2996 (1993).
CC -!- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND
COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-P-P-G-
E-R IN COLLAGEN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
CC ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD49a entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd49a.htm".
CC PIR; A45226; A45226.
DR PDB; 1OC5; 17-MAY-00.
DR Genew; HGNC:6134; ITGA1.
DR MIM; 192968; -.
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR -----

DR InterPro; IPR000413; Integrin_alpha.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01839; FG-GAP 3.
 DR Pfam; PF00357; Integrin_A; 1.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SMO0191; Int_alpha; 5.
 DR SMART; SMO0327; VWA; 1.
 DR SMART; SMO0327; VWA; 1.
 DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 DR PROSITE; PS0234; VWA; 1.
 DR Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 KW Repeat; Calcium; Magnesium; 3D-structure.
 FT DOMAIN 1 1113 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1114 1136 POTENTIAL.
 FT DOMAIN 1137 1151 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 16 75 FG-GAP 1.
 FT REPEAT ? 75 FG-GAP 2.
 FT DOMAIN 147 360 VWA.
 FT REPEAT 349 404 FG-GAP 3.
 FT REPEAT 405 457 FG-GAP 4.
 FT REPEAT 459 520 FG-GAP 5.
 FT REPEAT 540 599 FG-GAP 6.
 FT REPEAT 602 654 FG-GAP 7.
 FT CA_BIND 470 478 POTENTIAL.
 FT CA_BIND 552 560 POTENTIAL.
 FT CA_BIND 614 622 POTENTIAL.
 FT SITE 1139 1142 GFPR MOTIF.
 FT DISULFID 54 64 BY SIMILARITY.
 FT DISULFID 660 669 BY SIMILARITY.
 FT DISULFID 675 728 BY SIMILARITY.
 FT DISULFID 780 786 BY SIMILARITY.
 FT DISULFID 850 858 BY SIMILARITY.
 FT DISULFID 1002 1034 BY SIMILARITY.
 FT DISULFID 1037 1044 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 432 432 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 720 720 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 752 752 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 855 855 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 880 880 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 887 887 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 911 911 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 938 938 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 980 980 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1055 1055 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1074 1074 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1151 AA; 127837 MW; 6B3F3C1AABF52808 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 1151;
 Best Local Similarity 27.3%; Pred. No. 56;
 Matches 53; Conservative 25; Mismatches 66; Indels 50; Gaps 12;
 QY 72 GSTAATSEYEGSSV-----DLYGAYGYQCAGGTPNKACMYGGVTL----- 113
 DB 596 GGDGKTLKFFQSGIHGEMDLNG-----DGLTDVTIGLGGALFWSRDVAVVKTWN 647
 QY 114 HDNRLTESEKYPINLWIDGKOT-----TVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 168
 DB 648 FEPNKVNIQK---NCHMEGKETVCINATVCFE-VKLKSKEDTIYEADLQYRVTLDSURQ 703

QY 169 LYNDSDFEGG---KVORGLIVFHSSEGSTVSYDLFDAQGYPTDLARIYRD-----NT 217
 DB 704 ISSR-FESGTQERKVRQNTV-RKSECTKHSFYMLD-KHDFQDS-VAILDFNLTPDENG 759
 QY 218 TISSTSLISLYLY 231
 DB 760 PVLDDSLPNSVHEY 773
 RESULT 41
 YE64_PASMU
 ID YE64_PASMU STANDARD; PRT; 324 AA.
 AC Q9CKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical paba-like protein PM1464.
 GN PM1464.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RL "Complete genomic sequence of Pasteurella multocida Pm70.";
 CC Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -!- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE
 CC COMPONENT 1.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AB006183; AAK03548.1; .
 CC InterPro; IPR005801; Anth synth chor.
 CC Pfam; PF00425; chorismate_bind; 1.
 CC PRINTS; PRO0095; ANTSINHA5E1.
 CC PRODOM; PD000779; Anth synth chor; 1.
 CC KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 324 AA; 37309 MW; E9336FF3890A32AE CRC64;

Query Match 6.5%; Score 79.5; DB 1; Length 324;
 Best Local Similarity 27.3%; Pred. No. 13; Mismatches 13; Gaps 3;
 Matches 24; Conservative 17;
 QY 136 TTVPIDKVKTSKKEVTVOEL---DLQARHYLHGKFGLYNSDFGGKVGRLI-----V 185
 DB 236 TLLPAGSIGAPKEKTVIHAARPRGYTIGFGLFDGESLQSAVAIRFIQVDEKLI 295
 QY 186 FHSSEGSTVSYDLFDAQGYPTDLRIY 213
 DB 296 FRSGGGITLSELED---EYQELIQKY 320

RESULT 42
 VE1_HPV35
 ID VE1_HPV35 STANDARD; PRT; 637 AA.
 AC P27220;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Replication protein E1.
 GN E1.
 OS Human papillomavirus type 35.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.


```
OX NCBI_TaxID=10587;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124753; PubMed=1310198;
RA Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124753; PubMed=1310198;
RA Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
RT "The phylogenetic relationship and complete nucleotide sequence of
human papillomavirus type 35.";
RL Virology 186:770-776(1992).
CC CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC CC -!- SUBCELLULAR LOCATION: Nuclear.
CC CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; X74477; CRA52563.1; -.
DR EMBL; M74117; AAA46968.1; -.
DR PIR; A40824; X1ML35.
DR PIR; S36523; S36523.
DR InterPro; IPR001177; Papillom_E1.
DR Pfam; PF00519; E1; 1.
DR Pfam; PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 463 470 ATP (POTENTIAL).
FT CONFLICT 31 34 DPVS -> SSV (IN REF. 2).
FT CONFLICT 142 143 QQ -> HE (IN REF. 2).
FT CONFLICT 235 258 ESKTLKPYCLYHIQCLCSWG ->
NFKHTIYVYVYRVHGA (IN REF. 2).
FT CONFLICT 269 281 CAKNRTTIEKLS -> VEKREQLKTIDA (IN REF.
2).
FT CONFLICT 417 418 EK -> AO (IN REF. 2).
FT CONFLICT 515 552 WAYIDQYRLNALDGNPISLDVKKHALVOLKCPPLITS ->
GIYRPFKKCTRWKSYISFRCKALSIVHIMPTFTYII (IN
REF. 2).
FT CONFLICT 587 587 V -> E (IN REF. 2).
FT CONFLICT 613 613 D -> V (IN REF. 2).
FT SEQUENCE 637 AA; 72122 MW; 3C694D4451791003 CRC64;
Query Match 6.5%; Score 79.5; DB 1; Length 637;
Best Local Similarity 20.3%; Pred. No. 30;
Matches 50; Conservative 39; Mismatches 88; Indels 69; Gaps 11;
QY 21 TALGNLQIYYNSKAITSSSEKSDQFLTNLLKGFRTGHPWYNDLLVDLGSTAAATSEY 80
DB 310 TAMSINSEV-----DGETPWIORQIVLQHSF-----NDALFDL-SEWQWAY 351
QY 81 EGGSSVDLYGAYGYQAGGTGPNKTACMY-----GGVTLHDNNRLTEKKVPINL 129
DB 352 DNDFIDDSIAYKYAQLAET-NSNACFLKNSQAKIVKDCATMCRHYKRAEKREMTMSQ 410
QY 130 WIDGQKTTVPID-KVYTSKKEVTQELDLQA-----RHYLQCK-----FGLYNSDSF 175
DB 411 WTKRCEKVDGDDWRDVRFLRYQQQDFVAFLSALKNFLRGVPKNCILLYGAPNT--- 467
QY 176 GGVKVRGILTVHSSSGSTVSY-----DLFDAQ-----GOYPTDLIRIYR 214
DB 468 -CKSLFGLMSLMHFLQALISYNSKSHFWLQPLDYDAKIAMLDATSPCKWAYIDQYLRNAL 526
QY 215 DNTTIS 220
```

```
DB 527 DGNPIS 532
RESULT 43
Y650 METUA STANDARD; PRT; 692 AA.
AC Q57852;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0650 precursor.
GN MJ0650.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.B., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii";
RL Science 273:1058-1073(1996).
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC CC -----
DR EMBL; U67512; AAB98647.1; -.
DR PIR; B64381; B64381.
DR TIGR; MJ0650; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 24 HYPOTHETICAL PROTEIN MJ0650.
FT CHAIN 25 692 HYPOTHETICAL PROTEIN MJ0650.
FT SEQUENCE 692 AA; 80607 MW; 25D0A91A08177188 CRC64;
Query Match 6.5%; Score 79.5; DB 1; Length 692;
Best Local Similarity 19.1%; Pred. No. 33;
Matches 59; Conservative 39; Mismatches 98; Indels 109; Gaps 12;
QY 7 INEKDLRKXSELOGTAL-----GNLQIYYNSKAITSSSEKSDQFLTNLLIF 54
DB 363 INNSKIDKKIYKRGKLTSGYNGKYCLGGKVLGKLLYNGKNITDLTKAN--ISNSDLI 420
QY 55 KGF-----FTGHPWY-----NDLLVDLGS 73
DB 421 SSTAYGKDWLGLDEVNLHPSKSLIKEDGKFYDLTNISNITICKILSKNKEYILIGT 480
QY 74 TAATSYEGSSVDL-----YGAYGYQAGGTGPNKTACMYGGVTLHDNNRLTEKKV 125
DB 481 KNVLLIKYSGSFITINVTNYEKYGLCYIFEAMDYNEKERYWLVGGVCLY--NHPYSDAI 538
QY 126 PINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHVLHGKFG-----LYNSDSFG 176
DB 539 LYKYDNGSYESLFIN-----DNLHKIYDGFQFALVSLIKIYKPNKSNFL 582
QY 177 GRVQGLI-----IVFHSEGSTV--SYDLFDAQGYQPTLLRIYRDNNTTIS 220
DB 583 IKWVGLNDHWHLYKNNLTLEFVTQKNPGSIEIDNVTLYIF--NYNT-IEIYDNNKLLS 639
```

```

QY 221 STSL 224
DB 640 TVEL 643

RESULT 44
CHIT NPVAC
ID CHIT NPVAC STANDARD; PRT; 551 AA.
AC P41684;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable endochitinase precursor (EC 3.2.1.14).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus."
RL Virology 202:586-605(1994).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
acetyl-D-glucosamine polymers of chitin.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -!- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
hydrolases).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DB EMBL; L22858; AAA66756.1; -.
DR PIR; G72865; G72865.
DR HSSP; P07254; ICTN.
DR InterPro; IPR000886; ER target S.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00636; Glyco_18; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolyase; Glycosidase; Chitin degradation; Signal; Glycoprotein;
KW Endoplasmic reticulum.
FT SIGNAL 1 17
FT CHAIN 18 551
FT ACT_SITE 305 305
FT CARBOHYD 173 173
FT CARBOHYD 444 444
FT SITE 548 551
SQ SEQUENCE 551 AA; 61368 MW; 4DDAAD1873BBA2 CRC64;

Query Match
Best Local Similarity 23.8%; Pred. No. 27;
Matches 44; Conservative 22; Mismatches 71; Indels 48; Gaps 11;

QY 32 YNSKAITS---SEKSDAQFLTWLTFKGFTHPWYNDLVLGSLSTAATSEYEGSSVDLY 88
DB 358 YDKIAVYNAEAQKSLGKIFLMSYDFKG-----AWSN---TDLGYQTTVYAPSWNSEELY 409
QY 89 GAYGYQC---AGGTENKT---ACMYG---CVTLHDN-NRLTEKKYP-INLALDGGQT 136
```

```

Db 410 TTHYAVDALLKQGVDPNKIIIVGVAMYGRTGVTNTDNYFSGTNGPGSGTWEDG--- 466
QY 137 TVPIDKVKTSKKEYTVQELDLQARHYLHGKFLGFLYNSDSFGKQVQRGLIVFHSSEGSTVSY 196
Db 467 -----VVDFYQIQKDLNNY-----VTFPDS-----AAQASYVDFKSGKGLISF 504
QY 197 DLFDA 201
Db 505 DSVDS 509

RESULT 45
SLA2_BACAA
ID SLA2_BACAA STANDARD; PRT; 862 AA.
AC P94217;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-layer protein EAI precursor.
GN EAG OR BA0887.
OS Bacillus anthracis (strain Ames), and
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094; 1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames;
RX MEDLINE=32608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ralston J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Bertoni J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne / 9131;
RX MEDLINE=9726011; PubMed=9106206;
RA Mesnage S., Tosi-Couture E., Mock M., Gounon P., Fouet A.;
RT "Molecular characterization of the Bacillus anthracis main S-layer
RT component: evidence that it is the major cell-associated antigen.";
RL Mol. Microbiol. 23:1147-1155(1997).
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DB EMBL; AE017027; AAP24884.1; -.
DR EMBL; X99724; CAA68063.1; -.
DR TIGR; BA0887; -.
DR InterPro; IPR001119; SLH.
DR Pfam; PF00395; SLH; 3.
KW Signal; Repeat; Cell wall; S-layer; Complete proteome.
FT SIGNAL 1 29
FT CHAIN 30 862
FT DOMAIN 34 75
FT DOMAIN 95 136
FT DOMAIN SLH 1.
FT DOMAIN SLH 2.
```

```
FT DOMAIN 157 197 SLH 3.
SQ SEQUENCE 862 AA; 91362 MW; C816B202F62CCCA0 CRC64;

Query Match 6.5%; Score 79; DB 1; Length 862;
Best Local Similarity 22.6%; Pred.No. 48;
Matches 55; Conservative 29; Mismatches 97; Indels 62; Gaps 10;

QY 33 NSKAITSSKADQFLNTLLFKGFFTGHPWYNDLLVLDLSTAASTSEYSSVDLYGAYY 92
DB 432 NSQNLVVGKASLNKLVIATIGE-----DKVVDPGSISIKSSNHG-IISVNNYI 480
QY 93 GYOCAGGTPNTACTWYGGVT-----LHDNRLTEEKVPINLWIDGKQTTVPIDKVK 145
DB 481 TAEAGEA--TLTIKVGDTVQDVFKVTTDSRKLVSVKANPKLOV-VQNKTLIPVFVTT 537
QY 146 SK-----KEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQRLIVFHS 188
DB 538 DQYGDPPFGAATAIKEVLPKTVGVAEGGLDVTVDGSGISGTTIGVTGNDVGEQTVHFQ 597
QY 189 SEGSTV-----SYDLFDAQGY---PDTLLRIYRDNTTISTSLISLYL 230
DB 598 NGGATLGLSYNVTEGNAFKNFELSVKVGQYGQSPDKLDN-----VSTIVEYQJSK 651
QY 231 YTT 233
DB 652 YTS 654

RESULT 46
LMA5 HUMAN
ID LMA5 HUMAN STANDARD; PRT; 3695 AA.
AC 015230; Q9WZ47; Q9HLP1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DI 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LMA5 OR KIAA0533 OR KIAA1907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA DeCoukas P., Matthews L.H., Ashurst J., Buxton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguely C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahman D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA LeVaealaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McKay K., McMurray A.A.,
RA Mine S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.U.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromas A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RN Nature 414:865-871(2001).
RL [2]
RP SEQUENCE OF 197-1934 FROM N.A.
```

```
RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Res. 8:179-187(2001).
RN [3]
RP SEQUENCE OF 2051-3695 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 5:31-39(1998).
RN [4]
RP SEQUENCE OF 2743-3695 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97415425; PubMed=9271224;
RA Durkin M.E., Joehel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA Mewer U.M.;
RT "Tissue-specific expression of the human laminin alpha5-chain, and
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation."
RL FEBS Lett. 411:296-300(1997).
RN [5]
RP EXPRESSION IN RETINA.
RX MEDLINE=20422761; PubMed=10964957;
RA Libby R.T., Champlaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA Koch M., Burgeson R.E., Hunter D.D., Brunken W.J.;
RT "Laminin expression in adult and developing retinae: evidence of two
RT novel CNS laminins."
RL J. Neurosci. 20:6517-6528(2000).
CC -I- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -I- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
CC disulfide bonds into a cross-shaped molecule comprising one long
CC and three short arms with globules at each end.
CC -I- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -I- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
CC muscle, pancreas, retina and placenta. Little or no expression in
CC brain and liver.
CC -I- DOMAIN: Domain G is globular and is part of the major cell-binding
CC site located in the long arm of the laminin heterotrimer.
CC -I- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -I- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -I- SIMILARITY: Contains 2 laminin IV domains.
CC -I- SIMILARITY: Contains 5 laminin G-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to licenses@isb-sib.ch).
CC -----
CC EMBL; AJ354836; CAC22309.1; ALT_SEQ.
CC EMBL; AJ354836; CAC22310.1;
CC EMBL; AB067494; BAB67800.1;
CC EMBL; AB011105; BAA25459.1;
CC EMBL; Z95636; CAB09137.1;
CC HSP; P02468; IXL0.
CC Genew; HGNC:6485; LAMA5.
CC MIN; 601033;
CC InterPro; IPR008985; ConA_like_lec_gl.
CC InterPro; IPR006209; EGF_like.
```

```

DR InterPro; IPR008212; Lam_N2.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR008211; LamNT.
DR Pfam; PF00052; laminin_B; 1.
DR Pfam; PF00053; laminin_EGF; 18.
DR Pfam; PF00054; laminin_G; 2.
DR Pfam; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD002082; Lam_N2; 1.
DR ProDom; PD003031; Laminin_B; 1.
DR SMART; SM00180; EGF_Lam; 20.
DR SMART; SM00281; LamB; 1.
DR SMART; SM00282; LamG; 5.
DR SMART; SM00136; LamNT; 1.
DR PROSITE; PS00022; EGF_1; 19.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS01248; LAMININ TYPE EGF; 19.
DR PROSITE; PS50025; LAM G DOMAIN; 5.
DR GlycoProtID; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35
FT CHAIN 36 3695
FT DOMAIN 36 299 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 300 358 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 359 428 LAMININ EGF-LIKE 1.
FT DOMAIN 429 474 LAMININ EGF-LIKE 2.
FT DOMAIN 494 540 LAMININ EGF-LIKE 3.
FT DOMAIN 541 586 LAMININ EGF-LIKE 4.
FT DOMAIN 587 631 LAMININ EGF-LIKE 5.
FT DOMAIN 632 676 LAMININ EGF-LIKE 6.
FT DOMAIN 677 722 LAMININ EGF-LIKE 7.
FT DOMAIN 723 775 LAMININ EGF-LIKE 8.
FT DOMAIN 776 828 LAMININ EGF-LIKE 9.
FT DOMAIN 829 850 LAMININ EGF-LIKE 10.
FT DOMAIN 851 1437 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 1438 1483 LAMININ EGF-LIKE 12.
FT DOMAIN 1484 1527 LAMININ EGF-LIKE 13.
FT DOMAIN 1528 1576 LAMININ EGF-LIKE 14.
FT DOMAIN 1577 1627 LAMININ EGF-LIKE 15.
FT DOMAIN 1628 1637 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1638 1830 LAMININ EGF-LIKE 17 (C-TERMINAL).
FT DOMAIN 1831 1863 LAMININ EGF-LIKE 18.
FT DOMAIN 1864 1912 LAMININ EGF-LIKE 19.
FT DOMAIN 1913 1968 LAMININ EGF-LIKE 20.
FT DOMAIN 1969 2022 LAMININ EGF-LIKE 21.
FT DOMAIN 2023 2069 LAMININ EGF-LIKE 22.
FT DOMAIN 2070 2116 LAMININ EGF-LIKE 23.
FT DOMAIN 2117 2166 LAMININ EGF-LIKE 24.
FT DOMAIN 2167 2735 LAMININ EGF-LIKE 25.
FT DOMAIN 2736 2929 LAMININ EGF-LIKE 26.
FT DOMAIN 2941 3115 LAMININ EGF-LIKE 27.
FT DOMAIN 3124 3292 LAMININ EGF-LIKE 28.
FT DOMAIN 3340 3513 LAMININ EGF-LIKE 29.
FT DOMAIN 3520 3692 LAMININ EGF-LIKE 30.
FT DOMAIN 2203 2221 COILED COIL (POTENTIAL).
FT DOMAIN 2335 2466 COILED COIL (POTENTIAL).
FT DOMAIN 2510 2670 COILED COIL (POTENTIAL).
FT SITE 1722 1724 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1838 1840 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 300 309 BY SIMILARITY.
FT DISULFID 302 322 BY SIMILARITY.
FT DISULFID 324 333 BY SIMILARITY.
FT DISULFID 336 356 BY SIMILARITY.
FT DISULFID 359 368 BY SIMILARITY.
FT DISULFID 361 393 BY SIMILARITY.
FT DISULFID 396 405 BY SIMILARITY.
FT DISULFID 408 426 BY SIMILARITY.
FT DISULFID 429 440 BY SIMILARITY.
FT DISULFID 431 447 BY SIMILARITY.
FT DISULFID 449 458 BY SIMILARITY.
FT DISULFID 461 471 BY SIMILARITY.

Query Match 6.5%; Score 79; DB 1; Length 3695;
Best Local Similarity 29.4%; Pred. No. 2.9e+02;
Matches 58; Conservative 20; Mismatches 75; Indels 44; Gaps 13;

QY 56 GFTGHPWYNDLLVDLGSTAAATSEYEGSSV-----DLYGAYGYOCAGTGNKT- 104
DB 41 GGFSLHPPYPFNLA--GARIAASATCGEEAPARGSPRTEDLYCKLVGGFVAGGDPNQTI 98
QY 105 ACYGGVGLTHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVOELDL-QA 159
DB 99 QGVCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LGLGV 151
QY 160 RH--YLHGKFG-----LYNSDFGKGVQKGLIVFHSSEGSTVSYDLFDAGQGYPT 208
DB 152 FHVAYVLKFPANGPRPDLWLERSMDPGRVYQWQF-FASSK-----RDCLERFG--PQT 203
QY 209 LLRIYRNTTISSTLS 225
DB 204 LERITRDDAAICTEYS 220

RESULT 47
YJRL_YEAST STANDARD; PRT; 396 AA.
AC P46992;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 43.0 kDa protein in CPS1-FPP1 intergenic region.
GN YJL171C OR J0512
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Obermaier B., Piravandi E., Rinke M., Domdey H.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YJL162C.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49446; CAA89466.1; -.
DR PIR; S56954; S56954.
DR GenOnline; 141783; -.
DR SGD; S0003707; YJL171C.
KW Hypothetical protein.
SQ SEQUENCE 396 AA; 43014 MW; 279E58E57512670A CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 396;
Best Local Similarity 21.6%; Pred. No. 20;
Matches 64; Conservative 29; Mismatches 86; Indels 117; Gaps 16;

QY 26 LKQIYYNSKAIT-----SSKSAQDF-----LTNTLLF-K 55
||| :|||

```

Db 85 LKQAFYTPGFTVNNSSSDWRLAYESSKTDNVTLNHHGGASPCLGNALSYAS 144
 Qy 56 GFTTGHWPYNDLLVDLSTAATSEY-----EGSSVDLYG--AYGYQCAGG 99
 Db 145 SNGTGSASEATVLADGTLISDQEVIIYNSVCPKSGYDKGCVYRGIPAYGY--GG 201
 Qy 100 T-----PNKTACMYGGVTLHD-----NNRLTEKKVFN-----LWIDGKQTTV 138
 Db 202 TTKMPLFEFEMPTETERNSSSIGYDUPAIWLLNDHARTSQYPTNANCWSAG----- 256
 Qy 139 PIDKVKTSKKEVTQELDL-----QARHYLHGKFLGYNLS--DSFGGKVQ----- 180
 Db 257 -----CGEYDIFEAMNGTEKNHLYSIFHTFGQIEDLGTGIGSQSYIIRNTTG 303
 Qy 181 --RGLIVPHSSEGSTVSDYLFDA-----OGQPTDLLRIYRNTTISSTLSIS 227
 Db 304 TMKGWVFDSS-GNVVSP-ISDATFFNGTSGADTVNDLLAIPENETYSQMSIS 357
 RESULT 48
 SP74_YEAST STANDARD; PRT; 413 AA.
 AC P45819;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Sporulation-specific protein 74.
 GN SP074 OR YGL170C OR G1654.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1679;
 RX MEDLINE=97051590; PubMed=8996267;
 RA Kikma R., Cogliavina M., Zaccaria P., Bertani I., Bruschi C.V.;
 RA "A putative helicase, the SUA5, PMR1, TRN1YSL1 genes and four open
 RT reading frames have been detected in the DNA sequence of an 8.8 kb
 RT fragment of the left arm of chromosome VII of Saccharomyces
 RT cerevisiae.";
 RL Yeast 12:1033-1040(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97313265; PubMed=9169869;
 RA Tettelin H., Agostoni Carbone M.L., Albermann K., Albers K.,
 RA Arroyo K., Backes U., Barreiros T., Bertani I., Bjorson A.J.,
 RA Brueckner M., Bruschi C.V., Carignani G., Castagnoli L., Cerdan E.,
 RA Clemente M.L., Coblentz A., Cogliavina M., Colesac E., Defoor E.,
 RA Del Bino S., Delius H., Delner D., de Wergifosse P., Dufon B.,
 RA Durand P., Entian K.-D., Braso P., Escribano V., Fabiani L.,
 RA Fartmann B., Feroli F., Feuerhann M., Frontali L., Garcia-Gonzalez M.,
 RA Garcia-Saez M.I., Goffeau A., Guerreiro P., Hani J., Hansen M.,
 RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
 RA Indge K.J., James C.M., Kikma R., Koetter P., Kramer B., Kramer W.,
 RA Lauguin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
 RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,
 RA Melchiorotto P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
 RA Navrochi A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
 RA Paoluzi S., Plevani P., Portetelle D., Portillo F., Potier S.,
 RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
 RA Rodrigues-Pousada C., Rodriguez-Belmonte E., Rodriguez-Torres A.M.,
 RA Rose M., Ruzzi M., Sallola M., Sanchez-Perez M., Schaefer B.,
 RA Schaefer M., Scharte M., Schmidheini T., Schreier A., Skala J.,
 RA Souciet J.-L., Steensma H.Y., Talla E., Thierry A., Vandenbol M.,
 RA van der Aart Q.J.M., Van Dyck L., Vanoni M., Verhasselt P., Voet M.,
 RA Volckaert G., Wambutt R., Watson M.D., Weber N., Wedler H.,
 RA Wiefli P., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
 RA Zollner A., Kieune K.;
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome VII.";
 RL Nature 387:81-84(1997).
 RN [3]
 RP FUNCTION, SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, AND INTERACTION

RP WITH SP021 AND MPC54.
 RX MEDLINE=22680893; PubMed=12796288;
 RA Nickas M.E., Schwartz C., Neiman A.M.;
 RT "Ayd4p and Spo74p are components of the meiotic spindle pole body
 RT that promote growth of the prospore membrane in Saccharomyces
 RT cerevisiae.";
 RL Eukaryot. Cell 2:431-445(2003).
 CC -!- FUNCTION: Involved in the pathway that organizes the shaping and
 CC sizing of the prospore membrane (PSM) during sporulation. Probable
 CC component of a core structural unit of the scaffold that initiates
 CC synthesis of the prospore membrane.
 CC -!- SUBUNIT: Interacts with itself. Interacts with MPC54, NUD1 and
 CC SPO21/MPC70.
 CC -!- SUBCELLULAR LOCATION: Localizes to the meiotic outer plaque of the
 CC spindle pole body (SPB), at the end of the meiotic spindles.
 CC -!- DEVELOPMENTAL STAGE: Meiosis-specific.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X85757; CAA59759.1; -;
 CC EMBL: Z72692; CAA96882.1; -;
 CC EMBL: S59650; S59650.
 CC GenBank: 141218; -;
 CC SGD: S0003138; SPO74.
 CC GO: GO:0005816; C:spindle pole body; IDA.
 CC GO: GO:0005198; F:structural molecule activity; IDA.
 CC GO: GO:0007151; P:sporulation (sensu Saccharomycetes); IMP.
 KW Sporulation.
 SQ SEQUENCE 413 AA; 47700 MW; ACB8DA9A240B650 CRC64;
 Query Match 6.4%; Score 78.5; DB 1; Length 413;
 Best Local Similarity 20.3%; Pred. No. 21;
 Matches 47; Conservative 37; Mismatches 89; Indels 59; Gaps 9;
 QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNSKATSS----- 41
 Db 41 SKRNPVKQK--QKDEKSKMGTASNIFHENKIHSEHTDDFNDGLKLAPOSSPL 98
 QY 42 ----KSADQFLNTLLFKGFTTGH--PWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGY 94
 Db 99 KECQFNKSWESFCNT--EGYKTKMQPH-----FTSGLEEIKFVPWELNISTSPY 147
 QY 95 QCAGTPTNKTACMYGGVTLHDNNRLTEKKVFNLW-----IDGKQTTVPI--DKVKT 146
 Db 148 K--GQSPNSAPTEYSAATTAFTKQLEVSFLKTNLTLYIKKSIDICLSSVPPFDDAVQM 205
 QY 147 KKEVTQVELDLQARHYLHGKFLGYNLSDFGKVGQRLIVFHSSEGSTVSYDL 198
 Db 206 KKFLEVRDIDLDEVEL-----KILGELNDLNFHMQENSLNREL 247
 RESULT 49
 CLS1_BACAA
 ID CLS1_BACAA STANDARD; PRT; 509 AA.
 AC Q81V75;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cardiolipin synthetase 1 (EC 2.7.8.-) (Cardiolipin synthase 1) (CL
 DE synthase 1).
 GN CLS1 OR CLS-1 OR BA0625.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22608414; PubMed=12721629;

RA Read T.D., Peterson S.N., Tournasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzaple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nieman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
RT closely related bacteria";
RL Nature 423:81-86(2003).
CC -!- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
CC from one phosphatidylglycerol molecule to another to form
CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
CC diphosphatidylglycerol + glycerol.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -!- SIMILARITY: Belongs to the phospholipase D family. Cardiolipin
CC synthase subfamily.
CC -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL: AE017026; AAP24642.1; -
CC TIGR: BA0625; -
CC HAMAP: MF_00190; -; 1.
CC InterPro: IPR001736; PLD.
CC Pfam: PF00614; PLDC; 2.
CC SMART: SM00155; PLDC; 2.
CC DR PROSITE: PS00035; PLD; 2.
CC KW Transferase: Phospholipid biosynthesis; Transmembrane; Repeat;
CC Complete proteome.
CC FT TRANSMEM 5 22 Potential.
CC FT TRANSMEM 27 49 Potential.
CC FT TRANSMEM 58 80 Potential.
CC FT DOMAIN 238 265 PLD phosphodiesterase 1.
CC FT DOMAIN 422 449 PLD phosphodiesterase 2.
CC FT ACT_SITE 243 243 POTENTIAL.
CC FT ACT_SITE 427 427 POTENTIAL.
CC SQ SEQUENCE 509 AA; 58107 MW; 54AFD680CA095FA CRC64;
Query Match 6.4%; Score 78.5; DB 1; Length 509;
Best Local Similarity 25.6%; Pred. No. 27;
Matches 30; Conservative 26; Mismatches 30; Indels 31; Gaps 7;
QY 115 DNNRLTEKKVPIINLWIDGKQTVPIDKV-----KTSKKEVT-----VOE 154
DB 105 EGRRLSLKVLPLS-----ERSVHUTEVQVFGGPAADRTTKLLNGDGTFFSEILQA 158
QY 155 LDLDQARHYLHGKFGLYNSDSFGKVGORGLIVFHSBGSVSYDLDFAQOQYPTLLR 211
DB 159 IE-QAKSHHIHQYIYKSDIEGTVK-RDALIKKAKDGVIVRF-LYDGLGS--NLLRR 210

CC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
CC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=2125;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DSM 2030;
RC MEDLINE=90036724; PubMed=2681162;
RA Peters J., Peters M., Lottspeich F., Baumeister W.;
RT "S-layer protein gene of *Acetogenium kivui*: cloning and expression in
RT *Escherichia coli* and determination of the nucleotide sequence.";
RL J. Bacteriol. 171:6307-6315(1989).
[2]
RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
RC STRAIN=DSM 2030;
RC MEDLINE=92281680; PubMed=1596358;
RA Peters J., Rudolf S., Oschkinat H., Mengele R., Sumper M.,
RA Kellermann J., Lottspeich F., Baumeister W.;
RT "Evidence for tyrosine-linked glycosaminoglycan in a bacterial
RT surface protein.";
RL Biol. Chem. Hoppe-Seyler 373:171-176(1992).
[3]
RP DOMAINS.
RX MEDLINE=94156823; PubMed=8113161;
RA Lupas A., Engelhardt H., Peters J., Santarius U., Volker S.,
RA Baumeister W.;
RT "Domain structure of the *Acetogenium kivui* surface layer revealed by
RT electron crystallography and sequence analysis.";
RL J. Bacteriol. 176:1224-1233(1994).
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
CC layer with hexagonal symmetry.
CC -!- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS ABOUT 8% WHICH
CC CORRESPOND TO ABOUT 40 TO 50 SUGAR MOLECULES PER MONOMER. O-LINKED
CC GLYCANS CONSIST OF GLC, GALNAC AND GLCNAC.
CC -!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL: M31069; AAA21930.1; -
CC PIR: A34355; A34355.
CC InterPro: IPR001119; SLH.
CC Pfam: PF00395; SLH; 2.
CC DR PROSITE: PS01072; SLH_DOMAIN; 2.
CC KW Signal; Glycoprotein; Repeat; Cell wall; S-layer.
CC FT SIGNAL 1 26
CC FT CHAIN 27 762 CELL SURFACE PROTEIN.
CC FT DOMAIN 30 94 SLH 1.
CC FT DOMAIN 95 145 SLH 2.
CC FT DOMAIN 146 204 SLH 3.
CC FT DOMAIN 473 479 SER/THR-RICH.
CC FT DOMAIN 625 630 SER/THR-RICH.
CC FT CARBOHYD 297 297 O-LINKED (GLC. . .).
CC FT CARBOHYD 516 516 O-LINKED (GLC. . .).
CC FT CARBOHYD 520 520 O-LINKED (GLC. . .).
CC FT CARBOHYD 632 632 O-LINKED (GLC. . .).
CC SQ SEQUENCE 762 AA; 82785 MW; 34EC9C784DECA67E CRC64;
Query Match 6.4%; Score 78.5; DB 1; Length 762;
Best Local Similarity 24.8%; Pred. No. 45;
Matches 60; Conservative 28; Mismatches 105; Indels 49; Gaps 11;
QY 3 KSEINEKDLKRSKSELQGTALGNLKOIYY-----NSKAITSSSEKSDQFLNTLLFK 55
DB 90 KSEKSAFKDVPQNH-----WAVGQINLAYKLGLAQGVNGKFDNSSELRYAQAALFVLRL 145
QY 56 GFFTGHFWYNDLLVDLGLSTAAATSEYEGSSVDLYGAYYGQCAGGTNKTACMYGGVTLHD 115

RESULT 50

SLAP ACEKI

ID SLAP ACEKI

AC P22258;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cell surface protein precursor (S-layer protein).

OS Acetogenium kivui.

Db 146 GF-----KDLDPYFG-----YLAQAQL-GLVHGLNLA-----YGVKRG 180
 QY 116 NNRLEEK--KYPINLWIDGKQTTVP--IDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
 Db 181 DLALILDRALFVPMVKYVDGKEVLGKPLISKVAT-KAEYTVIATNAQDSRVEEGKVAULD 239
 QY 172 SPSPGKVGQGLIVFHSSEGSVSYDLDPDAQOQYPTDLLIRYDNTTISST-----SLSIS 227
 Db 240 KDGKLTINAGLVDFSEYLGKV-----IVYSRFGDPVIVAEAGDNVVSFTFEGQDSVGT 295
 QY 228 LY 229
 Db 296 VY 297

RESULT 51

ADH1_ORYSA
 ID ADH1_ORYSA STANDARD; PRT; 376 AA.
 AC P20306;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alcohol dehydrogenase 1 (EC 1.1.1.1).
 GN ADH1.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Indica-IR26; TISSUE=Seedling;
 RX MEDLINE=93357433; PubMed=2562760;
 RA Xie Y., Wu R.;
 RT "Rice alcohol dehydrogenase genes: anaerobic induction, organ
 specific expression and characterization of cDNA clones.";
 RL Plant Mol. Biol. 13:53-68(1989).
 CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
 NADH.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X16296; CAA34363.1; -
 DR PIR; JQ0474; JQ0474.
 DR HSSP; F11766; ITEX.
 DR Gramene; P20306; -
 DR InterPro; IPR002328; ADH zinc.
 DR InterPro; IPR002085; Adh zn family.
 DR InterPro; IPR002025; NAD_BS_
 DR Pfam; PF00107; ADH zinc_N; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family.
 FT METAL 45 45 ZINC 1 (CATALYTIC).
 FT METAL 67 67 ZINC 1 (CATALYTIC).
 FT METAL 98 98 ZINC 2.
 FT METAL 100 100 ZINC 2.
 FT METAL 103 103 ZINC 2.
 FT METAL 111 111 ZINC 2.
 FT METAL 175 175 ZINC 1 (CATALYTIC).
 SQ SEQUENCE 376 AA; 40852 MW; B8ED6E025863D64F CRC64;

Query Match 6.4%; Score 78; DB 1; Length 376;
 Best Local Similarity 23.8%; Pred. NO. 21;
 Matches 47; Conservative 29; Mismatches 77; Indels 46; Gaps 7;
 QY 3 KSEINEKDLRKSELQGTALGNLKIYYNSKAI-----TSSE-----KS 43
 Db 104 KSAESNCDLLRINTDRGVWIGDGKSRFSINGKPIVHFIGTSTFSEVTVMHVGCAKINP 163
 QY 44 ADQPLNTLLPKFFFTGHWPYNDLLVDLGSTAATSEYEGSSVDLYG-AYGYQCAGTGN 102
 Db 164 AAPLDKVCVLSGCIISTG-----LGATINVARPKGSTVAIFGLGAVGLAAAGARI 213
 QY 103 KTACMYGGVTLHDNNELTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELD----- 156
 Db 214 RGSRIIGIDL-NANRFEARKEGCTEFVNPDKHDPVQVLA---EMTNGGVDRSVECT 269
 QY 157 -----LQARHYLHGKFG 169
 Db 270 GNINAMIAFEVCVHDGWI 288

RESULT 52

DNAK_STRPN
 ID DNAK_STRPN STANDARD; PRT; 607 AA.
 AC P95829; O66035;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
 protein) (HSP70).
 DE DNAK OR SP0517.
 GN DNAK OR SP0517.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rioux C.R., Martin D., Hamel J., Brodeur B.R.;
 RT "Heat shock protein HSP70 and amino terminus of DnaJ of Streptococcus
 pneumoniae";
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rx / CP1200;
 RX MEDLINE=98231633; PubMed=9570114;
 RA Kim S.-W., Choi I.-H., Kim S.-N., Kim Y.-H., Pyo S.-N., Rhee D.-K.;
 RT "Molecular cloning, expression, and characterization of dnaK in
 Streptococcus pneumoniae";
 RL FEMS Microbiol. Lett. 161:217-224(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC BAA-334 / TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 Durkin A.S., Whitt M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 pneumoniae";
 RL Science 293:498-506(2001).

CC -!- FUNCTION: Acts as a chaperone (By similarity).
 CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC

Db 206 GNTSGMGTGSSVVVKAIVGVAHSDYSLTLTGRTA-NWNGPSYDLTGKIVPGQYNNVDFW 264
 QY 131 ---IDGKQTTVPIDKVKTSKEVTVOELDQARHY-----LHGKFGLYNSDSFGG 177
 Db 265 VKFVNGNDT---EQIKATVKATSDKONYIQVNDFAVNVKNGEWTEIKGSFTLPVAD----- 316
 QY 178 KVQKGLIVFHSSEGSTSVSY--DLFDAGQGYPDTLRLIYRD 215
 Db 317 --YSGISIVESQNPTEIFYIDDFSVGEISNNQIIOND 354

RESULT 56
 GTF2_STRDO
 ID -GTF2_STRDO STANDARD; PRT; 1592 AA.
 AC P27470;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucosyltransferase-I precursor (EC 2.4.1.5) (GTF-I) (Dextranucrase)
 DE (Sucrose 6-glucosyltransferase).
 OS Streptococcus downei (Streptococcus sobrinus),
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=13117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6715 / Serotype G;
 RX MEDLINE=91123227; PubMed=1704006;
 RA Abo H., Matsumura T., Kodama T., Ohta H., Fukui K., Kato K.,
 RA Kigawa H.;
 RT "Peptide sequences for sucrose splitting and glucan binding within
 RT Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
 RT synthetase).";
 RL J. Bacteriol. 173:989-996(1991).
 CC -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 CC TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 CC OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIANE THE
 CC AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -!- CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl} (N) = D-
 CC fructose + {(1,6)-alpha-D-glucosyl} (N+1).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA
 CC 1,3-LINKED GLUCOSE AND SOME 1,6-LINKAGES). GTF-S SYNTHESIZES
 CC WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
 CC FORMS OF GLUCANS.
 CC -!- SIMILARITY: Belongs to family 70 of glycosyl hydrolases.
 CC -!- SIMILARITY: Contains 16 cell wall binding repeats.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; D90213; BAA14241.1; --
 CC InterPro; IPR002479; CW binding.
 CC DR InterPro; IPR003318; Glyco_hydro_70.
 CC DR Pfam; PF01473; CW binding_1; 13.
 CC DR Pfam; PF02324; Glyco_hydro_70; 1.
 CC KW Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.
 FT SIGNAL 1 38 POTENTIAL.
 FT CHAIN 39 1592 GLUCOSYLTRANSFERASE-I.
 FT DOMAIN 39 1044 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1093 1592 GLUCAN-BINDING (APPROXIMATE).
 FT FT DOMAIN 1093 1592 6.5 X TANDEM REPEATS.
 FT REPEAT 1093 1142 1.
 FT REPEAT 1158 1207 2.
 FT REPEAT 1222 1272 3.
 FT REPEAT 1287 1337 4.
 FT REPEAT 1402 1451 5.
 FT REPEAT 1514 1563 6.

FT REPEAT 1577 1592 7 (INCOMPLETE).
 SQ SEQUENCE 1592 AA; 176167 MW; B0A66D079351ECF CRC64;
 Query Match 6.4%; Score 78; DB 1; Length 1592;
 Best Local Similarity 25.4%; Pred. No. 1.2e+02;
 Matches 48; Conservative 21; Mismatches 84; Indels 36; Gaps 8;
 QY 34 SKAITSSEKSAQDLNTLLFKGFTGHPWVNDLLVLSGTAATSEYEGS-SVDLYGAYY 92
 Db 28 ASALGASVASADTDTASDDSNQTVVTGDTNNQATQTSIAATATSEQASTD--AATD 85
 QY 93 GYQCAGGTTPNKTCMYGGV-----TLHDNNRLTEKKVPINLWIDGKQTVTP 139
 Db 86 QASAAEQGTGTTASTDTAAQTNNANEAKWPTENENQGTDEMLAEAKNVATAESDSIP 145
 QY 140 IDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVSYDLF 199
 Db 146 SDAKMS-----NVKQVD-----GKYYYDDQD---GNVRKNFAV---SVGDKIYY--F 185
 QY 200 DAQGYPDPT 208
 Db 186 DETGAYKDT 194

RESULT 57
 RLF_HUMAN
 ID -RLF_HUMAN STANDARD; PRT; 1914 AA.
 AC Q13129; Q5NU60;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein RLF (Rearranged L-myc fusion gene protein) (Zn-15
 DE related protein).
 DE
 GN RLF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96132723; PubMed=8545128;
 RA Makela T.P., Hellsten E., Vesa J., Hirvonen H., Palotie A.,
 RA Peltonen L., Altalo K.,
 RT The rearranged L-myc fusion gene (RLF) encodes a Zn-15 related zinc
 RT finger protein.";
 RL Oncogene 11:2699-2704(1995).
 RN [2]
 RP SEQUENCE OF 317-1914 FROM N.A.
 RA Donnelly S.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as a transcription factor.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- TISSUE SPECIFICITY: Widely expressed in fetal and adult tissues.
 CC -!- DISEASE: In some small cell lung carcinoma (SCLC) cell lines,
 CC there is an intrachromosomal rearrangements at ip32 fusing the
 CC first exon of the RLF gene with L-myc.
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; U23777; AAC50396.1; --
 CC EMBL; AL050341; CAB81608.1; --
 CC Genew; HGNC:10025; RLF.
 CC MIM; 180610; --
 CC GO; GO:0003700; F:transcription factor activity; TAS.
 CC GO; GO:0008270; F:zinc ion binding; TAS.

DR InterPro; IPR007087; Znf C2H2.
DR Pfam; PF00096; Znf C2H2; 12.
DR SMART; SM00355; Znf C2H2; 14.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 11.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
Nuclear protein; Repeat.
FT ZN_FING 582 604 C2H2-TYPE.
FT ZN_FING 671 696 C2H2-TYPE.
FT ZN_FING 714 736 C2H2-TYPE.
FT ZN_FING 742 766 C2H2-TYPE.
FT ZN_FING 771 795 C2H2-TYPE.
FT ZN_FING 801 825 C2H2-TYPE.
FT ZN_FING 954 979 C2H2-TYPE.
FT ZN_FING 1127 1152 C2H2-TYPE.
FT ZN_FING 1172 1195 C2H2-TYPE.
FT ZN_FING 1310 1335 C2H2-TYPE.
FT ZN_FING 1352 1387 C2H2-TYPE.
FT ZN_FING 1407 1432 C2H2-TYPE.
FT ZN_FING 1444 1469 C2H2-TYPE.
FT ZN_FING 1549 1574 C2H2-TYPE.
FT CONFLICT 1546 1548 LSL -> HTQ (IN REF. 2).
SQ SEQUENCE 1914 AA; 217899 MW; 1E7529139F6528AA CRC64;

Query Match 6.4%; Score 78; DB 1; Length 1914;
Best Local Similarity 23.9%; Pred. No. 1.6e+02;
Matches 51; Conservative 31; Mismatches 55; Indels 76; Gaps 11;

QY 7 INEKLKRSKELQGTALGNLQIYYNS--KATTSSEKSAQDF-----LTNTILF 54
DB 1745 VPXENFRKHSQPSFLDKTYKWPGESEFLKFIQSESEKEDFDWPESEHLTSLNSQS 1804
QY 55 KGFFTHGWPNVDLGLSTATSEYSGSVLDLYGAYGYQCAGGTPNKTACMYGGVTLH 114
DB 1805 SNDLTGNVANNMND-----SEPE--VDI-----PHSSS-----DSTIH 1837
QY 115 DNNRLTEKKVPINLWIDGKQTTVP-----IDKVKTSKKEVTQVELDQARHYLHGK 166
DB 1838 EN--LT-----AIPLLVAETTVPSLENLRVLDAKLTGELAKQL-----HYL---- 1882
QY 167 FGLYNSDFGGKVQRLIVFHSSEGSTVSYDLF 199
DB 1883 -----RPVVVLERSKFSTPLDLF 1901

RESULT 58
ID Y653 HAEIN STANDARD; PRT; 254 AA.
AC P44029;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative glycosyl transferase HI0653 (EC 2.-.-.-).
GN HI0653.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RP "whole-genome random sequencing and assembly of Haemophilus influenzae
RD.";

RL Science 269:496-512(1995).
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. WAAE/KDTX
CC SUBFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U32748; AAC23212.1; -.
DR PIR; B64011; B64011.
DR TIGR; HI0653; -.
DR InterPro; IPR001173; Glyco trans. 2.
DR Pfam; PF00535; Glycos transf 2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
Complete proteome.
SQ SEQUENCE 254 AA; 29137 MW; 1F520A67EC07B149 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 254;
Best Local Similarity 24.9%; Pred. No. 14;
Matches 48; Conservative 23; Mismatches 55; Indels 67; Gaps 12;

QY 42 KSADQFLTNTLLFKGFTGHPWVNDLLV-DLGSTAATSEYSGSVLDLYGA--YYGYQCAG 98
DB 11 KNEAQDLANCL-----DTVKQWVDEIIILDSGSTDKETALS----YGAKFYENSDWOG 61
QY 99 -GTPNKATACMYGVTGLDNNRLTEKKVPINLWIDGKQTTVP-----IDKVKTSKKEVT 151
DB 62 FGKQRLAQY-----VTSD-----YVLWLDADERTPKLQAAILSAVK-NDRENT 106
QY 152 VQELDQARHYLHGKGLYNSDSFGKQVORGLIVFHSSEGSTVSYDLFQAQGYPTLLR 211
DB 107 VYBIPRV-----SEVFGREIR-----HS-----GWYPDYVVR 133
QY 212 IYRDNITTSSTSL 224
DB 134 LYRTNVAQYNDL 146

RESULT 59
Y786 CORGL STANDARD; PRT; 985 AA.
AC Q8NS93;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0182 protein Cgi0786.
GN Cgi0786.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the UPF0182 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AP005276; BAB98179.1; -.

```

DR HAMAP; MF 01600; -; 1.
DR InterPro; IPR005372; UPF0182.
DR Pfam; PF03699; UPF0182.1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 21 43 POTENTIAL.
FT TRANSMEM 58 80 POTENTIAL.
FT TRANSMEM 115 132 POTENTIAL.
FT TRANSMEM 174 196 POTENTIAL.
FT TRANSMEM 217 234 POTENTIAL.
FT TRANSMEM 263 282 POTENTIAL.
FT TRANSMEM 287 309 POTENTIAL.
SQ SEQUENCE 985 AA; 109120 MW; 022E752333CF3824 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 985;
Best Local Similarity 20.4%; Pred. No. 76;
Matches 62; Conservative 37; Mismatches 94; Indels 111; Gaps 15;

QY 17 ELQGTALGNLKO-----IYYNSKAITSEKSADQFLNTLLFKGFTGHPWYNDLLV 69
DB 419 ELDPNALQQNQDQWNRHTYTHNGFIQAQAQNVDEVARDVGSTRG---GYPVYT--VS 473
QY 70 DLGASTAATSEYE-----GSSVDLYGAYG----- 93
DB 474 DLQSNAPAAASEDAEELGIKVEPRVYGLIASATGDADYAIVGTDGDPVEYDITDTS 533
QY 94 --YQAGGTP-----NKT--ACHYGGVTLHNNRLTEKKV-----PINLWIDG 133
DB 534 YTEGAGGVIGNVMNAMPALRYQENMMLLSDRVGSSEKILPERDPRSRVKVAPWLTT 593
QY 134 KQTTVP-ID-----KVKTSKKEVTVQEL--DLQARHYLHGKFG-LY 170
DB 594 DSKTYPIVIGRIKWIVDGVTTLDSLPYSTRSLTEATQDAVMDPTGQPLIDRVGVYR 653
QY 171 NS-----DSFGGKQV-----RGLIVPHSSEGSTVSVDLFDQAQGYDPDLLR 211
DB 654 NSVKAVVDAYDGVTELYEFDTEPVLKAWRGVFPDVTVDGSGEIS-DELRAHLRYPEDLFK 712
QY 212 IYRD 215
DB 713 VQRD 716

RESULT 60
MDR_PLAFF
ID MDR_PLAFF STANDARD; PRT; 1419 AA.
AC P13568;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein (Chloroquine resistance protein).
GN MDR1
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89288297; PubMed=2701941;
RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
RA Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium
RT falciparum has arisen as multiple independent events."
RL Mol. Cell. Biol. 11:5244-5250(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149200; PubMed=8426608;
RA Wilson C.M., Volkman S.K., Thaitong S., Martin R.K., Kyle D.E.,
RA Milhous W.K., Wirth D.F.;

```

"Amplification of pfmdr1 associated with mefloquine and halofantrine resistance in Plasmodium falciparum from Thailand.";
Mol. Biochem. Parasitol. 57:151-160(1993).
-!- FUNCTION: Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANEOUS: P.falciparum resistant to the drug chloroquine have multiple copies of the gene coding for MDR.
-!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; M29154; AA29646.1; -;
EMBL; X56851; CAA40180.1; -;
EMBL; S53996; AAD13870.1; -;
PIR; S18204; DVZQF.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PDOM0006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TMIF; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 82 POTENTIAL.
FT TRANSMEM 91 116 POTENTIAL.
FT TRANSMEM 160 188 POTENTIAL.
FT TRANSMEM 194 212 POTENTIAL.
FT TRANSMEM 279 298 POTENTIAL.
FT TRANSMEM 314 338 POTENTIAL.
FT TRANSMEM 339 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 807 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 908 928 POTENTIAL.
FT TRANSMEM 1028 1048 POTENTIAL.
FT TRANSMEM 1063 1083 POTENTIAL.
FT DOMAIN 1084 1419 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 643 661 POLY-ASN.
FT NP_BIND 413 420 ATP (POTENTIAL).
FT NP_BIND 1161 1168 ATP (POTENTIAL).
FT REPEAT 1 721
FT REPEAT 722 1419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 282 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;
Query Match 6.4%; Score 77.5; DB 1; Length 1419;
Best Local Similarity 21.3%; Pred. No. 1.2e+02;
Matches 47; Conservative 31; Mismatches 100; Indels 43; Gaps 8;
QY 27 KQIYYN-----SKAITSSEKSADQFLNTLLFKGFF---TGHPTWYNDLLVLDGST 74
DB 1011 KADYKNGKGRRIIVNAALWGFQSQAQLFINSFAYWFGSLIKRGITLVDDEPKSLFTE 1070
QY 75 AATSEYSGSSVDLYG-----AYGYQCA-----GTPNKIACMYGGVTLHD 115
DB 1071 IFTGSYAGKLSLKGDSENAKLSFEKYIPLMKRNSIDVRDDGGIRINKNLKGVDIKD 1130
QY 116 -NNRLTEKKVPI-----NLWIDGKQTTVPIDKVKTSKK-----EVTQELDLQARHYL---- 163
DB 1131 VNFYISRPVPIYKNLSFTCDSKTTAIVGCTSGSKSTFWNLLLRFYDLKNDHILKND 1190

QY 164 HGKFGYNSDFGGKVGRLVIFHSSEGSTVSVDLFDAGQ 204
 DB 1191 MTNFQYQNNNSLVKNNVFNQSGSABDYTFVNNNGE 1231

RESULT 61
 MOKC SCHPO
 ID MOKC SCHPO STANDARD; PRT; 2352 AA.
 AC Q9UTL4; O13605;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2004 (Rel. 43, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cell wall alpha-1,3-glucan synthase mok12 (EC 2.4.1.183).
 GN MOK12 OR SPBC32H8.13C OR P1011.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=99189260; PubMed=10087262;
 RA Katayama S., Hirata D., Arellano M., Perez P., Toda T.;
 RA "Fission yeast alpha-glucan synthase Moki requires the actin
 RT cytoskeleton to localize the sites of growth and plays an essential
 RT role in cell morphogenesis downstream of protein kinase C function.";
 RL J. Cell Biol. 144:1173-1186 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=20089027; PubMed=10620777;
 RA Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kuchida N., Jinno K.,
 RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
 RA Sakai M., Aoki K., Ogura K., Kudo H., Zhang M.Q.,
 RA Yanagida M.;
 RA "A 38 kb segment containing the cdc2 gene from the left arm of fission
 RT yeast chromosome II: sequence analysis and characterization of the
 RT genomic DNA and cDNAs encoded on the segment.";
 RL Yeast 16:71-80 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Collins M., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vanscheels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Frizc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
 RA Cerrutti L., Lowe I., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880 (2002).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) =
 CC UDP + {alpha-D-glucosyl-(1,3)}(N+1).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB018381; BAA76558.1; -
 DR EMBL; AB004534; BAA21388.1; ALT_INIT.
 DR EMBL; AL590971; CAC37503.1; -
 DR EIR; T43431; T43431.
 DR GeneDB; Spombe; SPBC32H8.13C; -
 DR InterPro; IPR006047; Alpha_amy_cat.
 DR InterPro; IPR001296; Glyco_transf_1.
 DR Pfam; PF00128; alpha-amyliase; 1.
 DR Pfam; PF00534; Glycosyltransf_1; 1.
 KW Cell wall; Transferase; Glycosyltransferase.
 SQ SEQUENCE 2352 AA; 266561 MW; 78ADPFC2P7140BBA CRC64;

 Query Match 6.4%; Score 77.5; DB 1; Length 2352;
 Best Local Similarity 20.5%; Pred. No. 2.2e+02;
 Matches 60; Conservative 35; Mismatches 72; Indels 125; Gaps 15;

 QY 4 SEINEKDLKKELOQTALGNLKIYYNKAITSS-----EKSADQFL 48
 DB 769 SEEVCKDLKFR-----IG-----FNSRLNSSPAKILEDISICGLDQAPQEV 814

 QY 49 TNTLLPKGFETG-----HPWYNDLLVDLGST----- 75
 DB 815 TNAPVTKWPNATLDSVPNGMHLLNEVSTNQTMQSKIALRIFEVNGEENPLVYPNN 874

 QY 76 ATSE-----YEGSSVDLYGAYYQCAGGTPNKACMYGVTLDHNNRLTEEKVPINLWI 131
 DB 875 ATFSPLLYKASNGDLYVNHGT---AGADKYRSLNYGPT---YSKW- 915

 QY 132 DGKQTTVPIDKV-KTSKKEVTVOELD-----LQARHYLHG-----RF--- 167
 DB 916 --KTVSTPSEKLRKPTWNGTNLQKWDGDLHVQWSSIALSTAHVQHGDTLNSYRQFENL 973

 QY 168 ---GLYNSDSFGKVGRLVIFHSSEGSTVSVDL-----FDAQGGYPD 207
 DB 974 FVQGAENRFYDGMFSPK---SYNLRNTWSYDLISTWPAELVLYNWMNPD 1023

 RESULT 62
 ID FEN AERPE STANDARD; PRT; 351 AA.
 AC Q9YFY5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Flap structure-specific endonuclease (EC 3.---).
 GN FEN OR APE0115.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococccaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki J., Kuchida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RA "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101 (1999).
 CC -1- FUNCTION: Endonuclease that cleave the 5'overhanging flap

structure that is generated by displacement synthesis when DNA polymerase encounters the 5' end of a downstream Okazaki fragment. Has 5' endo-/exonuclease and 5' pseudo-Y-endonuclease activities. Cleaves the junction between single and double-stranded regions of flap DNA (By similarity).
 CC COFACTOR: Binds 2 magnesium ions per subunit (By similarity).
 CC SIMILARITY: Belongs to the XPG/RAD2 endonuclease family. FEN1 subfamily.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AP000558; BAA79026.1; ALT_INIT.
 CC HSP; Q58839; IA76.
 CC HAMAP; MF 00614; 1.
 CC InterPro; IPR008918; 5_3_exo_C.
 CC InterPro; IPR000513; Exo_N_I.
 CC InterPro; IPR006086; XPG_I.
 CC InterPro; IPR006085; XPG_N.
 CC InterPro; IPR006084; XPGC_Rad.
 CC Pfam; PF00867; XPG_I; 1.
 CC Pfam; PF00752; XPG_N; 1.
 CC PRINTS; PR00853; XPGRADSUPER.
 CC SMART; SM00279; Hh2; 1.
 CC SMART; SM00484; XPGI; 1.
 CC SMART; SM00485; XPGN; 1.
 CC SMART; SM00485; XPGN; 1.
 CC PROSITE; PS00841; XPG_1; FALSE_NEG.
 CC HydroLase; Nuclease; Endonuclease; Magnesium; Metal-binding; Complete proteome.
 CC METAL 158 MAGNESIUM 1 (BY SIMILARITY).
 CC SEQUENCE 351 AA; 40153 MW; 28AD3B5598A5DA9 CRC64;
 CC
 CC Query Match 6.3%; Score 77; DB 1; Length 351;
 CC Best Local Similarity 21.4%; Pred. No. 23;
 CC Matches 50; Conservative 35; Mismatches 87; Indels 62; Gaps 11;
 CC
 CC 3 KSEINEKDLRKXSELO-----GTALGNLKOIYYVNSKA--ITSSEKSDQFLTNTLLPK 55
 CC Db 91 KSEVEER-LRKAEEAEARVRAVEAGEVEAEKAYMMARLITSDVVESEKELLDAM--- 146
 CC 56 GFTGTHIPWNLVDLGLSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHD 115
 CC Db 147 -----GMPW-----VQPAEGEAGAAAYMARKDAWATGSDYDLSLLFGSPRLVR 190
 CC 116 NNRLEEKVPINLWIDGKQTTVPIDKVTSKSEVTVQSLDQARHYLKGKGL----- 169
 CC Db 191 NLAITGRKKLP-----GRQYVEI-----KPEI-----LUSKLGITREQUI 231
 CC 170 -----YNSPSFGKVGQRLVPHFSSEGSTVSVDLFDAGQY-PDTLLRIY 213
 CC Db 232 AVGILLGTDYNGVGRVGYGKPTALRLVKLSLGDPMKVLASVPRGEYDPDYLRKVY 285
 CC
 CC RESULT 63
 CC MSN2 YEAST
 CC ID MSN2 YEAST STANDARD; PRT; 704 AA.
 CC AC P33748;
 CC DT 01-FEB-1994 (Rel. 28, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DT Zinc finger protein MSN2 (Multicopy suppressor of SNF1 protein 2).
 CC GN MSN2 OR YMR037C OR YM9532.02C.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CC [1]
 CC SEQUENCE FROM N.A.

RC STRAIN=S288c;
 RX MEDLINE=93309420; PubMed=8321194;
 RT "Two homologous zinc finger genes identified by multicopy suppression in a SNF1 protein kinase mutant of *Saccharomyces cerevisiae*.";
 RT Mol. Cell. Biol. 13:3872-3881(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / AB972;
 RX MEDLINE=97313268; PubMed=9169872;
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagals K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Bartell B.G., "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIII.";
 RT Nature 387:90-93(1997).
 RL [3]
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=96208509; PubMed=8641288;
 RA Martinez-Pastor M.T., Marchler G., Schueller C., Marchler-Bauer A., Ruiz H., Estruch F.;
 RT "The *Saccharomyces cerevisiae* zinc finger proteins Men2p and Msn4p are required for transcriptional induction through the stress response element (STRE).";
 RT EMBO J. 15:2227-2235(1996).
 RN [4]
 RP NUCLEOCYTOPLASMIC SHUTTLING.
 RX MEDLINE=22628141; PubMed=12732613;
 RA Jacquet M., Renault G., Lallet S., De Mey J., Goldbeter A.;
 RT "Oscillatory nucleocytoplasmic shuttling of the general stress response transcriptional activators Msn2 and Msn4 in *Saccharomyces cerevisiae*.";
 RT J. Cell Biol. 161:497-505(2003).
 CC -!- FUNCTION: POSITIVE TRANSCRIPTIONAL FACTOR THAT ACTS AS A COMPONENT OF THE STRESS RESPONSIVE SYSTEM. RECOGNIZES AND BINDS TO THE STRESS RESPONSE ELEMENT (STRE) WHICH IS INVOLVED IN THE RESPONSE TO VARIOUS FORMS OF STRESS (HEAT, OXIDATIVE, OSMOTIC, ETC.).
 CC INVOLVED IN THE REGULATION OF THE CTT1, DDR2, HSP12 GENES.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L08838; AAA34806.1; -;
 CC EMBL; Z48502; CAA88403.1; -;
 CC PIR; S39004; S39004.
 CC HSP; P08047; ISP1.
 CC GeneOnline; 142706; -;
 CC TRANSFAC; T01257; -;
 CC SGD; S0004640; MSN2.
 CC GO; GO:0005829; Cytoplasm; IDA.
 CC GO; GO:0005634; Nucleus; IDA.
 CC GO; GO:0006950; P:response to stress; IMP.
 CC InterPro; IPR007087; Znf_C2H2.
 CC Pfam; PF00096; zf-C2H2; 2.
 CC ProDom; PD000003; Znf_C2H2; 1.
 CC SMART; SM00355; Znf_C2H2; 2.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 CC PROSITE; PS00157; ZINC_FINGER_C2H2_2; 2.
 CC DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Activator; Transcription regulation; Repeat.
 CC DOMAIN 1 109 ASP-RICH (ACIDIC).
 CC DOMAIN 260 279 ASP-RICH (ACIDIC).
 CC ZN_FING 547 665 C2H2-TYPE 1.
 CC ZN_FING 676 698 C2H2-TYPE 2.
 CC SEQUENCE 704 AA; 77860 MW; EDF6F07446819DF1 CRC64;

SIGNAL 1 38 POTENTIAL.

DR PIR; S30302; S25437.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 284 AA; 33212 MW; 0E48AC80241417FE CRC64;

Query Match
Best Local Similarity 6.3%; Score 76.5; DB 1; Length 284;
Matches 35; Conservative 22; Mismatches 43; Indels 41; Gaps 8;

QY 25 NLKQIYYI-NSKAITSEKSAQDLNTLLFKGFF---TGHWPYNLDVLGSGTAATSEY 80
DB 114 NLQRMVYHLSNVLKRWPSGDMC-----FPDKTGS-----VDWGLASFLDL 157

QY 81 EGSSVDLYGAYGYQCAGGTGPNK-----TACMYGGVTLHDNNRLTEKKVPINLWID-- 132
DB 158 GGSKVDL-NEFNIRSNVDSKDNVLVQVADFAGLSVFSKSL-----GLYVDWK 208

QY 133 ---GKQTTVPIDKVKTSKKE 149
DB 209 FEKGGQQLVPEKIDLSKXD 229

RESULT 66
YQPI CAEEL STANDARD; PRT; 428 AA.
AC Q09302;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 48.3 kDa protein F07F6.1 in chromosome III.
GN F07F6.1.

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Chissee S.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; U23486; AAC46775.1; --
DR PIR; T15966; T15966.
DR Wormpep; F07F6.1; CE01894.
KW Hypothetical protein.
FT DOMAIN 9 13 POLY-SER.
FT DOMAIN 121 124 POLY-VAL.
FT DOMAIN 283 286 POLY-SER.
SQ SEQUENCE 428 AA; 48267 MW; 69A6A2AF86D5E2C CRC64;

Query Match
Best Local Similarity 26.7%; Pred. No. 33;
Matches 43; Conservative 16; Mismatches 63; Indels 39; Gaps 7;

QY 93 GYCAGGTPNKTACMYGGVTLHDNNRLTE-----BKK-----VPINLWID 133
DB 148 GYSYRGHILAVRFC-YPDGTYGDESALTQLVQCTNSAKGRILEKDDIVQDTFAVECW--- 203

QY 134 KQITVPIDKVKTSKKEVQVQELDLQARHYLHKGFLYN-SDSGGKVGQGLIVFHSSEGS 192
DB 204 --TKTFEDSLKPEKELTNL--LKAHAYLPYHTVLQSMRNLFTCKVQSEL----- 249

QY 193 TVSVLDPAQGVDPDTLLRIYRNTTISSTLSISLYTT 233
DB 250 -SSMFISDALAQWPTGLIRIFNRNKKVSNVTMCLSSSSSYT 289

RESULT 67
NUCD SALTY STANDARD; PRT; 600 AA.
ID NUCD SALTY STANDARD; PRT; 600 AA.
AC P33902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-quinone oxidoreductase chain C/D (EC 1.6.99.5) (NADH
dehydrogenase I, chain C/D) (NDH-1, chain C/D).
GN NUOC OR NUOCD OR NUOD OR STM2326 OR STY2556 OR T0538.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E.; Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 520-600 FROM N.A.
RX SPECIES=S.typhimurium;
RX MEDLINE=94052195; PubMed=8234329;
RA Archer C.D., Wang X., Elliott T.;
RT "Mutants defective in the energy-conserving NADH dehydrogenase of
Salmonella typhimurium identified by a decrease in energy-dependent
proteolysis after carbon starvation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9877-9881(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.B., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
sulfur (Fe-S) centers, to quinones in the respiratory chain. The
immediate electron acceptor for the enzyme in this species is
believed to be ubiquinone. Couples the redox reaction to proton
translocation (for every two electrons transferred, four hydrogen
ions are translocated across the cytoplasmic membrane), and thus
conserves the redox energy in a proton gradient (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -!- SUBUNIT: Composed of 13 different subunits. Subunits nuoCD, E, F,
and G constitute the peripheral sector of the complex.
CC -!- SIMILARITY: In the N-terminal section; belongs to the complex I 30
kDa subunit family.


```
CC -!- SIMILARITY: In the C-terminal section; belongs to the complex I 49
CC   kDa subunit family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB015885; BAA88798.1; -
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR002464; DEAH_box.
CC InterPro; IPR001650; Helicase_C.
CC Pfam; PF00271; Helicase_C; 1.
CC SMART; SM00487; DEXDC; 1.
CC PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
CC Helicase; Transcription regulation; Activator; ATP-binding.
CC NP BIND 45 52 ATP (POTENTIAL).
CC SITE 135 138 DEXH BOX.
CC SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 635;
Best Local Similarity 21.5%; Pred. No. 54;
Matches 55; Conservative

QY 6 EINEKD---LRK-----KSELQGTALGNLKOIYYNKAITSSEKSDQF---LTNT 51
DB 252 KLQEKDYNNVVKLCNNEMFEKNNVSLAVLGQLNFINNLDILFQEQDKELYPNLKISNG 311

QY 52 LLFKGFTGHPWNLDLLVGSTAATSEYEGSSVDLYG---AYGYQCAGTGNKTACMY 108
DB 312 IL-----YQDELTTNLSSKFKYFKITSLTGKQFIYFSNSTYGGLIKIYIMLS 361

QY 109 GGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSEKVTQVELDLQARHYLHGKFG 168
DB 362 NGYSEYNGSQTPK-----LINGKPTFAI---VTSKMKSSLEDL-----LN 401

QY 169 LYNDSFGKVGQRLIVFHSESGTSSVYDLF-----DAQGYPTLLRIYVDNT 217
DB 402 VYNSQL--NKDGSQIMFLPSSNIMSESYTLKEVINWFMTPDTFSQYNQILGERSIR-KF 458

QY 218 TISSTSLISLYLYTT 233
DB 459 SYFDISKPVNLYLLAT 474

RESULT 69
ID RPAL1 SCHPO STANDARD; PRT; 1689 AA.
AC P15398;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6).
GN RPAL OR NUC1 OR SPBC4C3.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9139548; PubMed=2537310;
RA Hirano T., Konoha G., Toda T., Yanagida M.;
RT "Essential roles of the RNA polymerase I largest subunit and DNA
RT topoisomerases in the formation of fission yeast nucleolus.";
RL J. Cell Biol. 108:243-253(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972 / HMI23;
RX MEDLINE=89232741; PubMed=2854522;
RA Yanagishi M., Nomura M.;
RT "Cloning and sequence determination of the gene encoding the largest
```

```
CC -!- SIMILARITY: In the C-terminal section; belongs to the complex I 49
CC   kDa subunit family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB015885; BAA88798.1; -
CC InterPro; IPR001410; DEAD.
CC InterPro; IPR002464; DEAH_box.
CC InterPro; IPR001650; Helicase_C.
CC Pfam; PF00271; Helicase_C; 1.
CC SMART; SM00487; DEXDC; 1.
CC PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
CC Helicase; Transcription regulation; Activator; ATP-binding.
CC NP BIND 45 52 ATP (POTENTIAL).
CC SITE 135 138 DEXH BOX.
CC SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 635;
Best Local Similarity 21.5%; Pred. No. 54;
Matches 55; Conservative

QY 6 EINEKD---LRK-----KSELQGTALGNLKOIYYNKAITSSEKSDQF---LTNT 51
DB 252 KLQEKDYNNVVKLCNNEMFEKNNVSLAVLGQLNFINNLDILFQEQDKELYPNLKISNG 311

QY 52 LLFKGFTGHPWNLDLLVGSTAATSEYEGSSVDLYG---AYGYQCAGTGNKTACMY 108
DB 312 IL-----YQDELTTNLSSKFKYFKITSLTGKQFIYFSNSTYGGLIKIYIMLS 361

QY 109 GGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSEKVTQVELDLQARHYLHGKFG 168
DB 362 NGYSEYNGSQTPK-----LINGKPTFAI---VTSKMKSSLEDL-----LN 401

QY 169 LYNDSFGKVGQRLIVFHSESGTSSVYDLF-----DAQGYPTLLRIYVDNT 217
DB 402 VYNSQL--NKDGSQIMFLPSSNIMSESYTLKEVINWFMTPDTFSQYNQILGERSIR-KF 458

QY 218 TISSTSLISLYLYTT 233
DB 459 SYFDISKPVNLYLLAT 474

RESULT 69
ID RPAL1 SCHPO STANDARD; PRT; 1689 AA.
AC P15398;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6).
GN RPAL OR NUC1 OR SPBC4C3.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9139548; PubMed=2537310;
RA Hirano T., Konoha G., Toda T., Yanagida M.;
RT "Essential roles of the RNA polymerase I largest subunit and DNA
RT topoisomerases in the formation of fission yeast nucleolus.";
RL J. Cell Biol. 108:243-253(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972 / HMI23;
RX MEDLINE=89232741; PubMed=2854522;
RA Yanagishi M., Nomura M.;
RT "Cloning and sequence determination of the gene encoding the largest
```

subunit of the fission yeast *Schizosaccharomyces pombe* RNA polymerase I.
 Gene 74:503-515(1988).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=972;
 MEDLINE=21849401; PubMed=11859360;
 Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jinenz J., Sanchez M., del Rey P., Benito J., Dominguez A., Revuelta J.B., Moreno S., Armstrong J., Forsburg S.J., Cerretti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J., Sipakowski G.V., Usery D., Barrell B.G., Nurse P.;
 "The genome sequence of *Schizosaccharomyces pombe*."
 Nature 415:871-880(2002).
 CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates. RNA polymerase I is essentially used to transcribe ribosomal DNA units.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA) (N).
 CC -!- SUBUNIT: Each class of RNA polymerase is assembled from 9 to 14 different polypeptides. This subunit is the largest component of RNA polymerase I.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- MISCELLANEOUS: Three distinct zinc-containing RNA polymerases were found in eukaryotic nuclei: polymerase I for the ribosomal RNA precursor, polymerase II for the mRNA precursor, and polymerase III for 5S and tRNA genes.
 CC -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X14783; CAA32887.1; -;
 CC EMBL; M37411; AAA35326.1; -;
 CC EMBL; AL021730; CAA16827.1; -;
 CC PIR; J50980; J50980.
 CC GeneDB Spombe; SPBC4C3.05c; -;
 CC InterPro; IPR007072; RNA_pol_A.
 CC InterPro; IPR007080; RNA_pol_Rpb1_1.
 CC InterPro; IPR007066; RNA_pol_Rpb1_3.
 CC InterPro; IPR007083; RNA_pol_Rpb1_4.
 CC InterPro; IPR007081; RNA_pol_Rpb1_5.
 CC InterPro; IPR006592; RNA_pol_A_N.
 CC Pfam; PF04997; RNA_pol_Rpb1_1.
 CC Pfam; PF00623; RNA_pol_Rpb1_2.
 CC Pfam; PF04983; RNA_pol_Rpb1_3.
 CC Pfam; PF05000; RNA_pol_Rpb1_4.
 CC Pfam; PF04998; RNA_pol_Rpb1_5.
 CC

DR SMART; SM00663; RPOLA_N; 1.
 KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
 RN Zinc-finger; Nuclear protein.
 FT ZN FING 63 79
 FT CONFLICT 69 69 D -> A (IN REF. 1).
 FT CONFLICT 84 84 I -> S (IN REF. 1).
 FT CONFLICT 704 704 T -> I (IN REF. 1).
 FT CONFLICT 1581 1581 A -> T (IN REF. 1).
 FT CONFLICT 1681 1681 T -> N (IN REF. 1).
 SQ SEQUENCE 1689 AA; 189244 MW; 2D2D3A2DEC94A497 CRC64;
 Query Match 6.3%; Score 76.5; DB 1; Length 1689;
 Best Local Similarity 24.7%; Pred. No. 1.8e+02;
 Matches 49; Conservative 32; Mismatches 52; Indels 65; Gaps 14;
 QY 25 NKQIYYNSK--ALTSEKSAQDLNTLLPK-----GFTGHFWYNDLLVDLGSTAATS 78
 DB 891 NLEEVYRDEKLQGLDAAMKGMKMGATSSIIKIPDGLTKFP--YNNHM-----QTMVTS 944
 QY 79 EYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ--T 136
 DB 945 GAKGSNNVV-----SQISCLLQOQL-----EGRRVP--LMVSGKSLPS 981
 QY 137 TVPIDKVKTSKE-----VTQVELDQARHYLH---GKFGLYNS---DSFGGKV 179
 DB 982 FVPYE---TSAKSGGFIASRELTGIAPQE-----YVPHCMAGREGLIDTAVKTSRSGYL 1032
 QY 180 QRGIVPHSHSGSTVSVD 197
 DB 1033 QRCLM--KHLSGLCQVQYD 1048
 RESULT 70
 YCX9 CHLRE STANDARD; PRT; 2971 AA.
 ID YCX9 CHLRE STANDARD; PRT; 2971 AA.
 AC Q32655; Q35635;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical 341.7 kDa protein in psbD-psbC intergenic region (ORF2971) (ORF).
 DE Chlamydomonas reinhardtii.
 OS Chlamydomonas reinhardtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadales; Chlamydomonadales.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=137c / CC-125;
 RA Watson A.I.; Purton S.;
 RT "Unidentified open reading frame ORF2971 (ORF) from the chloroplast genome of *Chlamydomonas reinhardtii*."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
 RP [2]
 RP SEQUENCE OF 2635-2971 FROM N.A.
 RC STRAIN=137c / CC-125;
 RX MEDLINE=89305500; PubMed=2663467;
 RA Rochaix J.D., Kuchka M., Mayfield S., Schirmer Rahire M., Girard Bascon J., Bemmoun P.;
 RT "Nuclear and chloroplast mutations affect the synthesis or stability of the chloroplast psbc gene product in *Chlamydomonas reinhardtii*."
 RL EMBL J. 8:1013-1021(1989).
 RN [3]
 RP COMPLETE PLASTID GENOME.
 RX MEDLINE=22305394; PubMed=12417694;
 RA Maul J.E., Lilly J.W., Cui L., Depamphilis C.W., Miller W., Harris E.H., Stern D.B.;
 RT "The *Chlamydomonas reinhardtii* plastid chromosome: islands of genes in a sea of repeats."
 RL Plant Cell 14:2659-2679(2002).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U62943; CAA05800.1; -
DR EMBL; X13879; CAA32083.1; -
DR EMBL; BX000554; DAA00965.1; -
DR InterPro; IPR003959; AAA_ATPase_centr.
DR Pfam; PF00004; AAA; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 2971 AA; 341663 MW; 3BE294AF2248348A CRC64;

Query Match 6.3%; Score 76.5; DB 1; Length 2971;
Best Local Similarity 19.8%; Pred. No. 3,7e+02;
Matches 54; Conservative 42; Mismatches 78; Indels 99; Gaps 13;
QY 4 SEINEKOLRKKSELOQT-ALGNLKOIYYNKAITSSEKSDQFLTNTLFGFTGHP 62
DB 2453 SKKLKELNWSKLIGSNGTSGQNVDLGVFAQIVNKKQKSLQQLPNSK-KSF----- 2505
QY 63 WYNDLVDLGSTAATSEYSSGVLDLYGAYGQCAGGTNTACMYGGVTLHD--NNRLT 120
DB 2506 -----KKYKXDKAIYYEV-----GKFLNLYFLNNQUT 2533
QY 121 BEKKVPINLWDGKQTVPIDKVTSKKEVTV---QELDLQARHYLHGKFLYNSDS--- 174
DB 2534 QSSIDKPSVNTKQI-----NDITFGDNFLNKINYL-----SLYNSKNKIL 2578
QY 175 -----FGKVGQGL-----IVFHSSEGSTVSVDLFDACQ-----YPTTLR 211
DB 2579 LQMLIFGKISQLSSKNLVSLSKQASINSYWEESGSSAGMPLGQTHLLPKALSV 2638
QY 212 I-----YRDNNTISSTLSISL-----YLY 231
DB 2639 LAKPMIFSQYNNQNLKTAITLLSFIHKRYLY 2671

RESULT 71
PCNA_HALMA
ID_PCNA_HALMA STANDARD; PRT; 247 AA.
AC Q9P9H8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase sliding clamp (Proliferating cell nuclear antigen
DE homolog) (PCNA).
GN PCN.
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP SEQUENCE FROM N.A.
RA Ichiki H., Tanaka Y., Mochizuki K., Yoshimatsu K., Sakurai T.,
RA Fujiwara T.;
RT Molecular and genetic analysis of copper-containing dissimilatory
RT nitrite reductase from a denitrifying halophilic archaeon, Haloarcula
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Sliding clamp subunit. Responsible for tethering the
CC catalytic subunit of DNA polymerase to DNA during high-speed
CC replication (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SIMILARITY: Belongs to the PCNA family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF442553; AAL35379.1; -
DR HAMAP; MF.00473; -; 1.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; G6I; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.

CC or send an email to license@isb-sib.ch.
CC
DR EMBL; AJ278286; CAB93143.1; ALT_INIT.
DR HSSP; O73947; IGE8.
DR HAMAP; MF.00317; -; 1.
DR InterPro; IPR000730; Pr_cel_nuc_antig.
DR Pfam; PF00705; PCNA; 1.
DR PRINTS; PR00339; PCNACYCLIN.
DR ProDom; PD002673; Pr_cel_nuc_antig; 1.
DR PROSITE; PS01251; PCNA_1; 1.
DR PROSITE; PS00293; PCNA_2; FALSE_NEG.
KW DNA-binding; DNA replication.
SQ SEQUENCE 247 AA; 27060 MW; 12EB3E2774A7FB3A CRC64;
Query Match 6.2%; Score 76; DB 1; Length 247;
Best Local Similarity 23.2%; Pred. No. 19;
Matches 38; Conservative 26; Mismatches 58; Indels 42; Gaps 6;
QY 68 LVDLGGSTAATSEYSSGVLDLYGAYGQCAGGTNTACMYGGVTLH-----DNNR 118
DB 46 MVDLRLDAA-----APESYETDGLI-----GVNLSRLIEDIAGMADAG 84
QY 119 LT-----BEKKVPINLWDGKQTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDS 174
DB 85 LVHLDDEETRKHLISIDGLEVTALIDPDSIKQEPDLPDLDSANIVIEGK-----DI 138
QY 175 FGKVGQGLIVFHSSEGSTVSVDLFDACQGYPTTLRIYRDN 216
DB 139 DRSVTAADMSVDHIALGVADATDELFFYVDASGDTDDVHLELTRDD 182

RESULT 72
G6PI_STRTR
ID_G6PI_STRTR STANDARD; PRT; 449 AA.
AC Q8VVB7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI.
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-250 / LMG 18311;
RA van den Bogaard P.T.C., Kleerebezem M., Hols P., Crispie F.,
RA Kuipers O.P., de Vos W.M.;
RT "Modulation of glycolysis by lactose availability in Streptococcus
RT thermophilus";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
CC phosphate.
CC -!- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the GPI family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF442553; AAL35379.1; -
DR HAMAP; MF.00473; -; 1.
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; G6I; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.

DR PROSITE; PS00174; P. GLUCOSE ISOMERASE 2; 1.
 KW Isomerase; Gluconeogenesis; Glycolysis.
 FT ACT SITE 312 BY SIMILARITY.
 FT ACT SITE 426 BY SIMILARITY.
 SQ SEQUENCE 449 AA; 49814 MW; 996D637623C6C72F CRC64;

Query Match
 Best Local Similarity 5.2%; Score 76; DB 1; Length 449;
 Matches 50; Conservative 31; Mismatches 74; Indels 60; Gaps 12;

QY 32 YNSKAITSSSEKSDQFLNTLLFKGFTGHPWYNDLLVDLGLGTAATSEYEGSSVDLYGAY 91
 DB 241 YSSSKISENEAYQAAARNILYRGY-----TTEILANYEPLS--QYFAE 283
 QY 92 YGYQCAGTPNK-----TACMYGGVTLHNNRLTBKKVPINLWDGKQTTVPIDKVK 144
 DB 284 WVKQLAGESEKQDQGIYPTISANP--STDLHSLGQFIQEG--TRNLF---ETVVRVDK-- 334
 QY 145 TSKEVTVQEL--DLQARHYLHGKFLGYNDSFGGKVGQGLIVFHSSEGSTVSVDLFDQAQ 202
 DB 335 -PRKNVPIPEALDGLGLQK-----DVFVNKATDGVLLAHT-----D 376
 QY 203 GQYPTDILLRI-YRDNMTIS-----STLSLSISLYL 230
 DB 377 GDVPMFTIPEQDAFTGLGVIYFFELALIALSGYL 411

RESULT 73
 YF08 MYCPN
 ID YF08 MYCPN STANDARD; PRT; 509 AA.
 AC P75278;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN508 (P02_orf509).
 GN MPN508 OR MP334.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=9948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae".
 RL Nucleic Acids; Res. 24:4420-4449 (1996).
 CC -!- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE000031; AAB95982.1; -.
 DR PIR; S73660; S73660.
 DR InterPro; IPR004306; MG032/096/288 1.
 DR InterPro; IPR004319; MG032/096/288-2.
 DR Pfam; PF03072; DUF237; 1.
 DR Pfam; PF03086; DUF240; 1.
 DR ProDom; PD004834; MG032/096/288 2; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 509 AA; 57625 MW; 8CDC95BB941A6987 CRC64;

Query Match
 Best Local Similarity 6.2%; Score 76; DB 1; Length 509;
 Matches 54; Conservative 35; Mismatches 97; Indels 52; Gaps 13;

QY 3 KSEINEKDLRKSELQGTALGNLQKIYYNSKAITSSEK-----SADQFLNTLL 52

DB 234 KAEYVKLEAREAFNKSLSLTAASEFKQYWSKKNDVTDKKOLAEALKISLEADNRRTSF 293
 QY 53 LFKGFTGHPWY-----NDLLVD-LGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKT 104
 DB 294 LIAGFTATDWMYNAKKENNDKAKAFSGSQGIFPKDG-----LANGIYMPDWLRLGSLTSS 349
 QY 105 ACMYGGVTLHNNRLTBKKV-----PINIWDGKQTTVPIDKVKTSKEVTVQELDLQ 158
 DB 350 -----NINLIKELKVNKIESPTINWDG--VGIKODKANPNFYAFEV-DIKYT 396
 QY 159 ARHYLHGKF---GLVNS--DSFGGKVGQGLIVFHSSEGSTVSVDLFDQAQGYPTLLR 211
 DB 397 GGYQLYGYFAAALFTKFPSSWSGEMNLKFIV---DGSIPVTV--AKKDYPSLQF 448

RESULT 74
 PBP STAAU
 ID PBP STAAU STANDARD; PRT; 670 AA.
 AC P07944;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Beta-lactam-inducible penicillin-binding protein.
 GN PBP.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87304805; PubMed=3305073;
 RA Song M.D., Wachi M., Doi M., Ishino F., Matsushashi M.;
 RT "Evolution of an inducible penicillin-target protein in methicillin-
 RT resistant Staphylococcus aureus by gene fusion."
 RL FEBS Lett. 221:167-171 (1987).
 CC -!- INDUCTION: IN THE PRESENCE OF BETA-LACTAM ANTIBIOTICS, MRSA
 CC CELLS PRODUCE THIS UNIQUE PBP IN EXCESSIVELY LARGE AMOUNTS AND
 CC CAN STILL PROLIFERATE, WHILE ALL THE NORMAL PBPS ARE INACTIVATED
 CC (REVERSIBLE SWITCHING ABILITY OF PBP FORMATION).
 CC -!- MISCELLANEOUS: PBP HAS EXTREMELY LOW AFFINITY TO PENICILLIN AND
 CC -!- MOST OTHER BETA-LACTAM ANTIBIOTICS
 CC -!- SIMILARITY: TWO DIFFERENT SETS OF CONSERVED SEQUENCES CONTAINING
 CC S-X-X-K FOR PENICILLIN-BINDING WERE FOUND IN MRSA PBP, THE FIRST
 CC BEING LOCATED AROUND SER-25 (HOMOLOGY WITH THE PENICILLIN-BINDING
 CC DOMAIN OF THE PENICILLINASE) AND THE SECOND AROUND SER-405 (HIGH
 CC HOMOLOGY WITH BOTH THE PUTATIVE TRANSGLYCOSYLASE (N-TERMINAL) AND
 CC TRANSPEPTIDASE (C-TERMINAL) PENICILLIN-BINDING DOMAIN OF E. COLI
 CC PBPS 2 AND 3). THE AUTHORS SUGGEST THE SER-405 RESIDUE TO BE THE
 CC PENICILLIN-BINDING SITE AND THE SEQUENCE AROUND SER-25 TO BE A
 CC RELIC OF THE EVOLUTION OF THIS DOMAIN FROM A PENICILLINASE GENE.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y00688; CAA68684.1; -.
 DR MEROPS; S12 UNW; -.
 DR InterPro; IPR007887; Meca.N.
 DR InterPro; IPR005311; PBP-dimer.
 DR InterPro; IPR001460; Transpeptidase.
 DR Pfam; PF05223; Meca.N; 1.
 DR Pfam; PF03717; PBP dimer; 1.
 DR Pfam; PF00905; Transpeptidase; 1.
 DR Peptidoglycan synthesis; Cell division; Antibiotic resistance;
 KW Cell wall.
 KW BINDING 25 25 PENICILLIN (PROBABLE).
 FT BINDING 405 405 PENICILLIN (PROBABLE).
 FT SEQUENCE 670 AA; 76463 MW; 2DAA14D35DA993A CRC64;

Query Match 6.2%; Score 76; DB 1; Length 670;
 Best Local Similarity 26.4%; Pred. No. 64;
 Matches 33; Conservative 19; Mismatches 41; Indels 32; Gaps 6;
 QY 64 YNDLLVGLSTAAATSEYEGS-----SVDLYGAYGYGACAGTGNKTYACMYGGVTLHD 115
 Db 339 YNNKNDYGGGTGTAHPOTGELLALVSTPSYDVTFMY-----GMSNEE 381
 QY 116 NNRLTEKKVP-INLWIDGKQTTP--IDKVKTSKKEVTVOELDLQARHYLHGKFGLYNS 172
 Db 382 YNKLTEDKKEPLNKF---QITSPGTSQILTAMIGLNKNTLDDKTSYKIDGK-GWQXD 437
 QY 173 DSFGG 177
 Db 438 KSWG 442

RESULT 75

NEUL_HUMAN
 ID NEUL_HUMAN STANDARD; PRT; 704 AA.
 AC Q95Y8; Q9ULJ4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurolysin, mitochondrial precursor (EC 3.4.24.16) (Neurotensin
 DE endopeptidase) (Mitochondrial oligopeptidase M) (Microsomal
 DE endopeptidase) (NEP).
 GN NLN OR KIAA1226.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen J.M., Rawlings N.D., Barrett A.J.;
 RT "Cloning and sequencing of human neurolysin, an oligopeptidase of
 RT family M3";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039619; PubMed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 RT for large proteins in vitro";
 RL DNA Res. 6:337-345(1999).
 CC -!- FUNCTION: Hydrolyzes oligopeptides such as neurotensin,
 CC bradykinin, dynorphin A, etc. (By similarity).
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage in neurotensin: 10-
 CC Pro-|-Tyr-11.
 CC -!- COPACITOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial intermembrane space and
 CC also cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M3.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ300837; CAC27329.1; --
 CC EMBL; AB033052; BAA86540.2; --
 CC Genbank; HGNC:16058; NLN.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR001567; Peptidase M3.
 CC Pfam; PF01432; Peptidase M3; 1.
 CC PROSITE; PS00142; ZINC PROTEASE; 1.
 CC Metalloprotease; Hydrolase; Zinc; Mitochondrion; Transit peptide.

FT TRANSIT 1 37 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 38 704 NEUROLYSIN.
 FT METAL 497 498 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 498 499 BY SIMILARITY.
 FT METAL 501 501 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 504 504 ZINC (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 704 AA; 80651 NW; 80136688D79BBD F CRC64;
 Query Match 6.2%; Score 76; DB 1; Length 704;
 Best Local Similarity 22.0%; Pred. No. 68;
 Matches 61; Conservative 32; Mismatches 92; Indels 92; Gaps 16;
 QY 1 SEKSEINEKD-----LRKKS-----ELQGTALGNLKOIYYVNSKAITSEK---SAD 45
 Db 323 SQKLPLGEAREREFLNKKCKEKGDFYDGI--NAWDLYY---MTQTEELKYSID 376
 QY 46 Q-----FLTNT-----LLFKGFFTHPWYNDLLVDLGSTAAATSEYEGS-S 84
 Db 377 QBFLEKYEPIEVVTEGLLNTYQELLGLSFEQMTDAHVWVNSVTLYTVKDKATGEVLGQFY 436
 QY 85 VDIY---GAYGYGACAGTGNKTCMYGGVTLHNNRLTEKKVPEINLW--IDGKQTTP 139
 Db 437 LDLYPREGKYNHACFGLOP-----GCLLPDGSRWVAALVNFSPQVAGRPSSLR 488
 QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQVOR--GLIVFHSSEGSTVS 197
 Db 489 HDEVRT-----YFH-----EFGHVMHQICAQTDFAFPSTGNTVETD 523
 QY 198 LFDAGQY-----PDILLRI---YRNTYISSTSL 224
 Db 524 FVEVPSQMLENWWVDVSLRLSKHYKDGSPIDALL 560

Search completed: August 12, 2004, 13:30:31
 Job time : 10.1186 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 20.2698 Seconds
(without alignments)

3626.866 Million cell updates/sec

US-09-900-766-2

Title: BLOSUM62

Perfect score: 1218

Sequence: 1 SEKSEENEDLKKKSELQK.....RDNTTISSTLSLSLYLYTT 233

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_plage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_ivirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	77.8	260	16 Q931M4	Q931M4 staphylococ
2	918	75.4	260	16 Q99SU3	Q99SU3 staphylococ
3	754	61.9	268	2 O85217	O85217 staphylococ
4	438.5	36.0	229	16 Q8NM97	Q8NM97 staphylococ
5	420.5	34.5	258	16 Q9EZM4	Q9EZM4 staphylococ
6	372.5	30.6	260	16 Q99T46	Q99T46 staphylococ
7	372.5	30.6	261	2 Q9EZM8	Q9EZM8 staphylococ
8	355	29.1	179	2 Q52075	Q52075 staphylococ
9	311	25.5	240	16 Q9F0L7	Q9F0L7 staphylococ
10	310	25.5	240	16 Q8NXJ5	Q8NXJ5 staphylococ
11	308	25.3	217	2 Q8RR76	Q8RR76 staphylococ
12	308	25.3	241	16 Q53585	Q53585 staphylococ
13	296.5	24.3	242	16 Q85383	Q85383 staphylococ
14	294.5	24.2	225	2 Q8VVM1	Q8VVM1 streptococ
15	293.5	24.1	225	2 Q91921	Q91921 streptococ
16	288.5	23.7	218	2 Q8RR75	Q8RR75 staphylococ

17	288.5	23.7	239	2	O05157	O05157 staphylococ
18	287.5	23.6	225	16	Q99Z21	Q99Z21 streptococ
19	287.5	23.6	239	2	O06535	O06535 staphylococ
20	284.5	23.4	239	2	O06531	O06531 staphylococ
21	284	23.3	239	2	Q9EZM7	Q9EZM7 staphylococ
22	282	23.2	239	16	Q99T47	Q99T47 staphylococ
23	278.5	22.9	242	16	Q8NMV3	Q8NMV3 staphylococ
24	278.5	22.9	256	2	Q8VLM7	Q8VLM7 staphylococ
25	278.5	22.9	266	16	Q8NXJ6	Q8NXJ6 staphylococ
26	277.5	22.8	239	2	O06532	O06532 staphylococ
27	277.5	22.8	239	2	O06533	O06533 staphylococ
28	276.5	22.7	234	2	Q9RSX4	Q9RSX4 staphylococ
29	276.5	22.7	242	2	Q93CC6	Q93CC6 staphylococ
30	275.5	22.6	207	2	Q7X0E8	Q7X0E8 staphylococ
31	271.5	22.3	218	2	Q7X0E7	Q7X0E7 staphylococ
32	270.5	22.2	218	2	Q7X0E9	Q7X0E9 staphylococ
33	268.5	22.0	251	16	Q8K6K5	Q8K6K5 streptococ
34	265.5	21.8	271	2	Q9F0L6	Q9F0L6 staphylococ
35	264.5	21.7	239	2	Q7X0E6	Q7X0E6 staphylococ
36	264.5	21.7	239	2	Q53678	Q53678 staphylococ
37	264	21.7	242	16	Q8NMV2	Q8NMV2 staphylococ
38	263	21.6	242	2	Q93CC5	Q93CC5 staphylococ
39	263	21.6	242	2	O54476	O54476 staphylococ
40	258.5	21.2	239	2	O06534	O06534 staphylococ
41	254.5	20.9	236	2	P97163	P97163 streptococ
42	253.5	20.8	236	2	Q54779	Q54779 streptococ
43	252.5	20.7	222	2	Q9R931	Q9R931 streptococ
44	251.5	20.6	236	2	Q54696	Q54696 streptococ
45	251	20.6	260	2	Q54738	Q54738 streptococ
46	251	20.6	260	2	Q54971	Q54971 streptococ
47	251	20.6	260	16	Q54739	Q54739 streptococ
48	250	20.5	222	2	Q9S5Z4	Q9S5Z4 streptococ
49	250	20.5	222	2	Q938P4	Q938P4 streptococ
50	249	20.4	258	2	Q92NF2	Q92NF2 staphylococ
51	248.5	20.4	236	2	Q57453	Q57453 streptococ
52	241	19.8	233	2	Q8RR77	Q8RR77 staphylococ
53	241	19.8	258	2	Q9EZM3	Q9EZM3 staphylococ
54	238.5	19.6	259	2	Q936G4	Q936G4 staphylococ
55	222	18.2	209	2	Q9RQJ5	Q9RQJ5 streptococ
56	219	18.0	209	2	Q9LAE0	Q9LAE0 streptococ
57	219	18.0	209	2	Q9LAD8	Q9LAD8 streptococ
58	217	17.8	209	2	Q9LAC6	Q9LAC6 streptococ
59	217	17.8	209	2	Q9LAD1	Q9LAD1 streptococ
60	215	17.7	209	2	Q9LAE1	Q9LAE1 streptococ
61	215	17.7	209	2	Q9LAC5	Q9LAC5 streptococ
62	213	17.5	209	2	Q9LAD9	Q9LAD9 streptococ
63	211	17.3	209	2	Q9LAD2	Q9LAD2 streptococ
64	210	17.2	209	2	Q9LAD6	Q9LAD6 streptococ
65	210	17.2	209	2	Q8NZ89	Q8NZ89 streptococ
66	209.5	17.2	233	16	Q8NZ89	Q8NZ89 streptococ
67	209	17.2	207	2	Q7WY99	Q7WY99 streptococ
68	207	17.0	209	2	Q9LAC9	Q9LAC9 streptococ
69	206	16.9	209	2	Q9LAC7	Q9LAC7 streptococ
70	206	16.9	209	2	Q9LAD4	Q9LAD4 streptococ
71	205	16.8	209	2	Q9LAC8	Q9LAC8 streptococ
72	205	16.8	209	2	Q9LAC3	Q9LAC3 streptococ
73	204.5	16.8	256	2	Q9SIH8	Q9SIH8 streptococ
74	203	16.7	209	2	Q9LAD5	Q9LAD5 streptococ
75	201	16.5	209	2	Q9LAD3	Q9LAD3 streptococ
76	200	16.4	209	2	Q9LAD7	Q9LAD7 streptococ
77	198.5	16.3	233	16	Q99XW1	Q99XW1 streptococ
78	198	16.3	209	2	Q9LAD0	Q9LAD0 streptococ
79	190	15.6	136	16	Q99T49	Q99T49 staphylococ
80	187	15.6	236	2	Q9L920	Q9L920 streptococ
81	186.5	15.3	234	16	Q8K8Q7	Q8K8Q7 streptococ
82	184	15.1	240	16	Q8P2R5	Q8P2R5 streptococ
83	182.5	15.0	210	2	Q9K2G9	Q9K2G9 streptococ
84	178	14.6	157	16	Q99TP7	Q99TP7 staphylococ
85	160	13.1	232	16	Q99QN1	Q99QN1 streptococ
86	156	12.8	234	2	Q53RR9	Q53RR9 streptococ
87	156	12.8	234	2	Q8G9K7	Q8G9K7 streptococ
88	153.5	12.6	108	2	Q9EZM5	Q9EZM5 staphylococ
89	153.5	12.6	235	16	Q8NXX2	Q8NXX2 streptococ

90 153.5 12.6 256 2 Q9X9R8 Q9X9R8 streptococc
 91 153.5 12.6 256 2 Q9S1H9 Q9S1H9 streptococc
 92 143 11.7 206 2 Q54512 Q54512 streptococc
 93 138.5 11.4 167 2 Q7X0E4 Q7X0E4 staphylococ
 94 130.5 10.7 167 2 Q7X0E5 Q7X0E5 staphylococ
 95 125.5 10.3 167 2 Q7WS59 Q7WS59 staphylococ
 96 119.5 9.8 227 2 Q843U3 Q843U3 streptococc
 97 118.5 9.7 262 16 Q8P0S0 Q8P0S0 streptococc
 98 117.5 9.6 259 16 Q938J1 Q938J1 streptococc
 99 115 9.2 62 16 Q99TP8 Q99TP8 staphylococ
 100 113.5 9.3 209 16 Q879B0 Q879B0 streptococc

ALIGNMENTS

RESULT 1

Q931M4 PRELIMINARY; PRT; 260 AA.
 AC Q931M4
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin P.
 GN SEP OR SAV1948.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizukami-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003364; BAB58110.1; --
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_cox_OB.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 77.8%; Score 948; DB 16; Length 260;
 Best Local Similarity 76.4%; Pred. No. 6.7e-69;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOCTALGNLKIYYNKAITSSEKSAQOPLNTLLFKGFTG 60
 DB 28 SEKSEINEKDLRKSELOCTALGNLKIYYNKAITSSEKSAQOPLNTLLFKGFTG 87
 QY 61 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLT 120
 DB 88 HWYNDLLVDFDSKOIVDKYKGVLDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLT 147
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 148 EEKVPINLWIDGKQNTVPLETVKTKNNVTQVELDLQARRYLQEKYLNLYNSDVPDGKQV 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNTTISTSLISLYLYTT 233
 DB 208 RGLIVFHTSTPSVNYDLFDAQGYSTNLLRIYRDNTINSNNHIDIYLYTS 260

RESULT 2

Q99SU3 PRELIMINARY; PRT; 260 AA.
 ID Q99SU3
 AC Q99SU3
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin P.
 GN SEP OR SAI761.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
 RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
 RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 RA Hiraoka H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
 RA Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003135; BAB43036.1; --
 DR PIR: C89984; C89984.
 DR HSP: P13163; 1SXT.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_cox_OB.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 75.4%; Score 918; DB 16; Length 260;
 Best Local Similarity 73.0%; Pred. No. 1.8e-66;
 Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOCTALGNLKIYYNKAITSSEKSAQOPLNTLLFKGFTG 60
 DB 28 SEKSEINEKDLRKSELOCTALGNLKIYYNKAITSSEKSAQOPLNTLLFKGFTG 87
 QY 61 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLT 120
 DB 88 HWYNDLLVDFDSKOIVDKYKGVLDLYGAYGYOCAGGTPNKTCMVGVTLDHNNRLT 147
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 148 EEKVPINLWIDGKQNTVPLETVKTKNNVTQVELDLQARRYLQEKYLNLYNSDVPDGKQV 207
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNTTISTSLISLYLYTT 233
 DB 208 RGLIEFHPSSGSDSVGYDLFDAQGYPTDLRIYRDNTIKSNKHIDIYLYTT 260

RESULT 3
 C85217

ID	Q85217	PRELIMINARY;	PRT;	268 AA.
AC	Q85217;			
DT	01-NOV-1998	(TrEMBLrel. 08, Created)		
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Enterotoxin J.			
GN	SEJ			
OS	Staphylococcus aureus.			
OC	Plasmid pIB485.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KSI11410;			
RX	MEDLINE=99052098; PubMed=9835033;			
RT	Zhang S., Iandolo J.J., Stewart G.C.;			
RT	"The enterotoxin D plasmid of Staphylococcus aureus encodes a second			
RT	enterotoxin determinant (sej).";			
RL	FEMS Microbiol. Lett. 168:227-233 (1998).			
DR	EMBL; AF053140; AAC78590.1; ..			
DR	HSP; P13163; IESF			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0046821; C:extrachromosomal DNA; IEA.			
DR	GO; GO:0015070; F:toxin activity; IEA.			
DR	GO; GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR008992; Bact_endotox.			
DR	InterPro; IPR006177; Bctr1_tox.			
DR	InterPro; IPR006123; Staph/Strep_toxin.			
DR	InterPro; IPR006126; Staph/Strep_tox.			
DR	InterPro; IPR006173; Staph_tox_OB.			
DR	Pfam; PF011123; Staph_Strep_toxin; 1.			
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.			
DR	PRINTS; PR00279; BACTRLTOXIN.			
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.			
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.			
KW	Plasmid.			
SQ	SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;			
	Query Match 61.9%; Score 754; DB 2; Length 268;			
	Best Local Similarity 59.3%; Pred. No. 3.7e-53;			
	Matches 137; Conservative 38; Mismatches 56; Indels 0; Gaps 0;			
Qy	3 KSEINKEKDLKKSELOGTALGNLKQIYYNSKAITSEKSAEQFLNTLLFKGFFTGHP 62			
Db	27 KNETIKENLKKSELSITLNNLRHYFFNEKGISSEKIMTDFLDYLLFKSFFSHS 86			
Qy	63 WYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGPNKTCMYGGVTLHDNNRLTEE 122			
Db	87 QYNDLLVQFDSKETVNFKEKQVDLYGSYGFCQSGGKPNKTCMYGGVTLHNNQLYDT 146			
Qy	123 KKVPINLWIDGQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQR 182			
Db	147 KKIPINLWIDSIRTVVPLDVKTNKKVKTICELDLQARYYVLLHKGYNLNPSTFGDKIQG 206			
Qy	183 LIVFHSSEGSVSYVDLFDPAQGYDPTLLRIYRDNNTTISSTLSLSLYLYTT 233			
Db	207 LIVFHTSKEPLVSVDLFNVIGQYDPDKLKIYQDNKLIHSENNHIDVLYTS 257			
RESULT 4				
Q8NW97	PRELIMINARY;			
ID	Q8NW97	PRT;	229 AA.	
AC	Q8NW97;			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	MW1552 protein.			
GN	MW1552			
OS	Staphylococcus aureus (strain MW2).			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=196620;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

```

RX MEDLINE=22040717; PubMed=1204378
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsutsu K.;
RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMEL; AP004827; BAE95417.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BctI_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF0123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTELTOXIN.
DR DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 229 AA; 26728 MW; AD3DAF9EA1AE3677 CRC64;

Query Match 36.0%; Score 438.5; DB 16; Length 229;
Best Local Similarity 35.5%; Pred. No. 1.le-27;
Matches 82; Conservative 47; Mismatches 97; Indels 5; Gaps 2;

QY 1 SEKSEINEKDKRKSELQGTALGNLKQIYYNYSKAITSEKSAQDQFLNTLLKPGFTG 60
DB 2 TNSASAIETSYDLHKHKKFDSKUSNAKMSPINPTQ--LEKNKNTDRLLKHDLFLHDMFVN 59
QY 61 HPWNLDLLDLGSTAATSEYGGSDVLYGAYGYQCAGGTPNKKTACMYGVTTLHDNNRLT 120
DB 60 DDMKDFKVFENEALSKKFKINDIDIFAGNYGCGHGATNTQCSYGVTLSDNKYD 119
QY 121 EEKKVPINLWIDGKQTVTPIDKYTKSEKVTVEQLDLQARHYLHGKPLNSDSFGSKVQ 180
DB 120 DYKNIPCNLWIDGHQAEILTAVTKTKKVIIOELDVQLANYLNKKYLYEQ---GGDIV 176
QY 181 RGLIVFHSSSGSVSYDLPLDAQQYPTLIRVDRNTTISSTLSISLYLY 231
DB 177 KGVKHNDDEQNIENFYNLNGEYEVLMKYADKNTINSDKLHDIYLF 227

RESULT 5
Q9EZM4 PRELIMINARY; PRT; 258 AA.
ID Q9EZM4
AC Q9EZM4
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sek (Enterotoxin SeN).
GN SEK OR SEN OR SAV1825 OR SA1643.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCBI_TaxID=158878, 158879, 1280;
[1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=A900322;
RX MEDLINE=20571956; PubMed=1123352;
RA Jarrard S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

```

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
RL Lancet 357:1225-1240 (2001).
DR EMBL; AF285760; AAC36956.1; -
DR EMBL; AP003363; BAB57987.1; -
DR EMBL; AP003335; BAB42911.1; -
DR PIR; H89968; H89968.
DR HSP; P13163; 1BSF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 34.5%; Score 420.5; DB 16; Length 258;
Best Local Similarity 38.0%; Pred. No. 3.7e-26;
Matches 87; Conservative 50; Mismatches 85; Indels 7; Gaps 4;

QY 6 EINEKRLKSELOGTALGNLKIYYNKAITSSEK-SADQFLTLTLFKGFFTHPWY 64
DB 32 EVKDKLKKSLDSSKFLNLTSTYDITWQDESNIKSTQDQLNLTILKIDISVLKT 91
QY 65 NDLVLVLGTAATSEYEGSSVDLYGAYGQAGGTPNKTACMYGGVTHDNRNTEKK 124
DB 92 SSLKVFNSDLNAPKGNIDITYGFGKCKVGLTEKTSCLYGGVTHDGNQDDEKV 151
QY 125 VPINLWDGKQTVPIDKVTSKEVTVOELDLQASHYLGKFGLYNSDFGKVGQGLI 184
DB 152 IGVNFKDGVQSGFV--IKTKAKTVQELDTKVFLENLYKYNKDT--GNIQKGI 207
QY 185 VFHS--SEGSTVSDYDFDAQGQVPTLLRIYRDNNTTSSISLSLYLT 231
DB 208 FFHSHNHQDSFYDLYNKGSGVGAFFQFQSDNRTVSSSNHYHDVFLY 256

RESULT 6
Q99T46 PRELIMINARY; PRT; 260 AA.
AC Q99T46;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin Sec.
GN SEC OR S4V1830 OR S41648.
OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699), and
OS *Staphylococcus aureus* (strain N315).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=1418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
RL Lancet 357:1225-1240 (2001).
DR EMBL; AP003363; BAB57992.1; -
DR EMBL; AP003335; BAB42916.1; -
DR PIR; E89969; E89969.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

Query Match 30.6%; Score 372.5; DB 16; Length 260;
Best Local Similarity 38.8%; Pred. No. 2.9e-22;
Matches 93; Conservative 32; Mismatches 92; Indels 23; Gaps 7;

QY 8 NEKD-----LRKSELOGTALGNLKIYYNKS-KAITSSEKSAQDQFLTLTLFKGFFTHG 61
DB 29 NEEDPKIESLCKSSVDPIALHNINDYINNRFTTKSVITTEKFLDFLLFKSI----- 84
QY 62 PW-----YNDLVLVLGTAATSEYEGSSVDLYGAYGQAGGTPNKTACMYGGVTLH 114
DB 85 NWLDGSAEFLKDLKAVEPSSAISKEFLGKTVDIVGVYKACHGCHQVDTACTYGGVTPH 144
QY 115 DNNPLTEKKVPINLWDGKQTVPIDKVTSKEVTVOELDLQASHYLGKFGLYNSDS 174
DB 145 ENNKLSFPGKIGVAVYKDNVNVNATFI--VTTDKKKVTQALDIKVRTKLNAYKLY--DR 200
QY 175 FGGVQVQGLIVFHSSEGSTVS--YDLFDAQGQVPTLLRIYRDNNTTSSISLSLYLT 232
DB 201 MTSVDQVGKIKFHSSESHSESFYDLFIKGNLPDQVLIYNDNKTIDSSDYHDVLYFT 260

RESULT 7
Q9EZM8 PRELIMINARY; PRT; 261 AA.
AC Q9EZM8;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE SEC.
GN SEC.
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed=1123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristant A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.,
RT "esc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in *Staphylococcus aureus*."
RL J. Immunol. 166:669-677 (2001).
DR EMBL; AF285760; AAC36951.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 29949 MW; 24DA4DDD766288EC CRC64;
Query Match 30.6%; Score 372.5; DB 2; Length 261;
Best Local Similarity 38.8%; Pred. No. 2.9e-22;
Matches 93; Conservative 32; Mismatches 92; Indels 23; Gaps 7;
QY 8 NEKD-----LRKSELOQTALGNLQIYYNS-KAITSSEKSAQOFLNTLLFGFTGH 61
DB 30 NEEDPKIESLCKSSVDPIALHNDDYINNRFTTVKSIIVSTTEKFLDFDLFSI---- 85
QY 62 PW-----YNDLLVDLGSTAITSYEGSSVDLYGAYGYOCAGTPTNKTCMYGGVTLH 114
DB 86 NWLDGISAEFKDLKVEFSSAISKEPLGKTVDIYGVYKACHGEHQVDTACTYGGVTPH 145
QY 115 DNNRLTEKKVPIINWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDS 174
DB 146 ENKLSSEPKNIGVAVYKDNVNVNTEI--VTDKKVTAQELDKVTKLNNAKLY--DR 201
QY 175 FGGKVORGLIVPHSSEGSTVS--YDLFAQGYPTLLRIYRDNTTISSTLSLSLYLT 232
DB 202 MTSVDYKGYKPHSHSEKESFYDLYFKGNLPQYLIQIYNDNKTIIDSSYDHIDVLYLT 261
RESULT 8
Q52075 PRELIMINARY; PRT; 179 AA.
AC Q52075;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Enterotoxin D.
GN VIRC2.
OS Staphylococcus aureus.
OG Plasmid p18485.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=25490000;
RA Bayles K.W., Iandolo J.U.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D";
RL J. Bacteriol. 171:4799-4806 (1989).
DR EMBL; M94872; AAA98133.1; -;
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact endotox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20563 MW; 579FFE811BC08747 CRC64;

Query Match 29.1%; Score 355; DB 2; Length 179;
Best Local Similarity 45.3%; Pred. No. 4.7e-21;
Matches 68; Conservative 26; Mismatches 56; Indels 0; Gaps 0;
QY 1 SEKSEBINEKDLRKKSELOQTALGNLQIYYNSKAITSSEKSAQOFLNTLLFGFTGH 60

DB 26 NENIDSVKEKELHKKSELSTALNNKHSYADKNPIIGENKSTGDFLENTLLYKKFFTD 85
QY 61 HPWYNDLLVDLGSTAITSYEGSSVDLYGAYGYOCAGTPTNKTCMYGGVTLHDNRLT 120
DB 86 LINFEDLLINFNSKEMAQHFKSKQVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 EEKKVPINWIDGKQTTVPIDKVKTSKEV 150
DB 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNL 175
RESULT 9
Q9F0L7 PRELIMINARY; PRT; 240 AA.
AC Q9F0L7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Sel [Extracellular enterotoxin L].
GN SEL OR SAV2008 OR SA1816.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus;
RX MEDLINE=20586668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine Staphylococcus aureus encoding multiple superantigens";
RL J. Bacteriol. 183:63-70 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus;
RX MEDLINE=20586668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine Staphylococcus aureus encoding multiple superantigens";
RL J. Bacteriol. 183:63-70 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J., Kaito C.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
RL Lancet 357:1225-1240 (2001).
DR EMBL; AF217235; AAC29598.1; -;
DR EMBL; AP003364; BAB58170.1; -;
DR EMBL; AP003135; BAB43096.1; -;
DR PIR; G89991; G89991.
DR HSSP; P13163; 1ESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 25.5%; Score 311; DB 16; Length 240;
Best Local Similarity 33.3%; Pred. No. 2.5e-17;
Matches 74; Conservative 36; Mismatches 78; Indels 34; Gaps 6;

```

QY 24 GNLKQIY-----YNSKAITSEKSADQFLNTLLFKGFTTGHFWYND-LLVDLGSTAATS 78
DB 31 GNLNRFYTKYEVNLRKXKNSPESHRL------YSKNDTLTYAEFDNEYITS 79
QY 79 EYEGSSVDLYGAYGYQCAGTNTKACMYGGVTLHNNRLTEKKVPINLMDGKQTV 138
DB 80 DLKGNVDVFGISYK-----GNSRT--YGGVTKAENKLDSPRIIPINLINGKHQTV 133
QY 139 PIDKVKTSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVQRLIYF 186
DB 134 TTKSVSTDKMWTQAEIDVKLRKYLODEFNIYGHNDTGKGEYGTSSKFGYSGFDKGVVF 193
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSLSL 228
DB 194 HMDGNSFSDLYFTYGLPESFLKIYKDNKTVDSQFHLVDV 235

RESULT 10
Q8NXJ5 PRELIMINARY; PRT; 240 AA.
AC Q8NXJ5, 20040717; PubMed=12044378;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Extracellular enterotoxin L.
GN SEL2 OR MW0760.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Ngai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94625.1; -.
DR GO: GO:000576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006173; Bact_tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 25.3%; Score 310; DB 16; Length 240;
Best Local Similarity 33.3%; Pred. No. 3e-17;
Matches 74; Conservative 36; Mismatches 78; Indels 34; Gaps 6;

QY 24 GNLKQIY-----YNSKAITSEKSADQFLNTLLFKGFTTGHFWYND-LLVDLGSTAATS 78
DB 31 GNLNRFYTKYEVNLRKXKNSPESHRL------YSKNDTLTYAEFDNEYITS 79
QY 79 EYEGSSVDLYGAYGYQCAGTNTKACMYGGVTLHNNRLTEKKVPINLMDGKQTV 138
DB 80 DLKGNVDVFGISYK-----GNSRT--YGGVTKAENKLDSPRIIPINLINGKHQTV 133
QY 139 PIDKVKTSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVQRLIYF 186
DB 134 TTKSVSTDKMWTQAEIDVKLRKYLODEFNIYGHNDTGKGEYGTSSKFGYSGFDKGVVF 193
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSLSL 228
DB 194 HMDGNSFSDLYFTYGLPESFLKIYKDNKTVDSQFHLVDV 235

RESULT 11
Q8RR76 PRELIMINARY; PRT; 217 AA.
AC Q8RR76, 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN SEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
RT isolates and Determination of the Enterotoxin Productivities of S.
RT aureus Isolates Harboring seg, seh, or sei Genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL: AB060536; BAB85990.1; -.
DR GO: GO:000576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact_tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 217 AA; 25143 MW; A8A44E23F31DE80D CRC64;

Query Match 25.3%; Score 108; DB 2; Length 217;
Best Local Similarity 33.9%; Pred. No. 3.9e-17;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

QY 10 KDLRKKSELTALGNLKIYYNSKAITSEKSADQFLNTLLFKGFTTGHFWYNDLLV 69
DB 1 EDLHDKSELTLALAN--AVGYNHPPFKENIKSDEISGEKDLIFRN--QGDG-NDLRV 55
QY 70 DLGTAATSEYEGSSVDLYGAYGYQCAGTNTKACMYGGVTLHNNRLTEKKVPINL 129
DB 56 KFATADLAQKFKKNKNDIYGASFYKCEKISENISECLYGGTLL-NSEKLAQSRVIGANV 114
QY 130 WIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIYFSS 189
DB 115 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSDKVKIYKDS---EISKGLIEFDMK 169
QY 190 EGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSLSL-LSLYLT 232
DB 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKNLTKSDSDISHIDVNLAT 213

RESULT 12
Q53585 PRELIMINARY; PRT; 241 AA.
AC Q53585, 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H.
GN SEH OR MW0051.
OS Staphylococcus aureus, and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 196620;

```

```

RN SEQUENCE FROM N.A.
RP STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453;
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fischetti V.A., Zabriskie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RL exotoxin.";
RN J. Exp. Med. 180:1675-1683(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yanamoto K., Hiramatsu K.;
RT "Genomic and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; U11702; AA19777.1; -.
DR EMBL; AF004822; BAB3916.1; -.
DR PDB; 1ENF; 10-JAN-01.
DR PDB; 1EMC; 10-JAN-01.
DR PDB; 1F77; 10-JAN-01.
DR PDB; 1JXY; 27-JUN-01.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 241 ENTEROTOXIN H.
SQ SEQUENCE 241 AA; 27858 MW; 70F7798587616CE CRC64;

Query Match 25.3%; Score 308; DB 16; Length 241;
Best Local Similarity 33.9%; Pred. No. 4.4e-17;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

QY 10 KDLRKSLQGTALGNLQIYYNSKAITSEKADQFLTWLTKGFTGHPYNDLV 69
DB 25 EDLHDKSLTDLALN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDG-NDLRV 79
QY 70 DLGSTAATSEYGGSDVLYGAYGQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINL 129
DB 80 KFTADLAQKFNKRVNDVIGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138
QY 130 WIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFLGYNDSFGKVQVGLIVFHS 189
DB 139 WVDGIQKTEL--ITNKKVNTLQELDKIRKILSDKYKIYKDS--EISKGLIEFDMK 193
QY 190 EGSTVYDLFAQQQYPTLLRIYRDNNTTISLSL--ISLYLT 232
DB 194 TPRDYFDIYDLKGNDYEIDKYEDNKLKSDDDISHIDVNLIT 237

RESULT 13
O85383 PRELIMINARY; PRT; 242 AA.
AC O85383;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Extracellular enterotoxin type I precursor (SET).
GN SEI OR SAV1828 OR SAV1646.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
```

```

OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 1280;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=S.aureus; STRAIN=FR1445;
RX MEDLINE=9898056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus.";
RL Infect. Immun. 66:3337-3348(1998).
[2]
RN SEQUENCE FROM N.A.
RP SPECIES=S.aureus; STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hizamatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF064774; AAC26661.1; -.
DR EMBL; AF285760; AAG36953.1; -.
DR EMBL; AP003363; BAB57990.1; -.
DR EMBL; AP003135; BAB42914.1; -.
DR PIR; C89969; C89969.
DR HSP; P3163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 242 ENTEROTOXIN TYPE I.
SQ SEQUENCE 242 AA; 27863 MW; C5C8B4ACEB5414A8 CRC64;

Query Match 24.3%; Score 296.5; DB 16; Length 242;
Best Local Similarity 32.4%; Pred. No. 3.8e-16;
Matches 77; Conservative 39; Mismatches 85; Indels 37; Gaps 10;

QY 8 NENDLKKSELOG-TALGNLQIY-----YNSKAITSEKADQFLTWLTKGFTGHP 62
DB 17 NIKDL---TVAQDVGIGVNLNRYFTXHDYIDLKGVTDKNLP-----IANQLEFS---TG-- 64
QY 63 WYNDLLVDLGSTAATSEYGGSDVLYGAYGQCAGGTPNKTACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISENNWDEISKFKGKLDIFGIDYNGPC-----KSKYMGATL-SGOYLNSA 116
QY 123 KKPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFLGYNDSFG-OK--- 178
DB 117 RKIPINLWNGKHTTSTDKIATNKKLVTAQEDVKRLRYLQBEVNIYGHNTGKGYG 176
QY 179 -----VQRGLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNNTTISLSLSL 228
```



```
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PFam; PF02876; Staph_strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 218 AA; 24909 MW; 101728FB71BF662 CRC64;

Query Match
Best Local Similarity 23.7%; Score 288.5; DB 2; Length 218;
Matches 70; Conservative 39; Mismatches 80; Indels 33; Gaps 8;

QY 23 LGNLKQIY---YNSKAITSSKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGLSTAATS 78
Db 6 VGNLRFYTKHDYIDLKGVTDKNLP-----IANQLEFS---TG---TNDLISESNWDEIS 55
QY 79 EYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
Db 56 KFKGKKLIDFIDYNGPC-----KSKYMFQCATL-SCQYLNSARKIPINLWVNGKHKT 108
QY 139 PIDKVTISKKEVTQVELDLOARHYLHGKFGLYNSDSFG-GK-----VQRGILVF 186
Db 109 STDKIATNKLVTAQIEDIVKURRLQBEYNIYGHNTKGKEYKSYGFGFNNGKVLV 168
QY 187 HSSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISL 228
Db 169 HLNNEKSFSDLYFTGDLGFLVPSFKLYEDNKIIESEKFLHDV 210

RESULT 17
ID O05157 PRELIMINARY; PRT; 239 AA..
AC O05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type C enterotoxin (fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91526; AAB50248.1; -.
DR HSP; P23313; 1JCK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PS00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match
Best Local Similarity 23.7%; Score 288.5; DB 2; Length 239;
Matches 81; Conservative 37; Mismatches 96; Indels 21; Gaps 9;

QY 11 DLKXSELQGTALGNLQIY--YNSKAITSSKSAQDFLNTLLFKGFFTGHPWYNDLL 68
Db 10 DLKXSEFTGT-MGNMKCLYDDYVS---ATKVKSVDFLAHDLIYNISDKKLKNDKVK 65

QY 69 VDLGSTAATSEYEGSSVDLYGAYGYOC-----AGGTPNKTCMYGGVTLHDNNRLTE 121
Db 66 TELLNEDLAKKYDEVDVYGSNYNCYFSKDNVKGVTGKTCMYGGITKEGHNFDN 125
QY 122 E--KKVPINLWIDGKQTTVPIDKVTISKKEVTQVELDLOARHYLHGKFGLYNSDSFGGKV 179
Db 126 GNLQNVLIIVY-ENKENTISFD-VQTDKKSVAQELDIKARFLINKOLYEFNS--SPY 181
QY 190 QRLIVFHSSGSTVSVDLFDAGQGYPD--TLRIYRDNTTISSTLSISLILYT 232
Db 182 EGTGIKFIENSDNTFWDMMPAPGDKFDQSKYLMYSDNKTVDSKSVKIEVHLTT 236

RESULT 18
QY9ZZI PRELIMINARY; PRT; 225 AA.
ID Q99ZZI;
AC Q99ZZI;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Streptococcal exotoxin I.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RA Ferrretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4659-4663 (2001).
DR EMBL; AS006546; AAK3906.1; -.
DR HSP; P3163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PS00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CC11CC04 CRC64;

Query Match
Best Local Similarity 23.6%; Score 287.5; DB 16; Length 225;
Matches 71; Conservative 40; Mismatches 86; Indels 25; Gaps 8;

QY 25 NLKQIY-YNSKAITSSKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGLSTAATSEY 80
Db 8 NLRLNLYTDPTTEVKCKINEGPPF-SGSLFYKNI-----PYGNSSIELKVELNSVERKANPF 62
QY 81 EGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDG---KQTT 137
Db 63 SGKRVDFITLEYSPPCNSNIKKNS---YGGITLSDGNRI-DKNIPVNI FIDGVQOKSY 118
QY 138 VPIDKVTISKKEVTQVELDLOARHYLHGKFGLY-----NSDSFGGKVQSGGLIVFHS 188
Db 119 TDLSTGTDKKEVTIQLDLVKSRYILQKHFNTYGFQGVKDFGSSFGSGFEGNIIFHL 178
QY 189 SEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISL 230
Db 179 NSGERISYNLFDTHGHDRESMLKKYKSDNKNTAYSDQLHIDIYL 220
```

RC	STRAIN=4446;
RR	MEDLINE=94011313; PubMed=8406814;
RX	Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT	"Characterization of novel type C staphylococcal enterotoxins:
RTT	biological and evolutionary implications";
RTL	Infect. Immun. 61:4254-4262(1993).
RL	EMBL; L13374; AAA26618.1; -
DR	HSSP; P34071; 1SE2.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPRO08992; Bact_endotox.
DR	InterPro; IPRO06177; BctrI tox.
DR	InterPro; IPRO06123; Staph/Strep_toxin.
DR	InterPro; IPRO06126; Staph/Strep_tox.
DR	InterPro; IPRO06173; Staph_tox_OB.
DR	Pfam; PF01123; Staph_strp_toxin; 1.
DR	Pfam; PF02876; Staph_strp_tox_C; 1.
DR	PRINTS; PR00279; BACTRLTOXIN.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER
FT	SEQUENCE
SQ	239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match	23.4%; Score 284.5; DB 2; Length 239;
Best Local Similarity	32.5%; Pred. No. 3.5e-15;
Matches	76; Conservative 45; Mismatches 94; Indels 19; Gaps

QY	11	DLRKSELQGTALGNLKIYYNSKAITSS-KSAQOFLTNLLFKGFTFGHPWYNDDLIV	69
Db	10	DLHKSSEFTGT-MGNMK--LYLDHYVSATKSVSKVDFLAHDJIYNISDKRLKYDKVKVT	66
QY	70	DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPNKTACMYGGVTLHDNNLTTEE	122
Db	67	ELLEDLAKYKDVEDVVGSYNYVCYFSSKDNVGVTKGKTCMGGITKEGHFPDG	126
QY	123	--KKVPINLWDIGQTTPIDIKVYTSKVEYTVGELDQAHHYLHGKGLYNSDSFGKVQ	180
Db	127	NLNQVLVRVY-ENKRNTISFE-VQTDKSVTAQELDIKARNFINKNLIEFNS--SPYE	182
QY	191	RGLVFHSSEGTSVSYDLFAAQGYPD--TLRLRYRDNNTTISTSLSIPLYLT	232
Db	183	TGYIKFENNNGTWFYDMMFAPGDKFDQSXYLMYNDNKTVDSKVKIEVHLT	236

RESULT 21	
Q9EZM7	PRELIMINARY; PRT; 239 AA.
ID Q9EZM7	
AC Q9EZM7	01-WAR-2001 (TrEMBLrel. 16, Created)
DT DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
SEM.	
DE SEM.	
GN SEM.	
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;	
RN [1]	SEQUENCE FROM N.A.
RP RP	STRAIN=A900322;
RC	MEDLINE=20571956; PubMed=11123352;
RX	Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA	Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT	"egc, A highly prevalent operon of enterocoxin gene,
RTL	nursery of superantigens in Staphylococcus aureus.";
RTL	J. Immunol. 166:669-677(2001).
DR	EMBL; AF285760; AAC36952.1; -
DR	HSSP; P13163; 1SXT.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPRO08992; Bact_endotox.
DR	InterPro; IPRO06177; BctrI tox.

forms a putative

```
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match      23.3%; Score 284; DB 2; Length 239;
Best Local Similarity 30.4%; Pred. No. 3.8e-15;
Matches 69; Conservative 38; Mismatches 80; Indels 40; Gaps 6;

QY 23 LGNLKQIYYNSKAIT--SSEKSAQDLNTLLFKGFFTGHPWYNLDLLVDLGSTAA----- 76
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 VGVNLNRYGSPYEDHQSIENPNNHLSHQLVES-----MDNSTVTABFKN 70
QY 77 ---TSEYEGSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEEEKKVPINLWDG 133
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 VDDVKFKNHADVYGLSYGYCL-----KNIYGGVTL-AGDYLEKSRRIPLNLWNG 124
QY 134 KQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLY-----NSDSFGGKQYR 181
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 EQHTTSTDKVTNKLVTAQEIDTKLRYLQEEYNIYGFNDTKNGRNYGNKSKFSSGFA 184
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISLSLSISL 228
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 KGLFHLNDGSSFSYDLFDGTGTGQAESFLKIYNDNKVTETKFKHLDV 231

RESULT 22
Q99T47 PRELIMINARY; PRT; 239 AA.
AC Q99T47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin SEM.
GN SEM OR SAV1829 OR SAI647.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1];
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanihisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003363; BAB57991.1; -.
DR EMBL; AF003135; BAB42915.1; -.
DR F01; D89969; D89969.
DR HSSP; F13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;
```

```
Query Match      23.2%; Score 282; DB 16; Length 239;
Best Local Similarity 29.7%; Pred. No. 5.6e-15;
Matches 68; Conservative 40; Mismatches 77; Indels 44; Gaps 6;

QY 23 LGNLKQIYYNSKAIT--SSEKSAQDLNTLLFKGFFTGHPWYNLDLLVDLGSTAA-- 79
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 VGVNLNRYGSPYEDHQSIENPNNHLSHQLVF-----SMNSTVTABF 68
QY 80 -----YEGSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEEEKKVPINLWI 131
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 KNVDVKKFKNHADVYGLSYGYCL-----KNIYGGVTL-AGDYLEKSRRIPLNLW 122
QY 132 DGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLY-----NSDSFGGKV 179
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 NGEHQITSTDKVTNKLVTAQEIDTKLRYLQEEYNIYGFNDTKNGRNYGNKSKFSSGF 182
QY 180 QRLGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISLSLSISL 228
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 NAGKILFHLNDGSSFSYDLFDGTGTGQAESFLKIYNDNKVTETKFKHLDV 231

RESULT 23
Q8NVN3 PRELIMINARY; PRT; 242 AA.
AC Q8NVN3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin Seg.
GN SEG2 OR MW1937.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004828; BAB95802.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PRINTS; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28138 MW; FFC689BB0E7A3BF5 CRC64;

Query Match      22.9%; Score 278.5; DB 16; Length 242;
Best Local Similarity 29.3%; Pred. No. 1.1e-14;
Matches 68; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

QY 17 ELQGTALGNLK---QIYYNSKAITSEKSAQDLNTLLFKGFFTGHPWYNLDLLVDLGS 73
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 44 KLGQVSSGNFSTGHQLEYIDGKTYLSQ-----FHN----- 74
QY 74 TAATSEYEGS-----SVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEEEKKVPIN 128
D  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 -----EYKRLKDKHVDIFGISYGLC-----NTKMYGGITLANQN-LDRPRNIPIN 122
```

```
QY 129 LWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHVLHGKFGLYN-----SDSFG 176
D 123 LWVNGKQNTISTDKVSTQKKEVTAQAEIDIKLRKYLQNEINYGNFKTKKQGVGYQSKEN 182
QY 177 GKVGRLIVHSHSGSTVSVLDLFAQQGYPTDLRLRIYRDNTTISSTLSISL 228
D 183 SGFNKGKITFHLNNEPSTYDLYFTGTGQAESFLKIYNDKNKTIDAENPHLDV 234

RESULT 24
Q8VLW7 PRELIMINARY; PRT; 256 AA.
AC Q8VLW7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcus enterotoxin Q.
GN ENTQ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RX MEDLINE=9835824; PubMed=9720870;
RA Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Novick R.P.;
RT "The gene for toxic shock toxin is carried by a family of mobile
pathogenicity islands in Staphylococcus aureus.";
RL Mol. Microbiol. 29:527-543(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RA Lindsay J.A., Kreiswirth B.N., Novick R.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RA Barry P.C., Novick R.P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0015070; F:toxin activity; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS02800; STAPHSTREP_TOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 256 AA; 29734 MW; 9E2F13790823A7DF CRC64;

Query Match 22.9%; Score 278.5; DB 2; Length 256;
Best Local Similarity 29.3%; Pred. No. 1.2e-14;
Matches 69; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

QY 17 ELQGTALGNLK---QIYYNSKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGS 73
D 58 KLGQVSGNFSHQLYIDGKVTLYSQ-----FHN----- 88

QY 74 TAATSEYGS-----SVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEEEKVPIN 128
D 89 -----EYEAELKDKHVDIFGISYGLC-----NTKMYGGITLANQN-LDKPRNIPIN 136

QY 129 LWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHVLHGKFGLYN-----SDSFG 176
D 137 LWVNGKQNTISTDKVSTQKKEVTAQAEIDIKLRKYLQNEINYGNFKTKKQGVGYQSKEN 196
```

```
QY 177 GKVGRLIVHSHSGSTVSVLDLFAQQGYPTDLRLRIYRDNTTISSTLSISL 228
D 197 SGFNKGKITFHLNNEPSTYDLYFTGTGQAESFLKIYNDKNKTIDAENPHLDV 248

RESULT 25
Q8NXJ6 PRELIMINARY; PRT; 266 AA.
AC Q8NXJ6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type C precursor.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94624.1; --
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0015070; F:toxin activity; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 22.9%; Score 278.5; DB 16; Length 266;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
Matches 76; Conservative 47; Mismatches 102; Indels 19; Gaps 9;

QY 1 SEKSEINEKDLRKKSBLQGTALGNLQIYYNSKAITSE-KSADQFLNTLLFKGFT 59
D 27 AESQPDPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNSDK 83

QY 60 GHPWYNDLLVDLGSSTAATSEYSGSVLYGAYGYQC-----AGTPNKTACMYGVT 112
D 84 KLRNYDKVKTLELNEDLAKYKQEVVDVYGSNYVYVYVYVYVYVYVYVYVYVYVYV 143

QY 113 LHDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHVLHGKFGLY 170
D 144 KHEGHNFDNGNLQNLVLRVY-ENKNTISPE-VQTDKSVTAQELDIKARFLINKNLY 201

QY 171 NSDFGKQVGRGLIVHSHSGSTVSVLDLFAQQGYPD--TLRLIYRDNTTISSTLSISL 228
D 202 EFNS--SPYETGYTKFTENNGNTFWYDMPAPGDKFDQSKYLMWYNDKNKTVDKRVKIEV 259

QY 229 YLYT 232
D 260 HLTT 263

RESULT 26
Q06532 PRELIMINARY; PRT; 239 AA.
ID Q06532
AC Q06532;
```

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; --
DR HSP; P34071; 1SE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F458C8D645 CRC64;
Query Match 22.8%; Score 277.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.3e-14;
Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;
QY 11 DLKSELOQTALGNLQIYYNSKAITSS-ESADQELTNTLLFKGFTGHPWYNDLLV 69
DB 10 DLKSEFTGT-MDNMK--LYDDHYVSATKVKSVDFKFLAHLIYNISDKKLNKYDKVT 66
QY 70 DLGTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKYACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGNHFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGVNSDPSGGKVQ 180
DB 127 NLQNVLRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYDP--TLRLIYRDNNTTISSTLSISLVLTT 232
DB 183 TGYIRFIENNGNTFWYDMMFAPGDKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236
RESULT 27
Q06533
ID Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).

DR EMBL; L13378; AAA26622.1; --
DR HSP; P34071; 1STE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;
Query Match 22.8%; Score 277.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 1.3e-14;
Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELOQTALGNLQIYYNSKAITSS-ESADQELTNTLLFKGFTG 60
DB 1 ESQDPTPDDELHKSSEFTGT-MGNMK--LYDDHYVSATKVKSVDFKFLAHLIYNISDKK 57
QY 61 HPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKYACMYGGVTL 113
DB 58 LKNDYKVKTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITK 117
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGV 171
DB 118 HEGNHDNGNLQNVLRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKNLYE 175
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQYDP--TLRLIYRDNNTTISSTLSIS 229
DB 176 FNS--SPYETGYIKFIENNGNTFWYDMMFAPGDKFDQSKYLMYNDNKTVDKSVKIEV 233
QY 230 LYT 232
DB 234 LTT 236
RESULT 28
Q095X4
ID Q095X4 PRELIMINARY; PRT; 234 AA.
AC Q095X4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ENTEROTOXIN-PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSP; P34071; 1SE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.

```
FT NON TER 1 1
FT NON TER 234 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 22.7%; Score 276.5; DB 2; Length 234;
Best Local Similarity 32.1%; Pred. No. 1.6e-14;
Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;

Qy 11 DLKKSSELOGTALGNLKOIYYNSKAITSE-KSADQFLNTLLFKGFFTGHPWYNDLLV 69
Db 5 DLKKSSEFTGT-MGNMK--VLYDDNYVSATKVKSVKFLAHLDIYNSDKRLKNVQKVT 61

Qy 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKTCMTYGGVTLHDNNRLTEE 122
Db 62 ELLNEDLAKKYKDBVVDVYGSNTYVNCYFSSKDNVGVTKGTCTMYGGITKEGHNFDNG 121

Qy 123 --KKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 122 NLQNVLRVT-ENKRNITSE-VQTDKSVTAQELDIKARFLINKNLKLYFNS--SPYE 177

Qy 181 RGLVHFSSSEGSTVSYDLFDAQOQYDP--TLRIYRDNTTISSTLSISLYLT 232
Db 178 TGYIKFIENNFTFYWDMPAPGDKPQSKYLMWYNDNKTVDKSKVKIEVHLTT 231

RESULT 29
Q93CC6 PRELIMINARY; PRT; 242 AA.
AC Q93CC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Seg.
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RA Yarwood J.M.; McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RT "Staphylococcus aureus pathogenicity island 3 (SapI3).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF110775; AAL04146.1;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact endotox.
DR InterPro: IPR006177; BctrI tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006125; Staph/Strep toxin.
DR InterPro: IPR008375; Staph exotoxin.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREPTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F6EEFD4AF8C30D85 CRC64;

Query Match 22.7%; Score 276.5; DB 2; Length 242;
Best Local Similarity 29.3%; Pred. No. 1.6e-14;
Matches 68; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

Qy 17 ELQGTALGNLK---QYYNSKAITSEKSAQOFLTNTLLFKGFFTGHPWYNDLLV 73
Db 44 KLOGVSGNFTSHQLEYIDGKTYLSQ-----FHN----- 74

Qy 74 TAATSEYEGS-----SVDLYGAYGYQCAGGTGPNKTCMTYGGVTLHDNNRLTEEKKVPIN 128
Db 75 -----EYEAKRLKDKHVDIFGSIYSLG-----NTKYMGGITLANQN-LDKPRNIPIN 122
```

```
Qy 129 LWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN-----SDSFG 176
Db 123 LWVNGKQNTISTDKVSTQKEVTAQEDIKURKYLQNEYNYGPNKTKGQGYQSKFN 182

Qy 177 GKVRGLVHFSSSEGSTVSYDLFDAQOQYDPDRLRIYRDNTTISSTLSISL 228
Db 183 SGFNKGKITFHLNNEPSFTYDLFTGTGQAESFLKIYDDNKTIDTFNPHLDV 234

RESULT 30
Q7XOE8 PRELIMINARY; PRT; 207 AA.
AC Q7XOE8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB-8802;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RT "Detection of staphylococcal enterotoxin type G precursors on
Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY291444; AAP78524.1;
DR NON_TER 207 207
SQ SEQUENCE 207 AA; 23953 MW; AE71FC176ES5842C CRC64;

Query Match 22.6%; Score 275.5; DB 2; Length 207;
Best Local Similarity 34.4%; Pred. No. 1.6e-14;
Matches 72; Conservative 34; Mismatches 66; Indels 37; Gaps 10;

Qy 8 NEKDLRKSELOG-TALGNLKQIY-----YNSKAITSEKSAQOFLTNTLLFKGFFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRNFYTKYDIDLKGVTDKNLP-----IANQLEFS---TG-- 64

Qy 63 WYNDLLVLAGSTAATSEYEGSSVDLYGAYGYQCAGGTGPNKTCMTYGGVTLHDNNRLTEE 122
Db 65 -TNDLSESNWDEISKFKGKWDIFGIDYNGPC-----KTKMYGATL-SQYLSA 116

Qy 123 KKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK--- 178
Db 117 RKIPINLWINGKHKTTISTDKIATNKKLIVTAQEDVKLRYLQBEYNTYGHNNNGKGEY 176

Qy 179 -----VORGLVHFSSSEGSTVSYDLF 199
Db 177 YKSFYSGFNKGVLFHLNDEKSFSDLF 205

RESULT 31
Q7XOE7 PRELIMINARY; PRT; 218 AA.
AC Q7XOE7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS14;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RT "Detection of staphylococcal enterotoxin type G precursors on
Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
```



```
QY 61 HPWYNDLLVLDLSTAATSEYEGSSVDLYGAYYQC-----AGGTENKTKACMYGGVTL 113
Db 58 LKNDKVKTELLNEDLAKYKDEVDVYGSNYNCYFSSKDNVGVTKGKTCMYGKITK 117
QY 114 HNNRLTEEK--KVPINLWIDGKQTTFEIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFNDKGLQNLIRVY-ENKRNITSE-VOITDKSVTAQELDIKARNELINKNLYE 175
QY 172 SDSFGGKQVGLIVPHSSEGSTVSVDLPDAQGYPD--TLRIYRDNTTISSTLSISLY 229
Db 176 FNS--SPYETGYKRIENNGNTFWYDMPAPGDKPDKQKYLMTYNDKNTVDSKSVKIEVH 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 37
Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC Q8NVW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin Sek.
GN SEK2 OR MW1938.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
SEQUENCE FROM N.A.
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.",
RL Lancet 359:1819-1827 (2002).
DR EMBL; AF004828; BAB95803.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin.
DR PRINTS; PR00279; Staph_Strep_toxin.
DR PROSITE; PS00278; BACTRLTOXIN.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;

Query Match 21.7%; Score 264; DB 16; Length 242;
Best Local Similarity 30.0%; Pred. No. 1.6e-13;
Matches 67; Conservative 38; Mismatches 84; Indels 34; Gaps 9;

QY 23 LGNLKQIY----YNSKAITSEKSAQDFLTNTLLFKGFFTHPWNLDLVLGSLTAATS 78
Db 29 IDNLRNFYTKDFINLKDY----KNDTFPIANQLQF-----SNESY-DLISEKDFNKFNS 78
QY 79 EYEGSSVDLYGAYYGCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQFTV 138
Db 79 NFKGKLDVFGISYNGQC-----NTKYIYGITA-TNEYLDKSRNIPINIWINGNHTKI 131
QY 139 FIDKVKTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGK-----VORGLIVF 186
Db 132 STNKVSTNKKFVTAQELDIKRLRYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVT 191
QY 187 HSESGSTVSVDLP-DAQGYPTTLRIYRDNTTISSTLSISL 228
Db 192 HLNNNDTFSDYDLFTGDDGLPKSFLKIYEDNKTVSEKFLHDV 234
```

RESULT 38

```
Q93CC5 PRELIMINARY; PRT; 242 AA.
ID Q93CC5;
AC Q93CC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sek.
GN SEK.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=COL;
RA Yarwood J.M., McCormick J.K., Faustian M.L., Orwin P.M., Kapur V.,
RA Shillevert F.M.;
RT "Staphylococcus aureus pathogenicity island 3 (SapI3).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410775; AAL04147.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin.
DR Pfam; PF02876; Staph_Strep_toxin.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B999DC9A9A CRC64;

Query Match 21.6%; Score 263; DB 2; Length 242;
Best Local Similarity 30.1%; Pred. No. 2e-13;
Matches 66; Conservative 35; Mismatches 92; Indels 26; Gaps 7;

QY 23 LGNLKQIY--YNSKAITSEKSAQDFLTNTLLFKGFFTHPWNLDLVLGSLTAATSEYEG 82
Db 29 IDNLRNFYTKDFVLDKVDKNDTPIANQLQF-----SNESY-DLISEKDFNKFNSFKG 82
QY 83 SSVLDLYGAYYGCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQFTVPIDK 142
Db 83 KLDVFGISYNGQC-----NTKYIYGITA-TNEYLDKSRNIPINIWINGNHTKISTNK 135
QY 143 VKTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGK-----VORGLIVFHSSE 190
Db 136 VSTNKKFVTAQELDIKRLRYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLNN 195
QY 191 GSTVSDYDLF-DAQGYPTTLRIYRDNTTISSTLSISL 228
Db 196 NDTFSYDLFTGDDGLPKSFLKIYEDNKTVSEKFLHDV 234
```

RESULT 39

```
O54476 PRELIMINARY; PRT; 242 AA.
ID O54476;
AC O54476;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin.
GN ENT.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
SEQUENCE FROM N.A.
RC STEAIN-RM4282; TRANSPOSON-Tn557;
RX MEDLINE=98385824; PubMed=9720870;
RA Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Novick R.P.;
```

"The gene for toxic shock toxin is carried by a family of mobile pathogenicity islands in *Staphylococcus aureus*.";
 Mol. Microbiol. 29:527-543 (1998).

DR EMBL; U93688; AAC28968.1; --
 DR HSP; P13163; ISX1.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 242 AA; 27720 MW; 28CB4F2EE6B66B9 CRC64;

Query Match 21.6%; Score 263; DB 2; Length 242;
 Best Local Similarity 30.1%; Pred. No. 2e-13;
 Matches 66; Conservative 35; Mismatches 92; Indels 26; Gaps 7;
 QY 23 LGNLKQIYYNKAITSSEKSDAOFNTLLFKGFTGHPWYNDLLVLDLGGSTAATSEYEG 82
 DB 29 IDNLRFYTKDFVLDKVDKNDTPIANQLQF-----SNESY-DLISEKDFNKSFNKG 82
 QY 83 SSVLDYGAAYGYQACGTPNKTACMGVTVLHNNRLTSEKVPINLWIDGKQTTVPIDK 142
 DB 83 KKLDFEISVNGQC-----NTRYIYGVTA-TNEYLDKSRNIPINWINGNHKTIISTNK 135
 QY 143 VKTSKKEVTQVELDQARHVLHCKFGLY-----NSDSFGK-----VQRLIVPHSSE 190
 DB 136 VSTNKKLVTAQELDVLRKYLQBEYINYGNGTKGEEYGHKSKFYSGNIGKVPFLNN 195
 QY 191 GSTVSYDLF-DAQGQVPTLLRIYRDNNTTISLSLSL 228
 DB 196 NDTFSYDLFTYGGDGLPKSLKIVEDNKTVESEKPHLDV 234

RESULT 40
 Q06534 PRELIMINARY; PRT; 239 AA.
 AC Q06534;
 DT 01-NOV-1996 (TEMBUREL. 01, Created)
 DT 01-NOV-1996 (TEMBUREL. 01, Last sequence update)
 DT 01-OCT-2003 (TEMBUREL. 25, Last annotation update)
 DE Enterotoxin (Fragment).
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RL biological and evolutionary implications.";
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13379; AAA26623.1; --
 DR HSP; P34071; ISE2.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1 1

SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;
 Query Match 21.2%; Score 258.5; DB 2; Length 239;
 Best Local Similarity 30.0%; Pred. No. 4.5e-13;
 Matches 73; Conservative 48; Mismatches 103; Indels 19; Gaps 9;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSE-KSADQPLTNTLLFKGFTG 60
 DB 1 ESQDPTPDELHKASKFTG-LMENMKVL--YDDRYVSATKVKSVKFLAHDLIYNISDKK 57
 QY 61 HPWNLDLVLGGSTAATSEYEGSSVDLYGAYGVQC-----AGGTPNKTACWYGGVTL 113
 DB 58 LKNYDKVKTLELLEDLAKKYDEVVDVYGSNYVNCFFSSKDNVGVKGTCHYGITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHVLHCKFGLYN 171
 DB 118 HEGNFDNGNLQNVLRVY-ENKENTISFE-VQTDKKSVAQELDIKARSLINKKNLYE 175
 QY 172 SDSFGGKQVQGLIVPHSSEGSTVSYDLFDAQGQYD--TLRIYRDNNTTISLSLSLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFWYDMWPAGKDFQSKYLMYNDNKTVDKSKVLEHV 233
 QY 230 LYT 232
 DB 234 LTT 236

RESULT 41
 P97163 PRELIMINARY; PRT; 236 AA.
 ID P97163;
 AC P97163; P97164;
 DT 01-MAY-1997 (TEMBUREL. 03, Created)
 DT 01-MAY-1997 (TEMBUREL. 03, Last sequence update)
 DT 01-OCT-2003 (TEMBUREL. 25, Last annotation update)
 DE Type A exotoxin precursor (Fragment).
 GN SPEA.
 OS *Streptococcus pyogenes*.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS156, and MGAS500;
 RX MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 RL J. Exp. Med. 174:1271-1274 (1991).
 DR EMBL; X61556; CAA43754.1; --
 DR EMBL; X61557; CAA43755.1; --
 DR EMBL; X61560; CAA43758.1; --
 DR EMBL; X61555; CAA43753.1; --
 DR EMBL; X61558; CAA43756.1; --
 DR EMBL; X61559; CAA43757.1; --
 DR EMBL; X61554; CAA43752.1; --
 DR PIR; A60108; A60108.
 DR HSP; P08095; 1BLZ.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1

FT	SIGNAL	<1	22	POTENTIAL.	
FT	CHAIN	23	>236	TYPE A EXOTOXIN.	
FT	NON TER	236			
SQ	SEQUENCE	236 AA;	27454 MW;	3PB3F41ABDC13A84 CRC64;	
	Query Match	20.9%;	Score 254.5;	DB 2;	Length 236;
	Best Local Similarity	32.0%;	Pred. No. 9.3e-13;		
	Matches	74;	Conservative 44;	Mismatches 94;	Indels 19; Gaps 10;
QY	4	SEBINEKDLRKKBELOGTAL-GNLKQIYY-YNSKAIT-SSEKSADQFETTLTKFGPFPTG	60		
Db	17	SQEVFAQQDDPQSLHRSSLVGNLQNIYFLYEGDPVTHENVKSVVDQLLSDLIYN--VS	73		
QY	61	HPHYNDLLVLGSTAATSEVEGGSVDLYGAYGYQC-AGGTPNKATACMYGGVTLHDNNRL	119		
Db	74	GPNYDKLTKEKQEMATLFDKRNVDYIGVEYHLCYLCENAEARSACIYGGVTHNEGHL	133		
QY	120	TEEKVPINLWIDGQKQTVTIDVKTSKEVTVOELDLQARHYLHGKFGYNSDSFGKV	179		
Db	134	EIPKIVVKSIDIGQ-SLSEF-IETNKKMWTAGELDYKRYKYLTDNKKLYTNGP--SKY	189		
QY	180	QRGLIVFHSSEGGSTVSYDLFD---AQGVDPDTLLRIYRDNNTTISSTLSI	226		
Db	190	ETGVKIPKPKNKESFWDFPEPEFTOSKY----LMYKONETLDSNTSO	236		

```

RESULT 42
Q54779 PRELIMINARY; PRT; 236 AA.
ID Q54779 Q54779 Q54736; Q54740; Q54741;
AC Q54779; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
NC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RN NCBI_TaxID=1314;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;
RC MEDLINE=92044323; PubMed=1940804;
RT Nelson K., Schlievert P.M., Seldander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.",
RL J. Exp. Med. 174:1271-1274 (1991).
DR ENBL; X61573; CAA43767.1; -
DR ENBL; X61572; CAA43770.1; -
DR ENBL; X61568; CAA43766.1; -
DR ENBL; X61570; CAA43768.1; -
DR ENBL; X61571; CAA43769.1; -
DR FIR; A60108; A60108.
DR HSP; P08095; IB1Z.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BctI_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS002477; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT FT SIGNAL 1 1
FT CHAIN <1 22
FT CHAIN 236 >236 TYPE A EXOTOXIN.
FT NON TER 236 236
FT NON TER 236 236

```

SEQ	SEQUENCE	236 AA; 27468 MW; 29DF2AD575623A84 CRC64;	
Query Match	20.8%; Score 253.5; DB 2; Length 236;		
Best Local Similarity	31.6%; Pred. No. 1.1e-12;		
Matches	73; Conservative 45; Mismatches 94; Indels 19; Gaps 10;		
QY	4	SEBINEKDLRKKELOQTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLFLKGFFTG 60	
Db	17	SQVFQAQDPDPQLHRSSLVKVLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VS 73	
QY	61	HPWYNLLVDLGSTAATSYEGSSVDLYGAYGYQC-AGGTPNKTAQMGYGVTLHNHNL 119	
Db	74	GPNYDKLTKELKNQEMATLFDKKNIDYGVVEYVHLCYLCENAFERSACIYGGVTNHEGNHL 133	
QY	120	TEBKYPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGKV 179	
Db	134	EIPKIVKVKSIDIGIQ-SLSFD-IEFNKQWTAQELDYKVRKVLTDNKQLYNGP---SKY 189	
QY	180	QRGLIVFHSSSEGSTVSYDIFD----RQGYPTDLLRIYRDNMTTISTSLSI 226	
Db	190	ETGVKIFPKNKESFWDFPEPTQSKY---LMYKDNETLDSNTSQI 236	
RESULT	43		
Q9R931	PRELIMINARY;	PRT; 222 AA.	
AC	Q9R931;		
DT	01-MAY-2000 (T-EMBLrel. 13, Created)		
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)		
DE	Exotoxin A (Fragment)		
GN	SPEA.		
OS	Streptococcus pyogenes.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=1314;		
EN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=D709;		
RX	MEDLINE=99137798; PubMed=9952369;		
RA	Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,		
RA	Hollingshead S.K., Beall B.;		
RT	"Genetic linkage of exotoxin alleles and emm gene markers for tissue		
RT	tropism in group A streptococci";		
RL	J. Infect. Dis. 179:627-636(1999).		
DR	EMBL; AF056598; A011624.1; -.		
DR	PIR; A60108; A60109.		
DR	HSP; P08095; IBI2.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0015070; P:toxin activity; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR008992; Bact_endotox.		
DR	InterPro; IPR006177; Bctr_tox.		
DR	InterPro; IPR006123; Staph/Strep_toxin.		
DR	InterPro; IPR006126; Staph/Strep_tox.		
DR	InterPro; IPR006173; Staph_tox_O8.		
DR	Pfam; PF01123; Staph_Strep_toxin; 1.		
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.		
DR	PRINTS; PR00279; BACTSLTOXIN		
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
FT	NON TER 1		
FT	NON TER 222		
SEQ	SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;		
Query Match	20.7%; Score 252.5; DB 2; Length 222;		
Best Local Similarity	32.0%; Pred. No. 1.2e-12;		
Matches	73; Conservative 44; Mismatches 92; Indels 19; Gaps 10;		
QY	4	SEBINEKDLRKKELOQTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLFLKGFFTG 60	
Db	5	SOEYFAQDPDPQLHRSSLVKVLQNIYFEGDPVTHENVKSVQDQLSHDLIYN---VS 61	

```

QY 61 HPWNLDLVLGTAATSEYEGSSVDLYGAYGYOC-AGGTPNKTACMYGGVTLHDNNRL 119
Db 62 GPNYDKLTKELKQEWATLFRKXNDVIGVEYVHLVCLNENASACTYGGVTHHEGNHL 121
QY 120 TEKKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 179
Db 122 EIPKILVKSVDIGIO-SLSFD-IETSKWVTAQELDYKVRKYLTNDKQLYTNGP--SKY 177
QY 180 ORGLIVPHSSEGSTVSVDLFD-----NQGQYPTLLRIYRDNNTTISLSI 223
Db 178 ETGYIKFIPKXKESFWDFPFPEFTQSKY----LMYIKDNETLDSNT 221

RESULT 44
Q54696 PRELIMINARY; PRT; 236 AA.
ID Q54696;
AC Q54696;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=3204333; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
J. Exp. Med. 174:1271-1274(1991).
DR EMBL,X61573; CAA43771.1; -.
DR PR; S18789; S18789.
DR HSP; P08095; IBLZ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008982; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 2575 MW; 70FS4120E79127DF CRC64;

Query Match 20.6%; Score 251.5; DB 2; Length 236;
Best Local Similarity 31.7%; Pred. No. 1.6e-12;
Matches 72; Conservative 42; Mismatches 102; Indels 11; Gaps 7;

```

```

QY 4 SERINEKDLKKSELOGTAL-GNLKQIY--YVNSKAITSEKSAQOFLNTLLFKGFTG 60
Db 17 SQEVFAQDNPQLHRSSVLKVLQNIYFLYEGDPVHENVKSVQDLQSHDIYN--VS 73
QY 61 HPWNLDLVLGTAATSEYEGSSVDLYGAYGYOC-AGGTPNKTACMYGGVTLHDNNRL 119
Db 74 GLNYDKLTKELKREWSLTFKKNKVDIYGVVEYVHCLCRNKRACIYGGVTHHEGNHL 133
QY 120 TEKKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 179
Db 134 EIPKILVKSVDIGIO-SLSFD-IETSKWVTAQELDYKVRKYLTNDKQLYTNGP--SKY 189

```

```

QY 180 ORGLIVPHSSEGSTVSVDLFDQAQGYPTLLRIYRDNNTTISLSI 226
Db 190 ETGYIKFISKDKETFWDFPFPEFNFQVKYLMYKDNETLDSSTSQI 236

```

RESULT 45

```

Q54738 PRELIMINARY; PRT; 260 AA.
ID Q54738;
AC Q54738;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Superantigen SSA.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
Infect. Immun. 62:1867-1874(1994).
DR EMBL; U48793; AAB02149.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29836 MW; C122141693B42AD6 CRC64;

```

```

Query Match 20.6%; Score 251; DB 2; Length 260;
Best Local Similarity 31.2%; Pred. No. 2e-12;
Matches 72; Conservative 44; Mismatches 97; Indels 18; Gaps 9;
QY 10 KDLKKSELOGTALGNLQIYYVNSKAITSEKSAQOFLNTLLFKGFTGHPWNLDLV 69
Db 35 EQLNKSQFTG-VGNLRCL-YDNHFVEGTNVASTGLQLQDLIFPKDLKLNYSVKT 92
QY 70 DLGTAATSEYEGSSVDLYGAYGYOCAGTNP-----KTACMYGGVTLHDNNRLTEKK 124
Db 93 EFNKDLAAKKNKVDIFGNTYNYCYSEGSKNAKATCMYGGVTHEHRNQI--EGK 150
QY 125 VPINLMT---DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 181
Db 151 FP-NITVKVVDENENILSPD-IITNKKQVTVQELDCDKTRKILVSRKNLYEFNN--SPYET 206
QY 182 GLIVPHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNNTTISLSISLYL 230
Db 207 GYIKFISSGDSFWMPPAPGAIFQSKYLMYNDNKTVSSSAIAIEVHL 257

```

```
RESULT 46
Q54971 PRELIMINARY; PRT; 260 AA.
ID Q54971
AC Q54971
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Superantigen.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Syiva G.L., Barbican K.B., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.P., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U48794; AAB02150.1; -
DR EMBL; U48792; AAB02148.1; -
DR EMBL; AE014155; AAM79527.1; -
DR EMBL; AP005144; BAC64214.1; -
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW SEQUENCE 260 AA; 29767 MW; EALP7CCAE80F99B CRC64;
SQ
Query Match 20.6%; Score 251; DB 2; Length 260;
Best Local Similarity 31.2%; Pred. No. 2e-12; Indels 18; Gaps 9;
Matches 72; Conservative 44; Mismatches 97; Indels 18; Gaps 9;
Oy 10 KDLRKSELOQTALGNLKOIYYNSKAITSSSEKSDQFLNTLLPKGFTGHPWYNLLV 69
Db 35 EQLNKKSQFTG-VMGNLRLC-LYDNHFVEGTNVSTGQLLQHLIPIKDLKKNYDSVKT 92
Oy 70 DLGSTAATSEYEGSSVDLYGAYGYOCAGTNP-----KTACMYGCVTLHNNRLTEKK 124
Db 93 EFNKSLATPKYKNDVDFSGSNYYNCYSEGNCKNAKKTCTMGYGVTEHHRNQI--EKG 150
Oy 125 VPINLMI---DGKQTTVPIDKTKSKVTVQELDQARHYLHGKFGLYNSDSFGKQYOR 181
Db 151 FP-NITVKYVENENILSPD-ITTNKQTVQELDCKTRKILVSRKNLYEFNN--SPYET 206
Oy 182 GLIVFHSSEGSTVSVDLPDAQOQYD--TLRIYRDNTTISTSTSLSYL 230
Db 207 GVIKFTIESSGDSFWYDMFAPGAIFDQSKYLMYNDKNTVSSSAIAIEVHL 257
RESULT 47
Q54739 PRELIMINARY; PRT; 260 AA.
ID Q54739
AC Q54739; Q54737;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE SUPERANTIGEN SSA (Streptococcal superantigen SSA-phase associated)
DE (SSA precursor).
GN SSA OR SPYM3 0920 OR SPS1119.
OS Streptococcus pyogenes, and
```



```

RESULT 51
Q57453
ID Q57453 PRELIMINARY; PRT; 236 AA.
AC Q57453;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61562; CAA43760.1; -
DR DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61567; CAA43765.1; -
DR DR EMBL; X61561; CAA43759.1; -
DR DR EMBL; X61564; CAA43762.1; -

```

```

ENBL; X61565; CAA43763.1; -.
DR EMBL; X61566; CAA43764.1; -.
DR PIR; A60108; A60108.
DR HSP; P08095; I312.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006136; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin1.
DR Pfam; PF02876; Stap_Strep_tox_C.
DR PRINTS; PR00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Signal.
KW NON_TER
FT SIGNAL
FT CHAIN
FT NON_TER
SQ SEQUENCE 236 AA; 27484 MW; 2EF7F41AAC853600 CRC64;

Query Match 20.4%; Score 248.5; DB 2; Length 236;
Best Local Similarity 31.6%; Pred.No. 2.ee-12;
Matches 73; Conservative 44; Mismatches 95; Indels 19; Gaps 10;

QY 4 SEINFEKDLKKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDELNTLLFKGFFTG 60
Db 17 SQVFQAQDDPDSQLHRSSVKNGLNIYFLYEGDPVTHENVKSDQLLSHDLIYN--VS 73
QY 61 HPWNLLVDLGSTAATSEYSGSVLDYGAAYGYQC-AGGTPNKATCMYGGVTLHDNNRL 119
Db 74 GPVYDKLXELKNQEMATLFDKKNVDIYSVEYVHLCVLCEAERSACIYGGVINHEGNHL 133
QY 120 TEKKVPINLWIDGKQTTPVIDKVKTSKEVTVQVELDLQARHYLHGKFLYNSDSFGKV 179
Db 134 EIPKIVKVKVSDIGIQ-SLSFD-IETNKKMTAQELDYKVRKYLTDNKQLYTNGP--SKY 189
QY 180 QRGILYVHSSGSGTSVSDYLFD---AQGGYEDTLRLIYRDNNTTISSTLSI 226
Db 190 ETGYIKPIPKNKESFWDFEPPEFTQSKY----LMYKDNELDSNTSQI 236

RESULT 52
Q8RR77
ID Q8RR77 PRELIMINARY; PRT; 233 AA.
AC Q8RR77;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Enterotoxin G (Fragment).
GN SEG.
OS Staphylococcus aureus.
OC Bacteria, Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RS SEQUENCE FROM N.A.
RA MEDLINE=21871379; PubMed=11880405;
RX Once K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
RT isolates and Determination of the enterotoxin Productivities of S.
RT aureus Isolates Harboring seg, seh, or sei Genes.";
RL J. Clin. Microbiol. 40:857-862 (2002).
DR EMBL; AB060535; BAB85989.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.

```

```

DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 233 AA; 27040 MW; ECE85287D63BF60D CRC64;

Query Match
Best Local Similarity 19.8%; Score 241; DB 2; Length 233;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINEKDLRKSELGQALGNLKOIYY---YNSKAITSSSEKSDAQFLNTLLFKGFFT 59
DB 5 KLDELNKVSDYKNN--KGT-MGNVMNLYTSPVVEGRGVNSR-----QFLSHDLIFP---I 54
QY 60 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCA-----GGTPNKTACM 107
DB 55 EYKSYNEVTELENTLANNYKDKVDIFGVPIFYTCIIPKSEPDINQFNG-----CCM 109
QY 108 YGGVTLH--DNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHG 165
DB 110 YGGLTFNSSNER---DKLITVQVTTIDNRQSLG--FTITTNKNMVTIQELDYKARHWLTK 164
QY 166 KFGLYNSDSFGKVGQRLIVFHSSEGSTVSYDLFDAQGGQYPTD---LLRIYRDNNTTISST 222
DB 165 EKLYEFD--GSAPESGYIKFTEKNNTSFWFDLPFKKELVPFVYKFLNIYGNKVVDSK 222
QY 223 SLISISLYLT 232
DB 223 SIRMEVFLNT 232

RESULT 53
Q9EZM3 PRELIMINARY; PRT; 258 AA.
ID Q9EZM3
AC Q9EZM3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SGL29P.
GN SGL29P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Jarrud S., Peyrat M.A., Lim A., Tristram A., Bes M., Mougel C.,
RX MEDLINE=20571956; PubMed=11123352;
RC STRAIN=A900322.
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAC36957.1; -.
DR HSP; P01552; ISB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 258 AA; 29956 MW; A85619E2FE21E3B7 CRC64;

Query Match
Best Local Similarity 19.8%; Score 241; DB 2; Length 258;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINEKDLRKSELGQALGNLKOIYY---YNSKAITSSSEKSDAQFLNTLLFKGFFT 59
DB 5 KLDELNKVSDYKNN--KGT-MGNVMNLYTSPVVEGRGVNSR-----QFLSHDLIFP---I 54
QY 60 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCA-----GGTPNKTACM 107
DB 55 EYKSYNEVTELENTLANNYKDKVDIFGVPIFYTCIIPKSEPDINQFNG-----CCM 109
QY 108 YGGVTLH--DNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHG 165
DB 110 YGGLTFNSSNER---DKLITVQVTTIDNRQSLG--FTITTNKNMVTIQELDYKARHWLTK 164
QY 166 KFGLYNSDSFGKVGQRLIVFHSSEGSTVSYDLFDAQGGQYPTD---LLRIYRDNNTTISST 222
DB 165 EKLYEFD--GSAPESGYIKFTEKNNTSFWFDLPFKKELVPFVYKFLNIYGNKVVDSK 222
QY 223 SLISISLYLT 232
DB 223 SIRMEVFLNT 232

RESULT 54
Q936G4 PRELIMINARY; PRT; 259 AA.
ID Q936G4
AC Q936G4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Enterotoxin-like protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RX MEDLINE=95050273; PubMed=7961465;
RC STRAIN=M.
RT "The Type1 Capsular Polysaccharide of Staphylococcus aureus is carried
RT in a Staphylococcal Cassette Chromosome Genetic Element.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10927; AAL26674.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR005566; Lipoclin_cytFABP.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 259 AA; 29981 MW; 783E1E4FEF057EDB CRC64;

Query Match
Best Local Similarity 19.6%; Score 238.5; DB 2; Length 259;
Matches 70; Conservative 43; Mismatches 106; Indels 25; Gaps 9;

QY 1 KSEINEKDLRKSELGQALGNLKOIYY---YNSKAITSSSEKSDAQFLNTLLFKGFFT 58

```

Db 24 ABTQNDPNISELNKSQY---TGSWHNIWLYNSDPVNAKKIKLSKDFLSHEFIVPINN 79
QY 59 TGHWPYNDLLDVGSTAATSEVGGSSVDLYGAYGYQC-----AGTGNKTACM 107
Db 80 PSH--YDVVKTELKOSTWASSFDGKEVDIFGVNVPDQCYFLNENIQDSNOGAGSKTTCM 137
QY 108 YGVGTLHDNNRLTEKKVPINLMI-DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGK 166
Db 138 YGGITLNN--TNNRIQIVVKKVENDSVTLSPD-INIDKETVTIQELDYKVRNKLISK 194
QY 167 FGLYNSDSFGKVQGLVHFHSSGTSVYDLFDAQGYPTLLRIYRDNTTISLSI 226
Db 195 INLYHLG--GTSYETGYIKFIENGRRYTYWMDPDGFTQSKYLMYIRGNSTVESAKTEI 252
QY 227 SLYL 230
Db 253 EVHL 256
RESULT 55
Q9RQ05 PRELIMINARY; PRT; 209 AA.
AC Q9RQ05; MEDLINE=9893;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z 2 (fragment).
GN SMEZ-2.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=9893428; PubMed=9874566;
RA Prof T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes";
RL J. Exp. Med. 189:189-192(1999).
DR EMBL; AF086626; AAD52087.1; -.
DR PDB; 1ET6; 24-MAY-00.
DR PDB; 1EU3; 24-MAY-00.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_tox_OB.
DR PRINTS; PR00279; Staph_tox_C; 1.
DR PRINTS; PR02876; Staph_tox_C; 1.
DR PROSITE; PS00278; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 18.2%; Score 222; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 3.4e-10;
Matches 58; Conservative 40; Mismatches 65; Indels 36; Gaps 6;
QY 50 NTLLFKGFTGHPWYNDLLVD-----LGSTAATSEVGGSSVDLYGAY----- 91
Db 6 NSLLRNISTIVVEYSDIVIDFKTSHNLVTKLDVDRDARDFINSEMEYANDFKTGDK 65
QY 92 -----YGYOCAGGTGNKTCMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNLKSG---KVTAITYGGITPYQKTSI--PKNIPVNLWINGKQISVPE 120
QY 143 VKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVQGLVHFHSSGGS-TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRFLIAQHQLYSS---GSSYKSGKLVFHTNDNSDKYSFDLYV 177

QY 202 QGOVPDTLLRIYRDNTTIS 220
Db 178 GYRDKESIPKVKDKNSFN 196
RESULT 56
Q9LAE0 PRELIMINARY; PRT; 209 AA.
AC Q9LAE0; MEDLINE=20273982; PubMed=10811869;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-4 (fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9893;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143654; AAF66655.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_C; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24108 MW; 67EC279BBC4A8247 CRC64;
Query Match 18.0%; Score 219; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 6e-10;
Matches 58; Conservative 39; Mismatches 66; Indels 36; Gaps 6;
QY 50 NTLLFKGFTGHPWYNDLLVD-----LGSTAATSEVGGSSVDLYGAY----- 91
Db 6 NSLLRNISTIVVEYSDIVIDFKTSHNLVTKLDVDRDARDFINSEMEYANDFKTGDK 65
QY 92 -----YGYOCAGGTGNKTCMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNLKSG---KVTAITYGGITPYQKTSI--PKNIPVNLWINGKQISVPE 120
QY 143 VKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVQGLVHFHSSGGS-TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRFLIAQHQLYSS---GSSYKSGKLVFHTNDNSDKYSFDLYV 177
QY 202 QGOVPDTLLRIYRDNTTIS 220
Db 178 GYRDKESIPKVKDKNSFN 196
RESULT 57
Q9LAD8 PRELIMINARY; PRT; 209 AA.
AC Q9LAD8; MEDLINE=9893;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-7 (fragment).
GN SMEZ-7.

```

DR HSP; Pf13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; BACTR_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24100 MW; 53049A11599BEA68 CRC64;

Query Match 17.8%; Score 217; DB 2; Length 209;
Best Local Similarity 29.1%; Pred.No.8.7e-10;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6

QY 50 NTLFLFKGFTGHVWYNDLLVD-----LGSATSEYEGSSVDLYGAY----- 99
Db 6 NSLLNIYTVITYYSVTDVDFKTHNLVYKLDVRDARDFINSEMDFAANDFKAGDK 65

QY 92 -----YQQCAGGTPNKACMYGVTLHDNNRLTEKKVPINLWIDGKOTTVPIDK 142
Db 66 IAVFSVPDWNYSKSG--KVTATYGGITPYQKTSI--PKNIPVNLWINGKQIPVPYNQ 120

QY 143 VKTSKKEVTVELDLQARHYLHGKFGLYNSDSGKVGQRLIVFHSSEGS-TVSYDLFA 201
Db 121 ISTNKTIVTAQEDLKVKFLIAHQLYSS---GSSYKSGRLVFNHINDSKYSFOLFYT 177

QY 202 QCGYPTDLLRIYRDNNTTIS 220
Db 178 GYRDKESIFKVKYKDKNSFN 196

RESULT 59
Q91AD1 PRELIMINARY; PRT; 209 AA.
ID Q91AD1 AC Q91AD1
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-14 (Fragment).
DE SMEZ-14.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4202;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776 (2000).
DR EMBL; AF143664; AAF66664.1; -.
DR HSP; Pf13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; BACTR_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24122 MW; 0CF5D429E1B39EFE CRC64;

```


Query Match 17.8%; Score 217; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 8.7e-10;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIMYEYSDTLIDFKTSHNLVTKKLDVRDARDFINSEMDYAAANDFKAGDK 65
QY 92 -----YGVOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120
QY 143 VKTSKEVTQVELDQARHLYHGKFLGYNDSFGKVGQGLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRKFLIAHQHLYSS---GSSYKSKGLVFNHNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 60
Q9LAE1 PRELIMINARY; PRT; 209 AA.
AC Q9LAE1;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11681;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143653; AAF66654.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN-
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24071 MW; FDADFCDIAA87271 CRC64;

Query Match 17.7%; Score 215; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 1.3e-09;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDYAAANDFKAGDK 65
QY 92 -----YGVOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120
QY 143 VKTSKEVTQVELDQARHLYHGKFLGYNDSFGKVGQGLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRKFLIAHQHLYSS---GSSYKSKGLVFNHNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 62
Q9LAC5 PRELIMINARY; PRT; 209 AA.
ID Q9LAC5
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN-
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6DE8 CRC64;

Db 121 ISTNKTVTVAQEIDLKVRKFLIAHQHLYSS---GSSYKSKGLVFNHNDNSDKYSLDLFT 177
QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 61
Q9LAC4 PRELIMINARY; PRT; 209 AA.
ID Q9LAC4
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN-
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6DE8 CRC64;

Query Match 17.7%; Score 215; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 1.3e-09;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDYAAANDFKAGDK 65
QY 92 -----YGVOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120
QY 143 VKTSKEVTQVELDQARHLYHGKFLGYNDSFGKVGQGLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRKFLIAHQHLYSS---GSSYKSKGLVFNHNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 62
Q9LAC5 PRELIMINARY; PRT; 209 AA.
ID Q9LAC5
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN-
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6DE8 CRC64;

```

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-21 (Fragment)
GN SMEZ-21
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11227;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
EMBL; AF143671; AAF66670.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 17.5%; Score 213; DB 2; Length 209;
Best Local Similarity 28.6%; Pred. No. 1.8e-09;
Matches 57; Conservative 39; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFFTHGHPWYNDLLVD-----LGSTAATSEYEGSVLYGAY----- 91
Db 6 NSLLRNISTVVEYSDTVIDFKTSHNLVTKLDVRDARDFTINSEMDYAADEFKDGK 65

QY 92 -----GYQCAGGTENKTCMYGGVTLHDNNLTTEEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVSPFDPWNYLSEG---KVIAITYGGITPYQKTSI--PKIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVTAQELDKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSFDLFT 177

QY 202 QGYPTDLLRIYRDNTIS 220
Db 178 GYRKESIFKVKYDNKSNF 196

RESULT 63
Q9LAD9 PRELIMINARY; PRT; 209 AA.
AC Q9LAD9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-5 (Fragment).
GN SMEZ-5.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11244;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
EMBL; AF143663; AAF66663.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 209 AA; 24079 MW; 24CA3885469CB99B CRC64;

Query Match 17.3%; Score 211; DB 2; Length 209;
Best Local Similarity 28.3%; Pred. No. 2.7e-09;
Matches 56; Conservative 43; Mismatches 75; Indels 24; Gaps 8;

QY 29 IYYNSKAITSSSEKSAQDFITNLLF---KGFTGHPWYNDLLVLDGSLTAATSEYEGSV 85
Db 17 VVEYSDTVI--DFKTSNHLVTKLDVRDARDKDFINS-----EMDEYAANDFKDGKI 66

QY 86 DLVGAYY--GYQCAGGTENKTCMYGGVTLHDNNLTTEEKKVPINLWIDGKQTTVPIDK 143
Db 67 AMSPVDPWNYLSEG---KVIAITYGGITPYQKTSI--KNIPVNLWINGKQISVPYNEI 121

QY 144 KTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS--TVSYDLFDA 202
Db 122 STNKTITVTAQELDKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSFDLFT 178

QY 203 QGYPTDLLRIYRDNTIS 220
Db 179 YRKESIFKVKYDNKSNF 196

RESULT 64
Q9LAD2 PRELIMINARY; PRT; 209 AA.
AC Q9LAD2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95/31;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
EMBL; AF143663; AAF66663.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
```

Db	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	66	IAVSVPPDWNLYSKG---KVTATYTGITPYQKTSI--PKNIPVNLWINRKQIPVPPVYNQ 120
FT	NON TER	143	VKTSKEVTQVELDLOARHLHGKFLGYNDSFGGKVQGRGLIVFHSSEGS--TVSYDLFDA 201
SQ	SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;	121	ISTNKTITVAQEIDLKVRKFLAQHQLYSS---GSSYKSGRLVFHTNDNSDKYSPDLFT 177
	Query Match 17.2%; Score 210; DB 2; Length 209;		
	Best Local Similarity 28.6%; Pred. No. 3.2e-09;		
	Matches 57; Conservative 38; Mismatches 68; Indels 36; Gaps 6;		
QY	50 NTLFPKGFFTGHPWYNLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91		
Db	6 NSLLRNIVSTIMYEYSDTVDFKTSNLTVKKLDVRDARDFFINSEMDVAANDFKAGDK 65		
QY	92 -----YGVQACAGTGNKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVIDK 142		
Db	66 IAVSVPPDWNLYSEG---KVIATYTGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120		
QY	143 VKTSKEVTQVELDLOARHLHGKFLGYNDSFGGKVQGRGLIVFHSSEGS--TVSYDLFDA 201		
Db	121 ISTNKTITVAQEIDLKVRKFLAQHQLYSS---GSSYKSGRLVFHTNDNSDKYSPDLFT 177		
QY	202 QGQYPTLLRIYRDNTTIS 220		
Db	178 GYRDKESIFKVKDKNSFN 196		
	RESULT 65		
QY	Q9LAD6 PRELIMINARY; PRT; 209 AA.		
AC	Q9LAD6; (TREMELrel. 15, Created)		
DT	01-OCT-2000 (TREMELrel. 15, Last sequence update)		
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)		
DE	Mitogenic exotoxin 2-9 (Fragment).		
GN	SMEZ-9.		
OS	Streptococcus pyogenes.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=1314;		
RN	[1] SEQUENCE FROM N.A.		
RP	STRAIN=11299;		
RC	MEDLINE=20273982; PubMed=10811869;		
RA	Prof T., Moffatt S.L., Weiler K.D., Paterson A., Martin D.,		
RA	Fraser J.D.;		
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,		
RT	Mosaic Structure, and Significant Antigenic Variation.";		
RL	J. Exp. Med. 191:1765-1776(2000).		
DR	EMBL; AF143659; AAF66659.1; -.		
DR	HSP; P13163; ISXT.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0015070; F:toxin activity; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR008992; Bact_endotox.		
DR	InterPro; IPR006177; Bctr1_tox.		
DR	InterPro; IPR006123; Staph/Strep_toxin.		
DR	Pfam; PF01123; Staph_strep_toxin; 1.		
DR	Pfam; PF02876; Staph_strep_tox_C; 1.		
DR	PRINTS; PR00279; BACTRLTOXIN.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
FT	NON TER		
SQ	SEQUENCE 209 AA; 24213 MW; B21587BA34385DD5 CRC64;		
	Query Match 17.2%; Score 210; DB 2; Length 209;		
	Best Local Similarity 29.1%; Pred. No. 3.2e-09;		
	Matches 58; Conservative 37; Mismatches 68; Indels 36; Gaps 6;		
QY	50 NTLFPKGFFTGHPWYNLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91		
Db	6 NSLLRNIVSTIMYEYSDTVDFKTSNLTVKKLDVRDARDFFINSEMDVAANDFKAGDK 65		
QY	92 -----YGVQACAGTGNKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVIDK 142		
	RESULT 67		
QY	Q8NZ89 PRELIMINARY; PRT; 233 AA.		
AC	Q8NZ89; (TREMELrel. 22, Created)		
DT	01-OCT-2002 (TREMELrel. 22, Last sequence update)		
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)		
DE	Mitogenic exotoxin Z.		
GN	SMEZ CR SPYM18_2064.		
OS	Streptococcus pyogenes (serotype M18).		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
OX	NCBI_TaxID=186103;		
RN	[1] SEQUENCE FROM N.A.		
RP	STRAIN=MGAS8232 / Serotype M18;		
RC	MEDLINE=21927593; PubMed=11917108;		
RA	Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,		
RA	Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,		
RA	Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,		
RA	Kapur V., Daly J.A., Veasy L.G., Musser J.M.;		
RT	"genome sequence and comparative microarray analysis of serotype M18		
RT	group A Streptococcus strains associated with acute rheumatic fever		
RT	outbreaks.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).		
DR	EMBL; AE010110; AAL98535.1; -.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0015070; F:toxin activity; IEA.		
DR	GO; GO:0009405; P:pathogenesis; IEA.		
DR	InterPro; IPR008992; Bact_endotox.		
DR	InterPro; IPR006177; Bctr1_tox.		
DR	InterPro; IPR006123; Staph/Strep_toxin.		
DR	Pfam; PF01123; Staph_strep_toxin; 1.		
DR	Pfam; PF02876; Staph_strep_tox_C; 1.		
DR	PRINTS; PR00279; BACTRLTOXIN.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
KW	Complete proteome.		
SQ	SEQUENCE 233 AA; 26859 MW; 23E07CC9C06AE866 CRC64;		
	Query Match 17.2%; Score 209.5; DB 16; Length 233;		
	Best Local Similarity 26.8%; Pred. No. 4e-09;		
	Matches 58; Conservative 43; Mismatches 70; Indels 47; Gaps 8;		
QY	34 SKAITSSEKSADQFLTN---TLFFKGFTHGHPWYNLLVD-----LGSTAATSE 79		
Db	19 SRPVIGLEVDNNSLLRNIVSTIMYE-----YSTVIDFKTSNLTVKKLDVRDARD 70		
QY	80 YEGSSVDLYGAY-----YGVQACAGTGNKTCACMYGGVTLHDNNRLTEK 123		
Db	71 FINSEMDVAANDFKDGDKIAMPSPVDFDWNLYSEG---KVIATYTGITPYQKTSI-- 125		
QY	124 KVPINLWIDGKQTTVIDKVKTSKEVTQVELDLOARHLHGKFLGYNDSFGGKVQGRGL 183		
Db	126 NIPVNLWINGKQISVPYNEISINKTIVTAGEIDLKVRKFLAQHQLYSS---GSSYKSGK 182		
QY	184 IVFHSSEGS--TVSYDLFDAQGVDPDLLRIYRDNTTIS 220		
Db	183 LVEHTNDNSDKYSPDLFTFYGYRDKESIFKVKDKNSFN 220		

Q7WY99 PRELIMINARY; PRT; 207 AA.
 ID Q7WY99
 AC Q7WY99
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z (Fragment).
 GN SNEZ-16.
 OS Streptococcus canis.
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igwe E.I., Gertz B.;
 RT "Streptococcal superantigen genes in human pathogenesis group G
 streptococcus."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AJ564198; CAD91900.1; -
 FT NON TER 1
 FT NON TER 207
 SQ SEQUENCE 207 AA; 24034 MW; C9D5C7B1603BDFC4 CRC64;

Query Match 17.2%; Score 209; DB 2; Length 207;
 Best Local Similarity 28.6%; Pred. No. 3.8e-09;
 Matches 57; Conservative 38; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFKGFFGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 5 NSLRLNIYSTIVVEYSVTVIDFKTSHNLVTKLDVRDARDFFINSEMDEYAANDFKAGDR 64
 QY 92 -----YGYCAGGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
 Db 65 IAVFSVPFDWNLYSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINRKQISVPYNE 119
 QY 143 VKTSKEVTVOELDLQARHVLHGKFLYNSDSFGGKVORGLIVFHSSEGS-TVSYDLFDA 201
 Db 120 ISTNKTIVTAQEDLKVRFKFLISQYQLYSS---GSNYKSGKLVFHTNDNSDKYSLDLFYT 176
 QY 202 QGOYPTLLRIYRDNTTIS 220
 Db 177 GYRDKESIFKVKDKNSFN 195

RESULT 68

Q9LAC9 PRELIMINARY; PRT; 209 AA.
 ID Q9LAC9
 AC Q9LAC9
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z-16 (Fragment).
 GN SNEZ-16.
 OS Streptococcus pyogenes.
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation."
 RL J. Exp. Med. 191:1765-1776(2000).
 DR ENBL; AF143666; AAF66666.1; -
 DR HSSP; P13163; 1SXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; P:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 QY 202 QGOYPTLLRIYRDNTTIS 220
 Db 177 GYRDKESIFKVKDKNSFN 195

DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 209 AA; 24172 MW; A1DB8FA187098BA5 CRC64;
 Query Match 17.0%; Score 207; DB 2; Length 209;
 Best Local Similarity 28.6%; Pred. No. 5.6e-09;
 Matches 57; Conservative 38; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFKGFFGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 6 NSLRLNIYSTIVVEYSVTVIDFKTSHNLVTKLDVRDARDFFINSEMDEYAANDFKAGDR 65
 QY 92 -----YGYCAGGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
 Db 66 IAVFSVPFDWNLYSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINRKQISVPYNE 120
 QY 143 VKTSKEVTVOELDLQARHVLHGKFLYNSDSFGGKVORGLIVFHSSEGS-TVSYDLFDA 201
 Db 121 ISTNKTIVTAQEDLKVRFKFLISQYQLYSS---GSNYKSGKLVFHTNDNSDKYSLDLFYT 177
 QY 202 QGOYPTLLRIYRDNTTIS 220
 Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 69

Q9LAC7 PRELIMINARY; PRT; 209 AA.
 ID Q9LAC7
 AC Q9LAC7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z-18 (Fragment).
 GN SNEZ-18.
 OS Streptococcus pyogenes.
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation."
 RL J. Exp. Med. 191:1765-1776(2000).
 DR ENBL; AF143666; AAF66666.1; -
 DR HSSP; P13163; 1SXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; P:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;
 Query Match 16.9%; Score 206; DB 2; Length 209;
 Best Local Similarity 35.6%; Pred. No. 6.8e-09;
 Matches 42; Conservative 30; Mismatches 40; Indels 6; Gaps 3;

QY 104 TACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDKTKTSKEVTVOELDLQARHVL 163

```
Db      84 TAYTYGGITPYQKTSI--PKNIPVNLWNRKQIPVPYNOISTNKTVTVAQEIIDLKVRKFL 141
Qy      164 HGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDLFDAQGGVDPDTLLRIYRDNNTTIS 220
Db      142 IAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSFDLFYTGGRDKESIFKYVKNKSNFN 196

RESULT 70
Q9LAD4 PRELIMINARY; PRT; 209 AA.
ID Q9LAD4
AC Q9LAD4
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9779;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph_tox.
DR InterPro; IPR006173; Staph_tox.
DR Pfam; PF01123; Staph_tox.
DR Pfam; PF02876; Staph_tox.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 16.9%; Score 206; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 6.8e-09;
Matches 58; Conservative 36; Mismatches 69; Indels 36; Gaps 6;

Qy      50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db      6 NSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAANDFKAGDR 65

Qy      92 -----YGYQCAGGTPTACMYGGVTLHDNNRLTEKKVFINLWIDGKQTTVPIDK 142
Db      66 IAVFSVPDMNYLSKG---KVTATYGGITPYQKTSI--PKNIPVNLWNRKQIPVPYNO 120

Qy      143 VKTSKEVTVOELDIQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDLFDA 201
Db      121 ISTNKTVTVAQEIIDLKVRKFLISQHLQYSS---GSSYKSGKLIVFHTNDNSDKYSLDLFYT 177

Qy      202 QGYPPDTLLRIYRDNNTTIS 220
Db      178 GYRDKESIFKYVKNKSNFN 196

RESULT 71
Q9LAC8 PRELIMINARY; PRT; 209 AA.
ID Q9LAC8
AC Q9LAC8
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
```

```
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-17 (Fragment).
GN SMEZ-17.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11686;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143667; AAF66667.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph_tox.
DR InterPro; IPR006173; Staph_tox.
DR Pfam; PF01123; Staph_tox.
DR Pfam; PF02876; Staph_tox.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24181 MW; A333F466398D9DC2 CRC64;

Query Match 16.8%; Score 205; DB 2; Length 209;
Best Local Similarity 28.6%; Pred. No. 8.2e-09;
Matches 57; Conservative 37; Mismatches 69; Indels 36; Gaps 6;

Qy      50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db      6 NSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAANDFKAGDR 65

Qy      92 -----YGYQCAGGTPTACMYGGVTLHDNNRLTEKKVFINLWIDGKQTTVPIDK 142
Db      66 IAVFSVPDMNYLSKG---KVTATYGGITPYQKTSI--PKNIPVNLWNRKQIPVPYNO 120

Qy      143 VKTSKEVTVOELDIQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDLFDA 201
Db      121 ISTNKTVTVAQEIIDLKVRKFLISQHLQYSS---GSSYKSGKLIVFHTNDNSDKYSLDLFYT 177

Qy      202 QGYPPDTLLRIYRDNNTTIS 220
Db      178 GYRDKESIFKYVKNKSNFN 196

RESULT 72
Q9LAC3 PRELIMINARY; PRT; 209 AA.
ID Q9LAC3
AC Q9LAC3
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-24 (Fragment).
GN SMEZ-24.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
```

FRAM, FF02878, SLAP SLIP COX C, I.
DR PRINTS: PR00279: BACTRLTÖXIN.

DB 6 NSLLRNISTIVYEYSDTVIDFKTSHNLVTKKLDVDRDARDFFINSEMDIYAANDFKDGDK 65

DR Pfam; PF01123; stap_strep_toxin; 1.
DR Pfam; PF02876; stap_strep_tox C. 1

Search completed: August 12, 2004, 13:32:30
Job time : 26.2698 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 29.2786 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-2
Perfect score: 1218
Sequence: 1 SEKSEINEKDLKKSELOG.....RDNTTISSTLSISLYVT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_29Jan04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	100.0	233	6	ABP58455 Engineere
2	1218	100.0	672	6	ABP58454 Engineere
3	1130	92.8	233	6	ABP58457 Engineere
4	1113	91.4	245	2	AAW35375 Staphyloc
5	1107	90.9	233	6	ABP58456 Staphyloc
6	1107	90.9	257	4	AAU14103 Peptide s
7	1107	90.9	257	6	ABO10268 S. aureus
8	1093	89.7	230	4	AAW67339 Staphyloc
9	1091	89.6	245	2	AAW35374 Staphyloc
10	1072	88.0	248	6	ABU79072 S. aureus
11	1048	86.0	230	2	AAW45012 Staphyloc
12	1044	85.7	230	5	ABW78235 Staphyloc
13	1035	85.0	230	2	AAW13204 Staphyloc
14	960	78.8	233	6	AAW13203 Staphyloc
15	948	77.8	233	6	ABP58458 Staphyloc
16	948	77.8	257	4	AAU14104 Peptide s
17	948	77.8	257	6	ABO10269 S. aureus
18	948	77.8	257	7	ADD44368 Staphyloc
19	944	77.5	233	2	AAW08738 Staphyloc
20	942	77.3	233	2	AAW45011 Staphyloc
21	941	77.3	233	2	AAW35373 Staphyloc
22	941	77.3	233	4	AAW67338 Staphyloc
23	935	76.8	257	6	ABU79068 S. aureus
24	933	76.6	233	5	ABB76234 Staphyloc
25	925	75.9	257	5	ABB79501 Staphyloc

26	925	75.9	257	6	ABU10081	Abu10081 Staphyloc
27	925	75.9	257	7	ABU62324	Abu62324 S. aureus
28	925	75.9	257	7	AAE37676	AAE37676 Protein #
29	921	75.6	233	3	AAV54463	AAV54463 Amino aci
30	921	75.6	233	5	ABW79502	ABW79502 Staphyloc
31	921	75.6	233	6	ABU10082	Abu10082 Staphyloc
32	921	75.6	233	7	ABU62325	ABU62325 S. aureus
33	921	75.6	233	7	AAE37677	AAE37677 Protein #
34	917	75.3	233	6	ABU10099	Abu10099 Staphyloc
35	912	74.9	233	6	ABU10098	Abu10098 Staphyloc
36	908	74.5	257	3	AAV70102	AAV70102 Staphyloc
37	903	74.1	233	3	AAU70103	AAU70103 Mutant St
38	611	50.2	258	6	ABU79071	Abu79071 S. aureus
39	605	49.7	228	2	AAW45013	AAW45013 Staphyloc
40	605	49.7	228	4	ABW67340	ABW67340 Staphyloc
41	605	49.7	228	5	ABW76236	ABW76236 Staphyloc
42	597	49.0	208	2	AAW13205	AAW13205 Staphyloc
43	485	39.8	203	6	ABP58459	ABP58459 Staphyloc
44	440.5	36.2	250	6	ABW70958	ABW70958 Staphyloc
45	406	33.3	82	6	ABU10091	Abu10091 Bacterial
46	406	33.3	82	7	ABU62338	ABU62338 S. aureus
47	370	30.4	91	2	AAW24299	AAW24299 Staphyloc
48	362	29.7	82	6	ABU10089	Abu10089 Bacterial
49	362	29.7	82	7	ABU62336	ABU62336 S. aureus
50	308	25.3	217	6	ABP58460	ABP58460 Staphyloc
51	291.5	23.9	259	5	ABP29357	ABP29357 Streptoco
52	287.5	23.6	239	2	AAW06254	AAW06254 Staphyloc
53	287.5	23.6	239	2	AAW06253	AAW06253 Staphyloc
54	287.5	23.6	240	6	ABG71369	ABG71369 Staphyloc
55	287.5	23.6	239	2	AAW06256	AAW06256 Staphyloc
56	282.5	23.2	240	6	ABG71370	ABG71370 Staphyloc
57	282.5	23.2	240	6	ABG71372	ABG71372 Staphyloc
58	280.5	23.0	239	2	AAW06255	AAW06255 Staphyloc
59	280.5	23.0	240	6	ABG71371	ABG71371 Staphyloc
60	279.5	22.9	239	2	AAW06252	AAW06252 Staphyloc
61	279.5	22.9	240	6	ABG71368	ABG71368 Staphyloc
62	277.5	22.8	238	2	AAW45016	AAW45016 Staphyloc
63	275.5	22.6	238	4	ABW67343	ABW67343 Staphyloc
64	275.5	22.6	238	5	ABW76239	ABW76239 Staphyloc
65	273.5	22.5	228	4	AAW63856	AAW63856 Amino aci
66	272.5	22.4	238	2	AAW13208	AAW13208 Staphyloc
67	271.5	22.3	251	2	AAW12153	AAW12153 Streptoco
68	270.5	22.2	221	2	AAW13209	AAW13209 Streptoco
69	270.5	22.2	221	2	AAW45017	AAW45017 Staphyloc
70	270.5	22.2	221	5	ABW76240	ABW76240 Staphyloc
71	270.5	22.2	251	2	AAW12151	AAW12151 Streptoco
72	270.5	22.2	251	2	AAW12150	AAW12150 Streptoco
73	268.5	22.0	251	2	AAW12154	AAW12154 Streptoco
74	268.5	22.0	251	2	AAW12146	AAW12146 Streptoco
75	268.5	22.0	251	2	AAW12097	AAW12097 Streptoco
76	268.5	22.0	251	2	AAW12147	AAW12147 Streptoco
77	268.5	22.0	251	2	AAW12148	AAW12148 Streptoco
78	268.5	22.0	251	2	AAW59780	AAW59780 Amino aci
79	268.5	22.0	266	6	ABU79069	ABU79069 S. aureus
80	267.5	22.0	239	2	AAW64847	AAW64847 Synthetic
81	267.5	22.0	239	4	ABW67341	ABW67341 Staphyloc
82	267.5	22.0	255	2	AAW06737	AAW06737 Staphyloc
83	266.5	21.9	221	4	AAW67344	AAW67344 Streptoco
84	264.5	21.7	239	2	AAW13207	AAW13207 Staphyloc
85	264.5	21.7	239	2	AAW45015	AAW45015 Staphyloc
86	264.5	21.7	239	5	ABW76238	ABW76238 Staphyloc
87	264.5	21.7	251	2	AAW59798	AAW59798 Amino aci
88	264.5	21.7	251	2	AAW59781	AAW59781 Amino aci
89	264.5	21.7	251	7	ABU62460	ABU62460 Streptoco
90	264.5	21.7	266	7	ABU62455	ABU62455 S. aureus
91	263.5	21.6	251	3	AAW70109	AAW70109 Streptoco
92	263.5	21.6	251	5	ABW79508	ABW79508 Streptoco
93	263.5	21.6	251	6	ABU10088	ABU10088 Streptoco
94	263.5	21.6	251	7	ABU62331	ABU62331 Streptoco
95	263.5	21.6	251	7	AAE37683	AAE37683 Streptoco
96	263.5	21.6	266	6	ABU79070	ABU79070 S. aureus
97	262.5	21.6	239	2	AAW06251	AAW06251 Staphyloc
98	262.5	21.6	239	4	AAW67342	AAW67342 Staphyloc

FT FT /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 452
 FT /note= "wild-type Asp substituted by Ser"
 FT Region 459..565
 FT /note= "574 variable light chain"
 FT Misc-difference 469
 FT /note= "wild-type Phe substituted by Ser"
 FT Misc-difference 504
 FT /note= "wild-type Thr substituted by Lys"
 FT Misc-difference 522
 FT /note= "wild-type Ile substituted by Ser"
 FT Misc-difference 532
 FT /note= "wild-type Phe substituted by Leu"
 FT Misc-difference 536
 FT /note= "wild-type Thr substituted by Ser"
 FT Misc-difference 537
 FT /note= "wild-type Leu substituted by Val"
 FT Misc-difference 542
 FT /note= "wild-type Leu substituted by Ala"
 FT Region 566..572
 FT /note= "C242 constant light chain"
 XX
 PN W02003002143-A1.
 XX
 XX 09-JAN-2003.
 XX
 XX 19-JUN-2002; 2002WO-SE001188.
 XX
 XX 28-JUN-2001; 2001SE-00002327.
 XX
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Claim 12; Fig 10; 102pp; English.
 XX
 CC The present sequence is a conjugate of a bacterial superantigen and an
 CC antibody moiety, and has been designed to target and destroy cancer
 CC cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
 CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
 CC of the following amino acid substitutions to reduce seroreactivity whilst
 CC maintaining production levels and biological activity: R20G, N21T, S24G,
 CC R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
 CC Fab moiety of the tumour reactive antibody 574. Substitutions were made
 CC in the 574 sequence to obtain higher yields: in the heavy chain, H41P,
 CC S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
 CC T77S, L78V and I83A. An expression vector comprising DNA encoding the
 CC conjugate can be used to transform host cells for recombinant production
 CC of the conjugate. The conjugate is useful for treating cancer, including
 CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
 CC cervix and prostate (claimed)
 XX
 SQ Sequence 672 AA;
 Query Match 100.0%; Score 1218; DB 6; Length 672;
 Best Local Similarity 100.0%; Pred. No. 3,2e-114;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTG 60
 DB 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTG 285
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLT 345

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 346 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 QY 181 RGLIVFHSSEGSTVSVDLPDAOGQYPTDLRIYRDNNTTISSTLSLSLYLYTT 233
 DB 406 RGLIVFHSSEGSTVSVDLPDAOGQYPTDLRIYRDNNTTISSTLSLSLYLYTT 458

RESULT 3
 ABP58457
 ID ABP58457 standard; protein; 233 AA.
 XX
 AC ABP58457;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Engineered superantigen SEA/E-18 for human cancer therapy.
 XX
 XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
 XX
 OS Staphylococcus sp.
 OS Synthetic.
 OS
 PN W02003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-18. The superantigen is based on staphylococcal
 CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
 CC to the N-terminal that were from enterotoxin A and one substitution in
 CC the C-terminal part, D227A. Models of new superantigen variants were
 CC constructed using the SEA/E-18 model as the template. These include the
 CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
 CC genetically fused to the Fab moiety of the tumour reactive antibody 574
 CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
 CC claimed example of novel conjugates of the invention comprising an
 CC engineered bacterial superantigen and an antibody moiety. The conjugates
 CC are designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 SQ Sequence 233 AA;
 Query Match 92.8%; Score 1130; DB 6; Length 233;
 Best Local Similarity 91.4%; Pred. No. 5,9e-106;
 Matches 233; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTG 60
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTCMYGGVTLHDNNRLT 120

Db 61 HPWYNDLLVLDGKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233

RESULT 4

AAW35375
 ID AAW35375 standard; peptide; 245 AA.
 AC AAW35375;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE Staphylococcus enterotoxin SEE modified superantigen.
 XX
 KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody; modified.
 XX
 OS Staphylococcus sp.
 XX
 Key Location/Qualifiers
 FH Misc-difference 20 /label= R20G
 FT /note= "wild-type Arg is replaced by Gly"
 FT Misc-difference 21 /label= N21T
 FT /note= "wild-type Asn is replaced by Thr"
 FT Misc-difference 24 /label= S24G
 FT /note= "wild-type Ser is replaced by Gly"
 FT Misc-difference 27 /label= R27K
 FT /note= "wild-type Arg is replaced by Lys"
 FT
 XX
 W09736932-A1.
 XX
 PD 09-OCT-1997.
 XX
 XX 26-MAR-1997; 97WO-SE000537.
 XX
 XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX
 PA (PHAA) PHARMACIA & UPJOHN AB.
 XX
 XX Antonsson P, Hansson J, Björk P, Dohlsten M, Kalland T;
 PI Abrahamsen L, Forsberg G;
 XX
 XX WPI; 1997-503052/46.
 XX
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX
 XX Claim 5; Page; 58pp; English.
 XX
 XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
 CC type SEE superantigen is modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. This modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused

CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 CC Note: This sequence is not provided in the specification. It has been
 CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
 CC 39 of the specification
 XX
 SQ Sequence 245 AA;

Query Match 91.4%; Score 1113; DB 2; Length 245;
 Best Local Similarity 86.9%; Pred. No. 3.3e-104;
 Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
 Qy 61 HPWYNDLLVLDGKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVLDGKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 228
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 228
 Qy 229 YLYTT 233
 Db 241 YLYTT 245

RESULT 5

ABP58456
 ID ABP58456 standard; protein; 233 AA.
 XX
 AC ABP58456;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin E.
 XX
 KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX
 OS Staphylococcus sp.
 XX
 FN W02003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 19-JUN-2002; 2002WO-SE001188.
 PF
 XX 28-JUN-2001; 2001SE-00002327.
 PR
 XX (ACTI-) ACTIVE BIOTECH AB.
 PA
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PI
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 XX receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX

PS Example 3; Fig 4; 102pp; English.

CC The present sequence is the protein sequence of staphylococcal

CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)

CC for human cancer therapy. These comprise an engineered bacterial

CC superantigen, such as novel SEA/3-120 (see ABP58455), which is based on

CC SEE, and an antibody moiety, such as tumour reactive antibody 514. The

CC superantigen is engineered to reduce seroreactivity whilst maintaining

CC biological activity and production levels. The conjugates are designed to

CC target and destroy cancer cells, including cancer of the lung, breast,

CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)

XX Sequence 233 AA;

SQ

Query Match 90.9%; Score 1107; DB 6; Length 233;

Best Local Similarity 89.7%; Pred. No. 1.3e-103;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLPKGFTG 60

DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLPKGFTG 60

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 61 HPWYNDLLVDLGSDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 121 BEKVPINLWIDGQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 121 BEKVPINLWIDGQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233

DB 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTINSENHIDLILYLYTT 233

RESULT 6

ID AAU14103

XX AAU14103;

AC AAU14103;

XX

DT 21-NOV-2001 (first entry)

XX

DE Peptide sequence from Staphylococcus aureus enterotoxin type E.

XX

KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;

KW antifusogenic; antiviral; HIV transmission.

XX

OS Staphylococcus aureus.

XX

FN WO200151673-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JUL-2000; 2000WO-US035727.

XX

PR 09-JUL-1999; 99US-00350841.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX

XX WPI; 2001-442157/47.

XX

PT Identifying a compound that inhibits the formation of or disrupts a

PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral

PT or intracellular modulatory activity, by detecting the formation of a

PT DP107/DP178 complex.

XX

PS Disclosure; Fig 41; 259pp; English.

XX

CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to

CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence or

CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including

CC small molecule compounds, which may themselves exhibit antifusogenic,

CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like

CC peptides are useful to inhibit human and non-human retroviral,

CC particularly HIV, transmission to uninfected cells. The present sequence

CC represents a peptide sequence from Staphylococcus aureus enterotoxin type

CC E

SQ Sequence 257 AA;

Query Match 90.9%; Score 1107; DB 4; Length 257;

Best Local Similarity 89.7%; Pred. No. 1.5e-103;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLPKGFTG 60

DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLPKGFTG 84

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 BEKVPINLWIDGQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 145 BEKVPINLWIDGQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233

DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTINSENHIDLILYLYTT 257

RESULT 7

ABO10268

ID ABO10268 standard; protein; 257 AA.

XX

AC ABO10268;

XX

DT 19-AUG-2003 (first entry)

XX

DE S. aureus enterotoxin E.

XX

KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;

KW Epstein-Barr virus infection; heptad repeat motif.

XX

OS Staphylococcus aureus.

XX

FN US6518013-B1.

XX

PD 11-FEB-2003.

XX

PF 07-JUN-1995; 95US-00485546.

XX

PR 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX

XX (TRIM-) TRIMERIS INC.

XX

PI Barney SO, Lambert DM, Petteway SR;

XX

XX WPI; 2003-465599/44.

XX

PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting

PT the cell with a peptide consisting of a region of Epstein-Barr virus

PT protein.

PT

XX Example; Fig 41; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of AL1MOT15, 107x1784 or P1Z1P sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group or macromolecular carrier group, and Z comprises a carboxyl group, amido group, hydrophobic group, or macromolecular carrier group, and fusion of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a protein from a pathogenic organism analysed for regions analogous to DP107 or DP178

XX Sequence 257 AA;

Query Match 90.9%; Score 1107; DB 6; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.5e-103;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINERKDLKKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFGFTG 60
Db 25 SEKSEINERKDLKKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFGFTG 84
QY 61 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTTPNKTACMGVTLHNNLT 120
Db 85 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTTPNKTACMGVTLHNNLT 144
QY 121 EEKVPINLWDGKTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWDGKTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQCQYPTDLRIYRDNNTTSSLSISLYTT 233
Db 205 RGLIVFHSSEGSTSVSYDLFDAQCQYPTDLRIYRDNNTTSSLSISLYTT 257

RESULT 8
AAB67339
ID AAB67339 standard; peptide; 230 AA.
AC AAB67339;
XX
XX 23-APR-2001 (first entry)
DT
DE Staphylococcus aureus enterotoxin E protein.
XX Tumour; cancer; immune; enterotoxin.
XX Staphylococcus aureus.
XX US6180097-B1.
XX 30-JAN-2001.
XX 30-OCT-1998; 98US-00183437.
XX 03-OCT-1989; 89US-00416530.
XX 17-JAN-1990; 90US-00466577.
XX 17-JAN-1991; 91WO-US000342.
XX 01-JUN-1992; 92US-00891718.
XX 02-MAR-1993; 93US-00025144.
XX 31-JAN-1994; 94US-00189424.

PR 19-JUN-1995; 95US-00491746.
PA (TERM/) TERVAN D S.
XX Terman DS;
XX WPI; 2001-158657/16.
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or in vivo comprises exogenous nucleic acids encoding a superantigen and a costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX The present invention relates to a tumour cell capable of stimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an anticancer immune response in vivo or ex vivo
XX Sequence 230 AA;

Query Match 89.7%; Score 1093; DB 4; Length 230;
Best Local Similarity 89.6%; Pred. No. 3.3e-102;
Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 4 SEENEDLKKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFGFTGHPW 63
Db 1 SEENEDLKKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFGFTGHPW 60
QY 64 YNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTTPNKTACMGVTLHNNLTTEK 123
Db 61 YNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTTPNKTACMGVTLHNNLTTEK 120
QY 124 KVPINLWDGKTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQRL 183
Db 121 KVPINLWDGKTTPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQRL 180
QY 184 IVFHSSEGSTSVSYDLFDAQCQYPTDLRIYRDNNTTSSLSISLYTT 233
Db 181 IVFHSSEGSTSVSYDLFDAQCQYPTDLRIYRDNNTTSSLSISLYTT 230

RESULT 9
AAW35374
ID AAW35374 standard; peptide; 245 AA.
XX
XX AAW35374;
XX
XX 20-APR-1998 (first entry)
DT
DE Staphylococcus enterotoxin SEE wild-type superantigen.
XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment; cancer; infection; autoimmune disease; antibody.
XX Staphylococcus sp.
XX Key Location/Qualifiers
XX Misc-difference 20 /note= "can be mutated at this position"
XX Misc-difference 21 /note= "can be mutated at this position"
XX Misc-difference 24 /note= "can be mutated at this position"
XX Misc-difference 27 /note= "can be mutated at this position"
XX WO9736932-A1.
XX 09-OCT-1997.

XX PF 26-MAR-1997; 97WO-SE000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX XX (PHAA) PHARMACIA & UPJOHN AB.
XX PA Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
XX PI Abrahamsen L, Forsberg G;
XX XX WPI; 1997-503052/46.
XX DR Conjugate of target seeking moiety and modified superantigen - useful for
XX PT activating the immune system to treat cancer, viral infections, parasitic
XX PT infestations and autoimmune diseases.
XX XX Claim 4; Page 38-39; 58pp; English.
XX XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
XX CC SEE superantigen can be modified to be used in a novel conjugate. The
XX CC novel conjugate comprises a target seeking moiety and a modified wild
XX CC type superantigen. The modified superantigen retains its ability to
XX CC activate a subset of T cells, even though 1 or more wild-type amino acid
XX CC residues in at least 1 region which functions in determining binding to T
XX CC cell receptor (TCR) and activation of a subset of T cells has/have been
XX CC replaced. Such a modified superantigen can optionally be used as part of
XX CC a conjugate with a target seeking moiety, for activating the immune
XX CC system to treat a mammalian disease. A pharmaceutical composition can be
XX CC prepared comprising a modified antibody (preferably a Fab fragment fused
XX CC to a peptide moiety providing activation of T cells in beta specific
XX CC manner) in which cysteines providing for interchain cysteine linkages in
XX CC the native antibody have been replaced (preferably by serine residues) to
XX CC prohibit cysteine formation. The modified wild-type superantigen is used
XX CC for treating cancer, viral infections, parasitic infestations and
XX CC autoimmune disease. The modified wild type superantigen has a lower
XX CC immunogenicity and reactivity with neutralising antibodies and has fewer
XX CC side-effects when used as a drug, compared to wild type superantigen
XX SQ Sequence 245 AA;
Query Match 89.6%; Score 1091; DB 2; Length 245;
Best Local Similarity 85.3%; Pred. No. 5,7e-102;
Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
QY 1 SEKSEINEKDLRKXSEIQALGNLKOIYYNKAITSSEKSDQFLNTLLPKGFPTG 60
DB 1 SEKSEINEKDLRKXSEIQALGNLKOIYYNKAITSSEKSDQFLNTLLPKGFPTG 60
QY 61 HPWNLDLVDLGSTAAATSEYEGSSVDLYGAVYGCAGGTENKTCAMVGGVTLHDNNRLT 120
DB 61 HPWNLDLVDLGSKDANKYKGGKVDLYGATYGCAGGTENKTCAMVGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLKGKGLYNSDSFGKVKQ 180
DB 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLKGKGLYNSDSFGKVKQ 180
QY 181 RGLVHFHSSSEGSTVSYDLFDAGQVPTLLIYRDNT-----TISSTLSLSL 228
DB 181 RGLVHFHSSSEGSTVSYDLFDAGQVPTLLIYRDNTINSENLIHDIYLTINSENLIHDL 240
QY 229 YLYTT 233
DB 241 YLYTT 245
RESULT 10
ID ABU79072
XX ABU79072 standard; protein; 248 AA.
XX AC ABU79072;
XX DT 18-JUN-2003 (first entry)

XX DE S. aureus SEE (staphylococcus enterotoxin E) protein.
XX XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX KW APC; antitumour.
XX OS Staphylococcus aureus.
XX XX US2002177551-A1.
XX PD 28-NOV-2002.
XX PF 30-MAY-2001; 2001US-00870759.
XX PR 31-MAY-2000; 2000US-0208128P.
XX XX (TERM/) Terman D S.
XX PA Terman DS;
XX PI WPI; 2003-361759/34.
XX DR N-PSDB; AC646498.
XX XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX PT to tumor associated lipids where the binding induces anergy or apoptosis
XX PT in T cells and antigen presenting cells.
XX XX Disclosure; Page; 167pp; English.
XX CC The invention relates to a mammalian cell receptor, useful in the
XX CC treatment of cancer, which binds to tumour associated lipids and induces
XX CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX CC Also included are a mammalian cell useful in the treatment of cancer
XX CC where the receptor which binds tumour associated lipids and induces
XX CC cellular inactivation or death is deleted or functionally deactivated,
XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX CC (by allowing tumour associated lipids to contact immunocytes in which
XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX CC deleted), a construct useful in the treatment of cancer comprising a
XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
XX CC useful in the treatment of cancer (where an adaptor protein which
XX CC inhibits T cell activation by tumour associated antigens is deleted or
XX CC functionally deactivated), a composition useful in the treatment of
XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing
XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX CC allowing tumour associated lipids to contact immunocytes, in which
XX CC receptors for the lipids are inactivated or deleted to produce a
XX CC tumouricidal immunocyte population, and administering the tumouricidal
XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to
XX CC contact T cells, in which adaptor proteins, which inhibit T cell
XX CC activation by tumour associated antigens, are deleted or functionally
XX CC deactivated to produce a tumouricidal population of T cells, and
XX CC administering the tumouricidally activated T cells to the host, or
XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
XX CC administering the tumouricidally activated T cells to the host), treating
XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which
XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a
XX CC tumour associated antigen to contact immunocytes in which adaptor
XX CC proteins which inhibit T cell activation by tumour associated antigens
XX CC are deleted or functionally deactivated) and producing (M7) a
XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
XX CC receptors, methods and compositions are useful for treating cancers and

CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 XX Sequence 248 AA;

Query Match 88.0%; Score 1072; DB 6; Length 248;
 Best Local Similarity 90.2%; Pred. No. 4.9e-100; Indels 0; Gaps 0;
 Matches 202; Conservative 9; Mismatches 13;
 QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSDQFLNTLLFKGFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSDQFLNTLLFKGFTG 84
 QY 61 HPWYNLLVDLSTAAITSEYSSVDLYGAYYQYQACGTPNKTACMYGGVTLHNNRLT 120
 Db 85 HPWYNLLVDLSTAAITSEYSSVDLYGAYYQYQACGTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNNTISSTLSLSLYTT 224
 Db 205 RGLIVFHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNNTISSTLSLSLYTT 248

RESULT 11
 AAR45012
 ID AAR45012 standard; protein; 230 AA.
 XX
 AC AAR45012;
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX
 XX Staphylococcal enterotoxin SEE.
 DE
 DE Staphylococcal enterotoxin; SE; cancer; tumour; agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 KW
 XX Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 120
 FT /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 121
 FT /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123
 FT /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124
 FT /note= "Given in the specification as U, no further
 FT details given"
 XX
 PN W09324136-A1.
 XX
 XX
 PD 09-DEC-1993.
 XX
 PD 01-JUN-1993; 93WO-05005213.
 XX
 PD 01-JUN-1992; 92US-00891718.
 XX
 XX (TERM/) Terman D S.
 XX (STON/) Stone J L.
 XX
 XX Terman DS, Stone JL;

XX WPI; 1993-405418/50.
 XX
 XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX
 XX Disclosure; Fig 1; 90pp; English.
 XX
 XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 230 AA;

Query Match 86.0%; Score 1048; DB 2; Length 230;
 Best Local Similarity 85.7%; Pred. No. 1.2e-97; Indels 0; Gaps 0;
 Matches 197; Conservative 12; Mismatches 21;
 QY 4 SEEINEXDLRKSELOQTALGNLQIYYNKAITSSEKSDQFLNTLLFKGFTGHPW 63
 Db 1 SEEINEXDLRKSELOQTALGNLQIYYNKAITSSEKSDQFLNTLLFKGFTGHPW 60
 QY 64 YNDLLVDLSTAAITSEYSSVDLYGAYYQYQACGTPNKTACMYGGVTLHNNRLTEK 123
 Db 61 YNDLLVDLSTAAITSEYSSVDLYGAYYQYQACGTPNKTACMYGGVTLHNNRLTEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQRL 183
 Db 121 YXXBKWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQRL 180
 QY 184 IVFHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNNTISSTLSLSLYTT 233
 Db 181 IVFHSSEGSTVSYDLFDQAQGYPTDLLRIYRDNNTISSTLSLSLYTT 230

RESULT 12
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 XX
 AC ABB76235;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 XX Staphylococcus aureus enterotoxin E.
 DE
 DE Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 KW
 XX Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 120
 FT /note= "Given as 'J' in the specification"
 FT Misc-difference 121
 FT /note= "Given as 'J' in the specification"
 FT Misc-difference 123
 FT /note= "Given as 'O' in the specification"
 FT Misc-difference 124
 FT /note= "Given as 'U' in the specification"
 FT Misc-difference 125
 FT /note= "Given as 'V' in the specification"
 XX
 PN US2002051765-A1.
 XX
 XX 02-MAY-2002.
 PD
 XX 19-DEC-2000; 2000US-00741503.
 XX
 XX 03-OCT-1989; 89US-00416530.
 PR

PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.
 PA
 XX
 XX
 PI Terman DS;
 XX
 DR WPI; 2002-415198/44.
 XX

PT Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX

PS Disclosure; Fig 2; 17pp; English.
 XX

CC The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see AB576234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX

SQ Sequence 230 AA;

Query Match 85.7%; Score 1044; DB 5; Length 230;
 Best Local Similarity 85.7%; Pred. No. 3e-97;
 Matches 197; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 4 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 63
 DB 1 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNLTTEK 123
 DB 61 YNDLLVDKSGKDANKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNLTTEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRL 183
 DB 121 XVQXKXKWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTINSENHDIYLYTT 230

RESULT 13

AAR13204
 ID AAR13204 standard; protein; 230 AA.
 XX
 AC AAR13204;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin E.

XX SEE; cancer treatment; pyrogen; tumouricide.

XX

OS Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1990; 90US-00466577.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX

XX Disclosure; Fig 1; 74pp; English.

CC SEE was isolated and purified from S. aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX

SQ Sequence 230 AA;

Query Match 85.0%; Score 1035; DB 2; Length 230;
 Best Local Similarity 84.3%; Pred. No. 2.5e-96;
 Matches 194; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 4 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 53
 DB 1 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNLTTEK 123
 DB 61 YNDLLVDKSGKDANKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNLTTEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRL 183
 DB 121 XVQXKXKWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTINSENHDIYLYTT 230

RESULT 14

AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX
 AC AAR13203;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin A.

XX SEA; cancer treatment; pyrogen; tumouricide.

XX Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1990; 90US-00466577.

XX PR 17-JAN-1990; 90US-00465577.
 XX (TERM/) Terman D S.
 XX Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity as
 PT *Staphylococcal* protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 XX SEA was isolated and purified from *S. aureus*. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEA. Synthetic polypeptides having structural homology to
 CC *Staphylococcal* exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See also AAR13204-R13211
 XX Sequence 233 AA;
 SQ

Query Match 78.8%; Score 960; DB 2; Length 233;
 Best Local Similarity 77.3%; Pred. No. 1e-88;
 Matches 180; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYYNKAITSSSEKSAQDFLTNTLLPKGFTG 60
 DB 1 SEKSEINEKDLRKSELOGTALGNLKIYYYNKAITSSSEKSHDQFLQHTILFKGFTD 60
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGYOCAGGTPNKTACMYGGVTLHDNNELT 120
 DB 61 HSWYNDLLVDLGSKSDIVDKYKGGKVDLYGAYYGYOCAGGTPNKTACMYGGVTLHDNNELT 120
 QY 121 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 121 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVPDGKQV 180
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQGOYPTDILLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 RGLIVFHTSTEPSVNYDLFDAQGOYSNTLLRIYRDNKNTINSENMHIDIYLYTS 233

RESULT 15
 ABP58458
 ID ABP58458 standard; protein; 233 AA.
 XX AC ABP58458;
 XX DT 14-APR-2003 (first entry)
 XX Staphylococcal enterotoxin A.
 XX Superantigen; *staphylococcal* enterotoxin A; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX *Staphylococcus* sp.
 XX WO2003002143-A1.
 XX 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001185.
 XX 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;

XX WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX Example 3; Fig 3; 102pp; English.
 XX The present sequence is the protein sequence of *staphylococcal*
 CC enterotoxin A (SEA). The invention provides novel conjugates (see
 CC APF58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see APF58453), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX Sequence 233 AA;
 SQ

Query Match 77.8%; Score 948; DB 6; Length 233;
 Best Local Similarity 76.4%; Pred. No. 1.7e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYYNKAITSSSEKSAQDFLTNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOGTALGNLKIYYYNKAITSSSEKSHDQFLQHTILFKGFTD 60
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGYOCAGGTPNKTACMYGGVTLHDNNELT 120
 DB 61 HSWYNDLLVDLGSKSDIVDKYKGGKVDLYGAYYGYOCAGGTPNKTACMYGGVTLHDNNELT 120
 QY 121 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 121 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVPDGKQV 180
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQGOYPTDILLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 RGLIVFHTSTEPSVNYDLFDAQGOYSNTLLRIYRDNKNTINSENMHIDIYLYTS 233

RESULT 16
 AAU14104
 ID AAU14104 standard; peptide; 257 AA.
 XX AC AAU14104;
 XX DT 21-NOV-2001 (first entry)
 XX Peptide sequence from *Staphylococcus aureus* enterotoxin A.
 XX Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
 KW antiviral; HIV transmission.
 XX *Staphylococcus aureus*.
 OS
 XX WO200151673-A2.
 XX 19-JUL-2001.
 XX 05-JUL-2000; 2000WO-US035727.
 XX 09-JUL-1999; 99US-00350841.
 XX (TRIM-) TRIMERIS INC.
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 XX WPI; 2001-442157/47.
 DR

XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Fig 42; 259pp; English.
 XX
 CC The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin A
 XX
 SQ Sequence 257 AA;

Query Match 77.8%; Score 948; DB 4; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNSKAITSSSEKSAQDLTNTLFGKFFTG 60
 Db 25 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHQDLQHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
 Db 85 HSWYNDLLVDFDSDKDIVDKYKGGKVDLYGAYYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
 QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQVQ 180
 Db 145 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLHGKFGLYNSDSVDFGKQV 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKNTINSENHIDILYLYTS 257

RESULT 17
 ABO10269
 XX ABO10269 standard; protein; 257 AA.
 XX ABO10269;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 XX *S. aureus* enterotoxin A.
 DE HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.
 XX
 OS *Staphylococcus aureus*.
 XX
 XX US6518013-B1.
 XX
 PD 11-FEB-2003.
 XX
 XX 07-JUN-1995; 95US-00485546.
 XX
 PR 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX

PA (TRIM-) TRIMERIS INC.
 XX
 XX Barney SO, Lambert DM, Petteway SR;
 PI
 DR WPI; 2003-465599/44.
 XX
 PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 PT
 PS Example; Fig 42; 716pp; English.
 XX
 CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 18-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALIMOTI5,
 CC 107x178x4 or PZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 SQ Sequence 257 AA;

Query Match 77.8%; Score 948; DB 6; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNSKAITSSSEKSAQDLTNTLFGKFFTG 60
 Db 25 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHQDLQHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
 Db 85 HSWYNDLLVDFDSDKDIVDKYKGGKVDLYGAYYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
 QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQVQ 180
 Db 145 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLHGKFGLYNSDSVDFGKQV 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKNTINSENHIDILYLYTS 257

RESULT 18
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX
 XX ADD44368;
 XX
 XX 15-JAN-2004 (first entry)
 XX
 XX *Staphylococcus aureus* enterotoxin A protein.
 DE enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 KW ice cream.
 XX
 XX *Staphylococcus aureus*.
 OS
 XX WO2003080865-A1.
 XX

PD XX 02-OCT-2003.
 XX PF 26-MAR-2002; 2002WO-IB001150.
 XX PF 26-MAR-2002; 2002WO-IB001150.
 XX PR 26-MAR-2002; 2002WO-IB001150.
 XX PA (COUL) COUNCIL SCI & IND RES.
 XX PA Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
 XX PI WPI; 2003-779273/73.
 XX DR N-PSDB; ADD44369.
 XX DR Novel oligonucleotide primers directed against enterotoxin A gene of
 PT Staphylococcus aureus and heat stable enterotoxin gene of *Yersinia*
 PT enterocolitica, useful for detecting food poisoning causing bacteria.
 XX Example 2; Page 14-15; 34pp; English.
 XX The invention relates to novel oligonucleotide primers directed against
 CC enterotoxin A gene (ent A) of *Staphylococcus aureus* and heat stable
 CC enterotoxin A gene (yst) of *Bacteria Yersinia enterocolitica*. The novel
 CC oligonucleotide primers are useful for simultaneously detecting food
 CC poisoning bacterial species *Staphylococcus aureus* and/or *Yersinia*
 CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
 CC without prior enrichment for preventing food poisoning outbreak. The PCR
 CC detection method is useful for detecting the bacteria strains in quantity
 CC as low as one cell. The method can be directly used for detecting
 CC bacterial strains. The oligonucleotide primers allow quick and highly
 CC sensitive detection of the food poisoning bacterial species. This
 CC sequence represents the protein derived from the enterotoxin A gene from
 CC *Staphylococcus aureus* of the invention.
 XX SQ Sequence 257 AA;
 Query Match 77.8%; Score 948; DB 7; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSAQDLFTNTLLPKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSHDQFLQHTILPKGFTD 84
 QY 61 HPYNDLLVDLSTAASTSEYSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSYNDLLVDLSTAASTSEYSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKKVPINLWIDGKQTTVPLETKNKVNTVQELDLQARHYLQEKYLYNSDVFQKQV 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPDTLRLRYRNTTISSTLSISLYLTT 233
 DB 205 RGLIVFHTSTPSVNYDLFGAQGYQNTLLRIYRNTKNTINSENHDIYLYTS 257

RESULT 19

AAW06738
 ID AAW06738 standard; protein; 233 AA.

XX AC AAW06738;
 XX AC

DT 08-MAR-1997 (first entry)
 XX

DE Staphylococcus enterotoxin A.

XX Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
 KW adjuvant.

XX Staphylococcus sp.
 XX

XX WO9636366-A1.
 PN

XX PD 21-NOV-1996.
 XX PF 20-MAY-1996; 96WO-US007432.
 XX PR 18-MAY-1995; 95US-00446918.
 XX PR 29-DEC-1995; 95US-00580806.
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX PI Dow SW, Elmelie RE, Potter TA;
 XX DR WPI; 1997-011857/01.
 XX DR N-PSDB; AAT45699.
 XX Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer.
 XX Example 1; Page 98-99; 131pp; English.
 XX A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
 CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
 CC AAW06739), esp. truncated forms of the superantigen lacking the leader
 CC peptide, can be used in the gene therapy of cancer, infectious diseases
 CC and immunological disorders. The nucleic acid, optionally in combination
 CC with cytokine or chemokine nucleic acids, is delivered to an animal using
 CC e.g. liposomes. It acts by controlling the activity of effector cells,
 CC such as T-cells, macrophages, monocytes and/or natural killer cells.
 CC Localised prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal
 XX SQ Sequence 233 AA;
 Query Match 77.5%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 4.3e-87;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSAQDLFTNTLLPKGFTG 61
 DB 2 EKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSHDQFLQHTILPKGFTD 61
 QY 62 PWYNDLLVDLSTAASTSEYSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVDLSTAASTSEYSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 181
 DB 122 EKVPINLWIDGKQTTVPLETKNKVNTVQELDLQARHYLQEKYLYNSDVFQKQV 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYPDTLRLRYRNTTISSTLSISLYLTT 233
 DB 182 GLIVFHTSTPSVNYDLFGAQGYQNTLLRIYRNTKNTINSENHDIYLYTS 233

RESULT 20

AAW45011

ID AAR45011 standard; protein; 233 AA.

XX AC AAR45011;
 XX AC

DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX

DE Staphylococcal enterotoxin SEA.

XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.

XX Staphylococcus aureus.
 XX

XX Key Location/Qualifiers
 XX Misc-difference 49
 FT

```

FT /note= "Given in the specification as O, no further
FT details given"
XX WO3224136-A1.
XX
XX 09-DEC-1993.
XX
XX 01-JUN-1993; 93WO-US005213.
XX
XX 01-JUN-1992; 92US-00891718.
XX
XX (TERM/) TERMAN D S.
XX PA (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
XX
XX WPI; 1993-405418/50.
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX in a patient or for the treatment of auto-immune diseases.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
XX which may be used in the methods of the invention for treating cancer in
XX a patient. These SEs, and homologues of them, can be used as tumouricidal
XX agents for treating cancers and autoimmune disease. They exhibit
XX tumouricidal activity and toxicity identical to that observed for the
XX Protein A perfusion system. They may be administered by i.v. injection.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 233 AA;
SQ
Query Match 77.3%; Score 942; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 6.8e-87;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLTNLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFLXHTILFKGFFTD 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTAQMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTAQMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 121 BEKKVPINLWLDGKQNTVPLETVKTKKQNTVQELDPQARRYLOEKYNLYNSDVFQKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENHDIYLYTS 233
RESULT 21
AAR35373
ID AAR35373 standard; peptide; 233 AA.
XX
XX AAR35373;
XX
XX 20-APR-1998 (first entry)
XX
XX Staphylococcus enterotoxin SEA wild-type superantigen.
XX
XX SE5; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody.
XX
XX Staphylococcus sp.
XX
XX WO9736932-A1.
XX
XX 09-OCT-1997.
XX

```

```

PF 26-MAR-1997; 97WO-SE0000537.
XX
XX 29-MAR-1996; 96SE-00001245.
XX
XX 12-AUG-1996; 96US-00695692.
XX
XX (PHRA ) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
XX Abrahmsen L, Forsberg G;
XX
XX WPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
XX activating the immune system to treat cancer, viral infections, parasitic
XX infestations and autoimmune diseases.
XX
XX Claim 8; Page 36-37; 58pp; English.
XX
XX This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
XX SEA superantigen can be modified to be used in a novel conjugate. The
XX novel conjugate comprises a target seeking moiety and a modified wild
XX type superantigen. The modified superantigen retains its ability to
XX activate a subset of T cells, even though 1 or more wild-type amino acid
XX residues in at least 1 region which functions in determining binding to T
XX cell receptor (TCR) and activation of a subset of T cells has/have been
XX replaced. Such a modified superantigen can optionally be used as part of
XX a conjugate with a target seeking moiety, for activating the immune
XX system to treat a mammalian disease. A pharmaceutical composition can be
XX prepared comprising a modified antibody (preferably a Fab fragment fused
XX to a peptide moiety providing activation of T cells in Vbeta specific
XX manner) in which cysteines providing for interchain cysteine linkages in
XX the native antibody have been replaced (preferably by serine residues) to
XX prohibit cysteine formation. The modified wild-type superantigen is used
XX for treating cancer, viral infections, parasitic infestations and
XX autoimmune disease. The modified wild type superantigen has a lower
XX immunogenicity and reactivity with neutralising antibodies and has fewer
XX side-effects when used as a drug, compared to wild type superantigen
XX
XX Sequence 233 AA;
SQ
Query Match 77.3%; Score 941; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 8.6e-87;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLTNLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFLQHTILFKGFFTD 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTAQMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTAQMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 121 BEKKVPINLWLDGKQNTVPLETVKTKKQNTVQELDLQARRYLOEKYNLYNSDVFQKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENHDIYLYTS 233
RESULT 22
AAR67338
ID AAR67338 standard; peptide; 233 AA.
XX
XX AAR67338;
XX
XX 23-APR-2001 (first entry)
XX
XX Staphylococcus aureus enterotoxin A protein.
XX
XX Tumour; cancer; immune; enterotoxin.
XX

```

OS Staphylococcus aureus.
 XX US6180097-B1.
 XX 30-JAN-2001.
 XX 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1991; 91WO-US000342.
 XX 01-JUN-1992; 92US-00891718.
 XX 02-MAR-1993; 93US-00025144.
 XX 21-JAN-1994; 94US-00189424.
 XX 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERNAN D S.
 XX Terman DS;
 XX WPI; 2001-158657/16.
 XX Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 233 AA;
 XX
 XX Query Match 77.3%; Score 941; DB 4; Length 233;
 XX Best Local Similarity 76.0%; Pred. No. 8.6e-87;
 XX Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNSTRATSSKSAOQFLTNILFKGFTG 60
 DB 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNSTRATSSKSAOQFLTNILFKGFTG 60
 QY 61 HPWYNLLVDLSTAASTSEYSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 DB 61 HSWYNLLVDLSTAASTSEYSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLWIDKQTVTIDKVTTSKVTVEQLDQARHYLHGKFGLYNSDSFGKVQ 180
 DB 121 EEKVPINLWIDKQTVTIDKVTTSKVTVEQLDQARHYLHGKFGLYNSDSFGKVQ 180
 QY 181 RGLIVFHSSEGSVSYDLDPAGQYEDTLRLRYRNTWISSLSLSLYLYTT 233
 DB 181 RGLIVFHTSTPSVNYDLFGAGQYVNTLRLRYRNTWISSLSLSLYLYTS 233
 RESULT 23
 ID ABU79068
 XX ABU79068 standard; protein; 257 AA.
 XX AC ABU79068;
 XX 18-JUN-2003 (first entry)
 XX S. aureus SEA (staphylococcus enterotoxin A) protein.
 XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 XX gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 XX T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 XX APC; antitumour.

XX OS Staphylococcus aureus.
 XX US2002177551-A1.
 XX 28-NOV-2002.
 XX 30-MAY-2001; 2001US-00870759.
 XX 31-MAY-2000; 2000US-0208128P.
 XX (TERM/) TERNAN D S.
 XX Terman DS;
 XX WPI; 2003-361759/34.
 XX N-PSDB; ACA84694.
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumour associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX Disclosure; Page; 167pp; English.
 XX The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX SQ Sequence 257 AA;
Query Match 76.8%; Score 935; DB 6; Length 257;
Best Local Similarity 75.5%; Pred. No. 4e-86;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSEIQGTALGNLQIYYNYSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSEIQGTALGNLQIYYNYSKAITSEKSDAQFLTNTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDPDSKDIVDKYKGVKVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 121 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 BEKVPINLWDGKQNTVPLETVTKNKNTVVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNNTTINSENHIDIYLYTS 257
RESULT 24
ID ABB76234 standard; protein; 233 AA.
XX AC ABB76234;
XX DT 09-AUG-2002 (first entry)
XX DE Staphylococcus aureus enterotoxin A.
XX KW Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
XX KW therapy.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Misc-difference 49 /note= "amino acid residue given as 'O' in the
FT specification"
XX PN US2002051765-A1.
XX PD 02-MAY-2002.
XX PF 19-DEC-2000; 2000US-00741503.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX FA (TERM/) TERMAN D S.
XX FI Terman DS;
XX WPI; 2002-415198/44.
XX DR WPI; 2002-415198/44.
XX PT Reagent for treating cancer without the need for e.g. radiotherapy,
XX PT comprises a specific V beta subset of T cells sensitized to a growing
XX PT tumor and stimulated with superantigens.
XX PS Disclosure; Fig 2; 17pp; English.
XX CC The present sequence is the protein sequence of enterotoxin A (SEA) of
XX CC Staphylococcus aureus. Similarity is shown, in several stretches of
XX CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic

CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydropathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumoricidal reaction
XX Sequence 233 AA;
SQ Query Match 76.6%; Score 933; DB 5; Length 233;
Best Local Similarity 75.5%; Pred. No. 5.6e-86;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSEIQGTALGNLQIYYNYSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSEIQGTALGNLQIYYNYSKAITSEKSDAQFLTNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDPDSKDIVDKYKGVKVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
QY 121 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 121 BEKVPINLWDGKQNTVPLETVTKNKNTVVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNNTTINSENHIDIYLYTS 233
RESULT 25
ID ABB79501 standard; protein; 257 AA.
XX AC ABB79501;
XX DT 23-SEP-2002 (first entry)
XX DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).
XX KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;
XX KW attenuation; mutant; mutein.
XX OS Staphylococcus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..257
FT -/label= Mature_protein
FT Misc-difference 72 /note= "wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "wild-type Asp substituted by Arg"
FT Misc-difference 116 /note= "wild-type Tyr substituted by Ala"
XX PN US6399332-B1.
XX PD 04-JUN-2002.
XX PF 01-SEP-1998; 98US-00144776.
XX

XX 25-JUN-1997; 97US-00882431.
 XX (USSA) US SEC OF ARMY.
 PA Ulrich RG, Olson MA, Bavari S;
 PI WPI; 2002-546281/58.
 XX N-PSDB; ABN84222.
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX Claim 4; Col 33-35; 46pp; English.
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The full-length expressed product is secreted into the periplasmic space
 CC of *Escherichia coli* host cells, and the leader peptide is recognised and
 CC cleaved by a native mechanism. The vaccine is used to protect against
 CC superantigen toxin infections. Superantigen attributes are absent, but
 CC the superantigen is effectively recognised by the immune system and an
 CC appropriate antibody response is produced. In examples from the
 CC invention, attenuated superantigen toxins were shown to protect animals
 CC against challenge with wild-type toxin. Methods of producing and using
 CC the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TST-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX Sequence 257 AA;
 XX
 Query Match 75.9%; Score 925; DB 5; Length 257;
 Best Local Similarity 75.1%; Pred. No. 4.2e-85;
 Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTTG 84
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYGYOCAGTTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKQV 180
 DB 145 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKQV 204
 QY 181 RGLIVPHSSSGSTVSVDLPDAQOYPTLLRIYRDNNTTSSLSLSLYLTT 233
 DB 205 RGLIVPHTSTPSVNYDLFGAQOQYNTLLRIYRDNNTTSSLSLSLYLTT 257
 RESULT 26
 ABU10081
 ID ABU10081 standard; protein; 257 AA.
 XX
 AC ABU10081;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin A #1.
 XX
 KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 XX superantigen toxin.
 XX Staphylococcus sp.
 XX US2003009015-A1.
 XX

XX 09-JAN-2003.
 XX 25-JUN-1997; 97US-00882431.
 XX 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2003-401542/38.
 DR N-PSDB; ACA61177.
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX Claim 10; Page 18-19; 50pp; English.
 XX The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #1
 XX Sequence 257 AA;
 XX
 Query Match 75.9%; Score 925; DB 6; Length 257;
 Best Local Similarity 75.1%; Pred. No. 4.2e-85;
 Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFTNTLLFKGFTTG 84
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYGYOCAGTTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKQV 180
 DB 145 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKQV 204
 QY 181 RGLIVPHSSSGSTVSVDLPDAQOYPTLLRIYRDNNTTSSLSLSLYLTT 233
 DB 205 RGLIVPHTSTPSVNYDLFGAQOQYNTLLRIYRDNNTTSSLSLSLYLTT 257
 RESULT 27
 ABU62324
 ID ABU62324 standard; protein; 257 AA.
 XX
 AC ABU62324;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE S. aureus periplasmic enterotoxin A mutant #1.
 XX
 KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX

OS Staphylococcus aureus.
OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT 25..257
FT Protein /label= Mature_SEA_mutant #1
FT Misc-difference 66 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116 /note= "Wild-type Tyr substituted by Ala"
XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX Ulrich RG;
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28894.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 22-23; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection, an
XX antiserum isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the
XX mature protein sequence) mutant of periplasmic SEA
XX Sequence 257 AA;
XX Query Match 75.9%; Score 925; DB 7; Length 257;
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITENKESHDPQRTIILFKGFTD 84
XX 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 85 HSWYNDLLVRFDSKDIIVDKYKGGKVDLYGAYAGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
XX 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
XX 145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
XX 181 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 233
XX 205 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 257
XX RESULT 28
XX AAE37676
XX ID AAE37676 standard; protein; 257 AA.
XX AC AAE37676;
XX 06-OCT-2003 (first entry)
XX Protein #1 related to the invention.
XX Superantigen toxin; vaccine; infection; gene therapy.
XX Unidentified.
XX WO2003056015-A1.
XX 10-JUL-2003.
XX 26-NOV-2001; 2001WO-US046540.
XX 26-NOV-2001; 2001US-00002784.
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX Ulrich RG;
XX WPI; 2003-492125/46.
XX N-PSDB; AAD56764.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 108-109; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is a protein related to the
XX CC invention
XX Sequence 257 AA;
XX Query Match 75.9%; Score 925; DB 7; Length 257;
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITENKESHDPQRTIILFKGFTD 84
XX 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 85 HSWYNDLLVRFDSKDIIVDKYKGGKVDLYGAYAGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
XX 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
XX 145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
XX 181 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 233
XX 205 RGLIVFHSSEGSTVSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 257

Db 205 RGLIVFHTSTPSVNYDLFGAQQGYSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 29
AA54463

ID AAY54463 standard; protein; 233 AA.

XX AAY54463;

AC

XX 25-APR-2000 (first entry)

DT

XX Amino acid sequence of a mutant Staphylococcal enterotoxin A.

DE

XX Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;

KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;

KW Staphylococcal intoxication; Staphylococcus exotoxin.

XX

OS Staphylococcus aureus.

XX

XX Key Location/Qualifiers

FH

FT Misc-difference 2 /note= "glu encoded by AGAA"

FT

FT Misc-difference 4 /note= "ser encoded by C"

FT

XX WO200002523-A2.

PN

XX 20-JAN-2000.

PD

XX 09-JUL-1999; 99WO-US015569.

PF

XX 10-JUL-1998; 98US-0092416P.

PR

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

PA

XX Lee JS, Pushko P, Smith JF, Ulrich RG;

PI

XX WPI; 2000-160826/14.

DR

XX N-PSDB; AA245833.

DR

XX New DNA construct useful as vaccines against enterotoxins of

PT Staphylococcus aureus which causes gastrointestinal distress, or toxic

PT shock syndrome.

PT

XX Disclosure; Page 28; 30pp; English.

PS

XX The present sequence is represents a mutant Staphylococcal enterotoxin A.

CC It is encoded by a mutant SEA gene. The mutant gene product is unable to

CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes

CC were inserted into a Venezuelan equine encephalitis (VEE) replicon

CC vector, to produce vaccine vectors. The mutant gene product is unable to

CC bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA

CC derived from the recombinant VEE vectors can be used as a nucleic acid

CC vaccine, or to transfect cells along with RNA from helper plasmids. The

CC recombinant proteins produced are used as vaccines for providing immunity

CC against Staphylococcal intoxication or as a diagnostic tool for detection

CC of Staphylococcus exotoxin. The transformed host cells are used to

CC analyse the effectiveness of drugs and agents which inhibit S. aureus

CC exotoxins or release of exotoxins. Infectious alpha-virus particles

CC comprising the mutant SEA or SEB genes are used for providing immunity

CC against Staphylococcal exotoxins by generating a protective immune

CC reaction in humans or animals. The vaccines are used to reduce disease

CC symptoms or reduce severity of disease caused by enterotoxins of S.

CC aureus

XX

XX Sequence 233 AA;

SQ

Query Match 75.6%; Score 921; DB 3; Length 233;

Best Local Similarity 75.0%; Pred. No. 9,2e-85;

Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

2 EKSEENEXDLRKSELOQTALGNLQIYYNEKAKTENKESHQPRQHTILFKGFFTDH 61

Db 2 EKSEENEXDLRKSELOQTALGNLQIYYNEKAKTENKESHQPRQHTILFKGFFTDH 61

QY 62 PWYNDLLVGLGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLLHNNRLTE 121

Db 62 SWYNDLLVGFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGVTLLHNNRLTE 121

QY 122 EKKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVOR 181

Db 122 EKKVPINLMDGKQNTVPLETATKNNKNTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181

QY 182 GLIVFHTSTPSVNYDLFGAQQGYSNTLLRIYRDNKTINSENHDIYLYTS 233

Db 182 GLIVFHTSTPSVNYDLFGAQQGYSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 30

ABB79502

ID ABB79502 standard; protein; 233 AA.

XX

AC ABB79502;

XX

DT 23-SEP-2002 (first entry)

XX

XX Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).

DE

XX Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;

KW attenuation; mutant; mutein.

KW

XX Staphylococcus sp.

OS

OS Synthetic.

XX

XX Key Location/Qualifiers

FH

FT Misc-difference 1 /note= "encoded by AT, apparent frameshift"

FT

FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"

FT

FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"

FT

FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"

FT

XX US6393332-B1.

PN

XX 04-JUN-2002.

PD

XX 01-SEP-1998; 98US-00144776.

PF

XX 25-JUN-1997; 97US-00882431.

PR

XX (USSA) US SEC OF ARMY.

XX

XX Ulrich RG, Olson MA, Bavari S;

XX WPI; 2002-546281/58.

DR

XX N-PSDB; ABN84223.

DR

XX Novel isolated and purified superantigen toxin DNA fragment which has

XX been genetically altered, useful for producing vaccine for treatment of

XX superantigen toxin-associated bacterial diseases.

XX

XX Claim 5; Col 37-39; 46pp; English.

CC

CC The present sequence is the protein sequence of staphylococcal

CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine

CC comprises 3 amino acid substitutions introduced into the SEA sequence:

CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to

CC major histocompatibility complex (MHC) Class II and/or T cell receptors.

CC The protein is expressed as a nonsecreted product within host Escherichia

CC coli cells. The vaccine is used to protect against superantigen toxin

CC infections. Superantigen attributes are absent, but the superantigen is

CC effectively recognised by the immune system and an appropriate antibody

CC response is produced. In examples from the invention, attenuated

CC superantigen toxins were shown to protect animals against challenge with

CC wild-type toxin. Methods of producing and using the altered superantigen
CC toxins as vaccines, and in diagnosis and therapy, are provided. A
CC multivalent vaccine consisting of altered superantigen toxins from SEA,
CC SEB, SEC-1, TSST-1 and streptococcal SpA is predicted to provide
CC protective immunity against the majority of bacterial superantigen toxins
XX
XX Sequence 233 AA;
SQ
Query Match 75.6%; Score 921; DB 5; Length 233;
Best Local Similarity 75.0%; Pred. No. 9.2e-85;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLNTLLPKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDPFRQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYCAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRPDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVPDGVQR 181
QY 182 GLIVFHSSEGSTVSDYDLFDAQOQYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHMDIYLYTS 233
RESULT 31
ABU10082
ID ABU10082 standard; protein; 233 AA.
XX
AC ABU10082;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcal enterotoxin A #2.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by AT"
FT
XX
PN US2003009015-A1.
XX
PD 09-JAN-2003.
XX
PF 25-JUN-1997; 97US-00882431.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2003-401542/38.
DR N-PSDE; ACA61178.
XX
FT New superantigen toxin and/or DNA fragment with an altered binding of the
FT encoded altered toxin to either MHC class II or T cell antigen receptor,
FT useful for treating or ameliorating superantigen-associated bacterial
FT infection.
XX
PS Claim 11; Page 20-21; 50pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin

CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC A #2
XX
XX Sequence 233 AA;
SQ
Query Match 75.6%; Score 921; DB 6; Length 233;
Best Local Similarity 75.0%; Pred. No. 9.2e-85;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLNTLLPKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDPFRQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYCAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRPDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVPDGVQR 181
QY 182 GLIVFHSSEGSTVSDYDLFDAQOQYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHMDIYLYTS 233
RESULT 32
ABU62325
ID ABU62325 standard; protein; 233 AA.
XX
AC ABU62325;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus cytoplasmic enterotoxin A mutant #1.
XX
KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1.2 /note= "Encoded by ATGAG"
FT
FT Misc-difference 42 /note= "Wild-type Leu substituted by Glu"
FT
FT Misc-difference 48 /note= "Wild-type Leu substituted by Arg"
FT
FT Misc-difference 70 /note= "Wild-type Asp substituted by Arg"
FT
FT Misc-difference 89 /note= "Wild-type Tyr substituted by Gly"
FT
FT Misc-difference 92 /note= "Wild-type Tyr substituted by Ala"
FT
XX
PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
PF 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.

XX (ULRI/) ULRICH R G.

XX PI

XX Ulrich RG;

XX WPI: 2003-492125/46.

XX N-PSDB; AC28895.

XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.

XX Disclosure; Page 24-25; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
CC SEA

XX Sequence 233 AA;

Query Match 75.6%; Score 921; DB 7; Length 233;

Best Local Similarity 75.0%; Pred. No. 9.2e-85;

Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSDADQLNTLLFKGFFTGH 61

DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSHDQFRQHTILFKGFFTDH 61

QY 62 PWYNDLLVLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

DB 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181

DB 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181

QY 182 GLIVFHSSEGSTSVSYDLFDAQGQYPTLLRIYRDNTTISSTLSLSLYLYTT 233

DB 182 GLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNTKNTINSENHIDIVLYTS 233

RESULT 33

AAE37677

ID AAE37677 standard; protein; 233 AA.

XX AAE37677;

XX 06-OCT-2003 (first entry)

XX Protein #2 related to the invention.

XX Superantigen toxin; vaccine; infection; gene therapy.

XX Unidentified.

XX Key

XX Location/Qualifiers

FT Misc-difference 1 /note= "Encoded by AT"

XX WO2003056015-A1.

XX 10-JUL-2003.

XX 26-NOV-2001; 2001WO-US046540.

XX 26-NOV-2001; 2001US-00002784.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX Ulrich RG;

XX WPI: 2003-492125/46.

XX N-PSDB; AAD56765.

XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.

XX Disclosure; Page 110-112; 141pp; English.

XX The invention provides a superantigen toxin DNA fragment which has been
CC genetically altered such that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is disrupted or
CC altered. DNA fragments of the invention are useful in the production of
CC vaccines against bacterial superantigen toxin infections. They are also
CC useful in gene therapy. The present sequence is a protein related to the
CC invention

XX Sequence 233 AA;

Query Match 75.6%; Score 921; DB 7; Length 233;

Best Local Similarity 75.0%; Pred. No. 9.2e-85;

Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSDADQLNTLLFKGFFTGH 61

DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSHDQFRQHTILFKGFFTDH 61

QY 62 PWYNDLLVLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

DB 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181

DB 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181

QY 182 GLIVFHSSEGSTSVSYDLFDAQGQYPTLLRIYRDNTTISSTLSLSLYLYTT 233

DB 182 GLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNTKNTINSENHIDIVLYTS 233

RESULT 34

ABU10099

ID ABU10099 standard; protein; 233 AA.

XX ABU10099;

XX 11-AUG-2003 (first entry)

XX Staphylococcus enterotoxin A K14E substitution mutant.

XX Enterotoxin A; superantigen-associated bacterial infection; mutant;

XX superantigen toxin; vaccine; munein.

XX Staphylococcus sp.

XX Synthetic.

XX Key

XX Location/Qualifiers

XX Misc-difference 14 /note= "Wild-type Lys substituted by Glu"

XX PN US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX PA (ULRI/) ULRICH R G.
 XX PA (OLSO/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 7; Page; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analyzing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the staphylococcus
 CC enterotoxin A K14E mutant. Note: The present sequence is not present in
 CC the specification but was created by the indexer from the wild-type
 CC staphylococcus enterotoxin A sequence (see ACA61178)
 XX SQ Sequence 233 AA;
 Query Match 75.3%; Score 917; DB 6; Length 233;
 Best Local Similarity 74.6%; Pred. No. 2.3e-84;
 Matches 173; Conservative 22; Mismatches 37; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAOPLNTLLFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHDQPRQHTILFKGFTDH 61
 QY 62 PWYNDLLVDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 QY 182 GLIVFHSSEGSTVSVDLPDAQGYDPDILLRIYRDNNTTSSLSLSLYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFQAQGYSNLLRIYRDNKNTINSENHMDIYLYTS 233
 RESULT 35
 ID ABU10098
 XX ABU10098 standard; protein; 233 AA.
 XX AC ABU10098;
 XX DT 11-AUG-2003 (first entry)
 XX DE Staphylococcus enterotoxin A Y64A substitution mutant.
 XX KW Enterotoxin A; superantigen-associated bacterial infection; mutant;

KW superantigen toxin; vaccine; mutein.
 XX OS Staphylococcus sp.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
 FT US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX PA (ULRI/) ULRICH R G.
 XX PA (OLSO/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 7; Page; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the staphylococcus
 CC enterotoxin A Y64A mutant. Note: The present sequence is not present in
 CC the specification but was created by the indexer from the wild-type
 CC staphylococcus enterotoxin A sequence (see ACA61178)
 XX SQ Sequence 233 AA;
 Query Match 74.9%; Score 912; DB 6; Length 233;
 Best Local Similarity 74.6%; Pred. No. 7.5e-84;
 Matches 173; Conservative 21; Mismatches 38; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAOPLNTLLFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHDQPRQHTILFKGFTDH 61
 QY 62 PWYNDLLVDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 QY 182 GLIVFHSSEGSTVSVDLPDAQGYDPDILLRIYRDNNTTSSLSLSLYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFQAQGYSNLLRIYRDNKNTINSENHMDIYLYTS 233
 RESULT 36
 ID AAY70102
 ID AAY70102 standard; protein; 257 AA.

XX AAY70102;
 AC Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 XX antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 XX antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
 XX treatment; superantigen-associated bacterial infection.
 XX Staphylococcus sp.
 XX Key Location/Qualifiers
 XX Peptide 2..25
 XX /label= Leader peptide
 XX Protein 26..253
 XX /label= Mature Staphylococcal enterotoxin A
 XX /note= "Includes transcription start site residue, Met-"
 XX Misc-difference 42
 XX /note= "Encoded by TTG"
 XX Misc-difference 125
 XX /note= "Encoded by CCA"
 XX WO200009154-A1.
 XX -24-FEB-2000.
 XX 13-AUG-1998; 98WO-US016766.
 XX 13-AUG-1998; 98WO-US016766.
 XX (REED-) REED ARMY INST RES WALTER.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2000-224177/19.
 XX N-PSDB; AAZ51105.
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 XX diagnosis of superantigen-associated bacterial infections.
 XX Claim 7; Page 72-73; 118pp; English.
 XX The present amino acid sequence is the Staphylococcal enterotoxin A
 XX (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
 XX toxin when altered by site directed mutagenesis, results in disruption of
 XX binding of the toxin to both the MHC class II or T-cell antigen receptor.
 XX SEA has antibacterial and cytostatic activity. This sequence is useful
 XX for the production of SEA vaccines and specific antibodies. This vaccine
 XX overcomes the disadvantages of the chemically inactivated toxins and is
 XX designed to protect individuals against one or several related
 XX staphylococcal and streptococcal toxins. It is used for the diagnosis and
 XX treatment or amelioration of superantigen-associated bacterial
 XX infections
 XX Sequence 257 AA;
 Query Match 74.5%; Score 908; DB 3; Length 257;
 Best Local Similarity 74.2%; Pred. No. 2.2e-83;
 Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSEKLGCTALGNLQIYYNKSALTSEKSAQOFLNTLLKGFPTG 60
 DB 25 SEKSEINEKDLRKSEKLGCTALGNLQIYYNKSALTSEKSHQOFRGHTILFKGFTD 84
 QY 61 HPWYNLLVDLGSTAATSEYSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNRILT 120
 DB 85 HSWYNLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNRILT 144
 QY 121 EEKKVPINLWLDGKQNTVPLETVTKTKQNVTVQELDLQARRYLQEKYNYNSDVFQKQV 180

DB 145 EEKKVPINLWLDGKQNTVPLETVTKTKQNVTVQELDLQARRYLQEKYNYNSDVFQKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFPAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFPAQGYNTLLRIYRDNTKNTINSENWHIDVLYTS 257
 RESULT 37
 AAY70103
 ID AAY70103 standard; protein; 233 AA.
 XX AAY70103;
 AC AAY70103;
 XX 05-JUN-2000 (first entry)
 XX Mutant Staphylococcal enterotoxin A for vaccine A489270P.
 XX Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 XX antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 XX antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
 XX treatment; superantigen-associated bacterial infection; A489270P.
 XX Staphylococcus sp.
 XX Key Location/Qualifiers
 XX Protein 1..233
 XX /label= Mature Staphylococcal enterotoxin_A
 XX /note= "Mutant sequence without the leader peptide"
 XX Misc-difference 2
 XX /note= "Encoded by AG"
 XX Misc-difference 18
 XX /note= "Encoded by TTG"
 XX Misc-difference 48
 XX /note= "Wild type Leu substituted with Arg"
 XX Misc-difference 70
 XX /note= "Wild type Asp substituted with Arg"
 XX Misc-difference 92
 XX /note= "Wild type Tyr substituted with Ala"
 XX Misc-difference 157
 XX /note= "Encoded by CTT"
 XX Misc-difference 180
 XX /note= "Encoded by CAG"
 XX WO200009154-A1.
 XX 24-FEB-2000.
 XX 13-AUG-1998; 98WO-US016766.
 XX 13-AUG-1998; 98WO-US016766.
 XX (REED-) REED ARMY INST RES WALTER.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2000-224177/19.
 XX N-PSDB; AAZ51106.
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 XX diagnosis of superantigen-associated bacterial infections.
 XX Claim 8; Page 74-76; 118pp; English.

The present amino acid sequence is the mutant Staphylococcal enterotoxin
 A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
 of SEA vaccine A489270P. The coding region of this SAG toxin is altered
 by site directed mutagenesis, that results in disruption of binding of
 the toxin to both the MHC class II or T-cell antigen receptor. This
 altered SAG toxin has the leader peptide cleaved by native bacterial
 enzymatic mechanism and the first residue of the mature protein is
 encoded by the transcriptional start site (ATG). SEA has antibacterial
 and cytostatic activity. This sequence is useful for the production of
 SEA vaccines and specific antibodies. This vaccine overcomes the

disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections

Query Match 74.1%; Score 903; DB 3; Length 233;
Best Local Similarity 73.7%; Pred. No. 6.1e-83;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

2 EKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFLTNLLFKGPTCH 61
2 EKSEINEKDLRKSEKOGTALGNLKOIYYNEKAKTENKESHQOFOHLLFKGPTDH 61
62 PWNDDLVLGSLTAATSEYEGSSVDLYGAYYGQAGTGNKTKACMYGGVTLHDNNELTE 121
62 SWYNDLLVRPDSKDINDYKGGKVDLYGAYYGQAGTGNKTKACMYGGVTLHDNNELTE 121
122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFLGYNDSFGGKQVR 181
122 EKKVPINLWIDGKONTVPLETKNKXNTVQELDKQARYLQBYNLYNSDVFDDGKVAR 181
182 GLIVFHSSEGTSTVSDYLDFAQOQYPTLLRIYRNTTISSTLSISLYLYTT 233
182 GLIVFHSSTEPSVNYDLFAGAGQYNTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 38
ABU79071
ID ABU79071 standard; protein; 258 AA.
AC ABU79071;
XX
XX
DT 18-JUN-2003 (first entry)
DE
DE S. aureus SED (staphylococcus enterotoxin D) protein.
XX
XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
XX Staphylococcus aureus.
OS
XX
XX US2002177551-A1.
PN
XX
XX 28-NOV-2002.
PD
XX
XX 30-MAY-2001; 2001US-00870759.
XX
XX 31-MAY-2000; 2000US-0208129P.
XX
XX (TERM/) TERMAN D S.
FA
XX
XX Terman DS;
PI
XX
XX WPI; 2003-361759/34.
DR
XX
XX N-PSDB; ACA64697.
XX
XX
XX A mammalian cell receptor, useful in the treatment of cancer by binding
PI to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
PT
XX
XX Disclosure; Page; 167pp; English.
PS
XX
XX The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal

(by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated lipids to a tumour associated antigen population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal) by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?docid=20020177551"

XX
XX
XX Sequence 258 AA;
Query Match 50.2%; Score 611; DB 6; Length 258;
Best Local Similarity 51.1%; Pred. No. 2.9e-53;
Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFLTNLLFKGPTG 60
26 NENIDSVKEKELHKKSELSTALNNKHSYADKNPIIGENKSTGQFLENTLLYKKFFTD 85
61 HPWYNDLLVDLSTATSEYEGSSVDLYGAYYGQAGTGNKTKACMYGGVTLHDNNRLT 120
86 LINFEDLLINFNSEKEMAQHFKSKNDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
121 BEKKVPINLWIDGKOTTPIDKVKTSKEVTVOELDLQARHYLHGKFLGYNDSFGGKQV 180
146 ERKKVPINLWINGVQKESVLDKVKQTDKNVTQVELDAQARYLQDXDLKLYNNDTLOGK 205
181 RGLIVFHSSEGTSTVSDYLDFAQOQYPTLLRIYRNTTISSTLSISLYLY 231
206 RGKIEFDSDDSGSKVSDYLDVKGDFPEKQLRIYSNDKNTLSTLHLDIYLY 256

RESULT 39
AAR45013
ID AAR45013 standard; protein; 228 AA.
XX
XX AAR45013;
XX
XX 25-MAR-2003 (revised)
DT

DT 08-JUN-1994 (first entry)
 XX Staphylococcal enterotoxin SED.
 DE Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 XX autoimmune disease; toxicity; Protein A; perfusion system.
 KW Staphylococcus aureus.
 XX WO9324136-A1.
 XX 09-DEC-1993.
 PD 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 XX (TERM/) Terman D S.
 PA (STON/) STONE J L.
 XX Terman DS, Stone JL;
 XX WPI; 1993-405418/50.
 XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX Disclosure; Fig 1; 90pp; English.
 PS The sequences given in ARA45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 228 AA;
 SQ

Query Match 49.7%; Score 605; DB 2; Length 228;
 Best Local Similarity 52.0%; Pred. No. 9.9e-53;
 Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;
 QY 7 INEKDLRKSELOGTALGNLKOIYYNNSKAITSSSEKSDQFLNTLLPKGFTGHPWYND 66
 Db 2 VKEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGQDFLENTLLYKKFFTDLINFED 61
 QY 67 LLVLDGSTAATSEYEGSSVDLYGAYYGYOCAGTTPNKTACMYGVTLHDNNRLTEKKVP 126
 Db 62 LLINFNSEKMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNVTVQELDAQARYLQKDLKLYNNDTLGGKIQRKIEF 181
 QY 187 HSEGSTSVSYDLFDAQGYQYPTLLRIYRDNNTTSSLSLSLYLY 231
 Db 182 DSSDGSKVSVDLFDVKDGFPEKQLRIYSNKLSTLSTLHLDIYLY 226

RESULT 40
 AAB67340
 ID AAB67340 standard; peptide; 228 AA.
 XX AAB67340;
 AC AAB67340;
 XX 23-APR-2001 (first entry)
 DT Staphylococcus aureus enterotoxin D protein.
 DE Tumour; cancer; immune; enterotoxin.
 KW Staphylococcus aureus.
 XX

XX US6180097-B1.
 PN 30-JAN-2001.
 PD 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-USC00342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) Terman D S.
 PA Terman DS;
 PI WPI; 2001-158657/16.
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 PS The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 228 AA;
 SQ

Query Match 49.7%; Score 605; DB 4; Length 228;
 Best Local Similarity 52.0%; Pred. No. 9.9e-53;
 Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;
 QY 7 INEKDLRKSELOGTALGNLKOIYYNNSKAITSSSEKSDQFLNTLLPKGFTGHPWYND 66
 Db 2 VKEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGQDFLENTLLYKKFFTDLINFED 61
 QY 67 LLVLDGSTAATSEYEGSSVDLYGAYYGYOCAGTTPNKTACMYGVTLHDNNRLTEKKVP 126
 Db 62 LLINFNSEKMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNVTVQELDAQARYLQKDLKLYNNDTLGGKIQRKIEF 181
 QY 187 HSEGSTSVSYDLFDAQGYQYPTLLRIYRDNNTTSSLSLSLYLY 231
 Db 182 DSSDGSKVSVDLFDVKDGFPEKQLRIYSNKLSTLSTLHLDIYLY 226

RESULT 41
 ABB76236
 ID ABB76236 standard; protein; 228 AA.
 XX ABB76236;
 AC ABB76236;
 XX 09-AUG-2002 (first entry)
 DT Staphylococcus aureus enterotoxin D.
 DE Enterotoxin D; SED; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 KW Staphylococcus aureus.
 XX

P	N		US2002051765-A1.
X	D		
P	D		
X	F		02-MAY-2002.
P	F		
X	F		19-DEC-2000; 2000US-00741503.
P	F		
X	P		03-OCT-1989; 83US-00416530.
P	R		17-JAN-1990; 90US-00466377.
P	R		17-JAN-1991; 91WO-US000342.
P	R		01-JUN-1992; 92US-00891718.
P	R		02-MAR-1993; 93US-00025144.
P	R		31-JAN-1994; 94US-00189424.
P	R		19-JUN-1995; 95US-00491746.
X	X		(TERM/) Terman D S.
P	A		
X	X		Terman DS;
P	I		
X	X		WPI; 2002-415198/44.
P	R		
X	X		Reagent for treating cancer without the need for e.g. radiotherapy; PT Comprises a specific V beta subset of T cells sensitized to a growing P tumor and stimulated with superantigens. T XX Disclosure; Fig 2; 17pp; English.
P	S		The present sequence is the protein sequence of enterotoxin D (SED) of CC Staphylococcus aureus. Similarity is shown, in several stretches of CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the CC present invention, synthetic polypeptides useful in tumour therapy and in CC blocking or destroying autoreactive T and B lymphocyte populations are CC characterised by substantial structural homology to staphylococcal CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic CC exotoxins, with statistically significant sequence homology and CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo CC analysis exceeding 6) to include alignment of cysteine residues and CC similar hydropathy profiles. These superantigens are used to treat solid CC tumours, including their metastases, without radiation, surgery or CC standard chemotherapeutic agents. A claimed method of human cancer CC treatment involves contacting haematopoietic cells from a patient with CC one or more superantigens ex vivo to generate stimulated cells, selecting CC a specific v beta subset of cells, and reintroducing these cells into the CC patient to induce an in vivo therapeutic, tumoricidal reaction X SQ Sequence 228 AA;
P	Q		Query Match 49.7%; Score 605; DB 5; Length 228;
B	E		Best Local Similarity 52.0%; Pred.No. 9.9e-53;
M	A		Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;
Q	Y		7 INEXDLRKSELOQTALGNLKLQIYYNSKAITSEKSADQLNTLLFKGFTTGHPWIND 66
D	b		2 VKRELHKHKSLSSTALNNMKHSYADKNPIIGENKSTGTQFLNTLLYKKFTDLINPED 61
Q	Y		67 LLYVDLGSTAATSEVEGSSVDLYGNYGYCQAGGTPNKTACMTGGVTLHDNRLTEEKVP 126
D	b		62 LLINFNSKEMAQHFKSKNVDPVIPIRYSYNGCYGEIDRTACTYGGVTPEHGKLNKERKIP 121
Q	Y		127 INLMWDGQTTVPDIDVKTKSKEVTVOELDLQARHYLHGKFGLYNSDSFGGVKGVRGLTVF 186
D	b		122 INLMINGVQKEVSLDKVTQDKKNVTQVELDAQARRYLOKDLKYNDNLILGSKI QEGKIEF 181
Q	Y		187 HSGEGSVTSVYDLFPDAQGYEDTLRIYRDNTTISSTLSISLYL 231
D	b		182 DSSDGSKVSYDLFPVGDFEKKQLRIYSNDKNLTSLTEHLHIDIYLY 226
RESULT	42		
ID	AAR:13205		
XX	AA		AAR:13205 standard; protein; 228 AA.
XX	AC		AAR:13205;

XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX Burnham MKR, Hodgson JE;
 XX WPI: 1997-435166/40.
 XX N-PSDB; AA01865.
 XX New Staphylococcus aureus polynucleotide and polypeptide(s) - for
 PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
 XX Claim 11; Page 33; 117pp; English.
 XX The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40711. The polypeptide, and polynucleotide encoding
 CC it, are derived from Staphylococcus aureus. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds that
 CC bind and inhibit the activity of the polypeptide. Such compounds can be
 CC used as anti-bacterial compounds. The polypeptide may also be used as an
 CC immunogen to vaccinate an animal for protection against Staphylococcus
 CC aureus caused disease
 XX Sequence 91 AA;
 SQ Query Match 30.4%; Score 370; DB 2; Length 91;
 Best Local Similarity 76.9%; Pred. No. 1.8e-29;
 Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 107 MYGGVTLHDNNRLTEKKVPIINLWIDGKOTTVPIDKVTSKEVTVQELDLQARHYLHGK 166
 DB 1 MYGGVTLHDNNRLTEKKVPIINLWIDGKXNTVPLETVTKNKNVTQVELDLQARRYLOEK 60
 QY 167 FGLYNSDSFGCKVQKRGVLIVFHSSEGSTVSVD 197
 DB 61 YNLNSDVFQKVGKRGVLIVFHSSTEPSVNYD 91
 RESULT 48
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 AC ABU10089;
 XX 11-AUG-2003 (first entry)
 DT Bacterial superantigen toxin SEA.
 DE Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 KW SEA.
 OS Unidentified.
 XX US2003009015-A1.
 PN 09-JAN-2003.
 PD 25-JUN-1997; 97US-00882431.
 PF 25-JUN-1997; 97US-00882431.
 PR (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2003-401542/38.
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX

PS Example 1; Page 35; 50pp; English.
 XX The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEA
 XX Sequence 82 AA;
 SQ Query Match 29.7%; Score 362; DB 6; Length 82;
 Best Local Similarity 79.3%; Pred. No. 9.9e-29;
 Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 43 SAQOFLNTLLFKGFFTGHEWYNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGGTPN 102
 DB 1 SHQOFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 49
 ABU62336
 ID ABU62336 standard; protein; 82 AA.
 AC ABU62336;
 XX 27-AUG-2003 (first entry)
 DT S. aureus enterotoxin A, SEA, MHC binding region.
 DE SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 XX Staphylococcus aureus.
 OS US2003036644-A1.
 PN 20-FEB-2003.
 PD 26-NOV-2001; 2001US-00002784.
 PF 25-JUN-1997; 97US-00882431.
 PR 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRICH R G.
 PA Ulrich RG;
 XX WPI; 2003-492125/46.
 DR New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX Disclosure; Fig 3; 68pp; English.
 XX The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSS1-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic responses resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antisera isolated from individuals immunised with one or more altered
CC TSS-1 superantigen toxin and an antibody which recognises altered TSS-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the *S. aureus* enterotoxin A, SEA, MHC binding region
XX
XX

SQ Sequence 82 AA;

Query Match 29.7%; Score 362; DB 7; Length 82;
Best Local Similarity 79.3%; Pred. No. 9.9e-29;
Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 43 SADQFLNTLFGKFFTHGHPYNDLLVLDLSTAASTSEYEGSSVDLYGAYGYOCAGGTPN 102

Db 1 SHDQFLQHTLFGKFFTHGHPYNDLLVLDLSTAASTSEYEGSSVDLYGAYGYOCAGGTPN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 50

ABP58460

ID ABP58460 standard; protein; 217 AA.

XX AC

XX ABP58460;

XX DT

14-APR-2003 (first entry)

XX DE

Staphylococcal enterotoxin H.

XX KW

Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;

XX KW

cytostatic; vaccine.

XX OS

Staphylococcus sp.

XX DN

WO2003002143-A1.

XX PD

09-JAN-2003.

XX PF

19-JUN-2002; 2002WO-SE001188.

XX PR

28-JUN-2001; 2001SE-00002327.

XX PA

(ACTI-) ACTIVE BIOTECH AB.

XX PI

Forsberg G, Erlandsson E, Antonsson P, Walse B;

XX DR

WPI; 2003-201467/19.

XX PT

Conjugate for therapy, has bacterial superantigen with a region in T-cell

XX PT

receptor and four regions to determine binding to class II major

XX PT

histocompatibility complex, antibody to cancer associated cell surface

XX PS

Example 3; Fig 3; 102pp; English.

XX CC

The present sequence is the protein sequence of staphylococcal

XX CC

enterotoxin D (SED). The invention provides novel conjugates (see

XX CC

ABP58454) for human cancer therapy. These comprise an engineered

XX CC

bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an

XX CC

antibody moiety, such as tumour reactive antibody 574. Bacterial

XX CC

enterotoxins such as SEA, SED, and SEH were used in the molecular

XX CC

modelling of the engineered superantigens. The superantigens were

XX CC

engineered to reduce seroreactivity whilst maintaining biological

XX CC

activity and production levels. The novel conjugates were designed to

CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 217 AA;

Query Match 25.3%; Score 308; DB 6; Length 217;

Best Local Similarity 33.9%; Pred. No. 1.2e-22;

Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

QY 10 KDLRKSELOQTALGNLKOIYYNSKAITSSKSDAQFLNTLLFKGFTGHPWYNDLLV 69

Db 1 EDLHKSEITDLALAN--AYQYNHFFIKENTKSDSEISGEKDLIFRN--QDSG-NDLRV 55

QY 70 DLGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129

Db 56 KATADLAOKFNKQVDIYGASFYKCEKISENISECLYGGTLL-NSEKLAERIVGANV 114

QY 130 WIDGKQTTVPIDKVKTSKEVTQBELDQARHVLHGKFLYNSDSFGGKQVQRLIVFHSS 189

Db 115 WVDGQKETEL--IRTNKKNVTQLBDIKIRKILSDKVKIYYKDS---EISKGLIEFDWK 169

QY 190 EGSTVSYDLFDAQQQYPTDLLRIYRDNNTTISTSLIS-LSLYLYT 232

Db 170 TPRDYSFDIYDLKGENDYBIDKIYEDNKTLSKDDISHIDVNLTY 213

RESULT 51

ABP29357

ID ABP29357 standard; protein; 259 AA.

XX AC

ABP29357;

XX DT

02-JUL-2002 (first entry)

XX DE

Streptococcus polypeptide SEQ ID NO 7890.

XX KW

Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;

XX KW

group A streptococcus; Streptococcus pyogenes; antibacterial;

XX KW

antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX OS

Streptococcus pyogenes.

XX PN

WO200234771-A2.

XX PD

02-MAY-2002.

XX PF

29-OCT-2001; 2001WO-GB004789.

XX PR

27-OCT-2000; 2000GB-00026333.

XX PR

24-NOV-2000; 2000GB-00028727.

XX PR

07-MAR-2001; 2001GB-00005640.

XX PA

(CHIR-) CHIRON SPA.

XX PI

(GENO-) INST GENOMIC RES.

XX PI

Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;

XX PT

Tettelin H;

XX DR

WPI; 2002-352536/38.

XX DR

N-PSDB; ABN69988.

XX PT

New Streptococcus protein for the treatment or prevention of infection or

XX PT

disease caused by Streptococcus bacteria, such as meningitis, and for

XX PT

detecting a compound that binds to the protein.

XX CC

Claim 1; Page 3920; 4525pp; English.

XX CC

The invention relates to a protein (ABP25413-ABP30895) from group B

XX CC

streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

XX CC

(Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in

XX CC

the specification. The proteins have antibacterial and antiinflammatory

XX CC

activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and

XX CC

antibodies that bind (I) are used in the manufacture of medicaments for

the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus (I) may be prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX
 SQ Sequence 259 AA;

Query Match 23.9%; Score 291.5; DB 5; Length 259;
 Best Local Similarity 31.3%; Pred. No. 7.3e-21;
 Matches 72; Conservative 42; Mismatches 91; Indels 25; Gaps 8;

QY 17 ELQGTALGNLQY-YNSKAITSEKSDQFLTLTLFKGFTGHPWYN---DLLVDLG 72
 DB 34 EMSVGVIINRLSYDTEVKGKINEGPPF-SGLFYKNI---PYGNSIEIKVLEIN 88
 QY 73 STAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMGVTLHDNNRLTEEEKVPIINLWID 132
 DB 89 SVEKANFFSGKRVDFTEVSPPCNSNIKNS---YGGITLSDGNRI-DKKNIPVNIID 144
 QY 133 G---KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKVKQ 180
 DB 145 GVQKYSYTDISTGSDKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKVKQ 204
 QY 181 RGLIVFHSSGSSVSDLYGAYGYQCAGGTENKTCACMGVTLHDNNRLTEEEKVPIINLWID 230
 DB 205 EGNIIHLNSGERISYLNFDTGHDRESMLKYSNDKNTAYSQDLHIDIVL 254

RESULT 52
 AAY06254
 ID AAY06254 standard; protein; 239 AA.
 XX
 AC AAY06254;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC3-FRI909.
 XX
 KW Enterotoxin; SEC3-FRI909; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI909. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production.

CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX
 SQ Sequence 239 AA;

Query Match 23.6%; Score 287.5; DB 2; Length 239;
 Best Local Similarity 33.3%; Pred. No. 1.7e-20;
 Matches 78; Conservative 45; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSELOQTALGNLQYIYNSKAITSE-KSQDQFLTNLTLFKGFTGHPWYNDLLV 69
 DB 10 DLKHSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNINDKLNNDKVKVT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTGNKTCACMGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANIKDEVDVYGSNYVNCYFSSKDNVGVTSKTCMGYGGITKHEGHDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNLVLRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSGSSVSDLYGAYGYQCAGGTENKTCACMGVTLHDNNRLTEEEKVPIINLWID 232
 DB 183 TGYIKFIESNGNTFWYDMFPAPGDKFDQSKYLMYKDNKVKDSKVIEVHLTT 236

RESULT 53
 AAY06253
 ID AAY06253 standard; protein; 239 AA.
 XX
 AC AAY06253;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC3-FRI913.
 XX
 KW Enterotoxin; SEC3-FRI913; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.

This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 -FRI913. The invention relates to pyrogenic toxins, such as
 staphylococcal enterotoxins, modified in the disulfide loop region.
 Typically, the modification involves deletions within the disulfide loop
 region of SEC (see AAY06261). The modified toxins retain useful
 biological properties, such as the ability to induce cytokine production.

CC but have substantially reduced toxicity compared to the corresponding
CC unmodified native toxin. Emetic response inducing activity and fever
CC inducing activity are typically decreased by at least about 100-fold,
CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
CC native toxin
XX
SQ Sequence 239 AA;

Query Match 23.6%; Score 287.5; DB 2; Length 239;
Best Local Similarity 32.5%; Pred. No. 1.7e-20;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;
QY 11 DLKKESELOQTALGNLKIYYNSKAITSS-KSADQFLTNTLLFKGFTGHPWYNDLLV 69
Db 10 DLKSSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLIYNSDKLKNYDKVKT 66
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKACMYGGVTLHDNNRLTEE 122
Db 67 ELLNEDLAKYKDEVDVYGSNYVYCYFSSKDNVGVTKGTCMYGGITKHEGNHFDNG 126
QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYD--TLRLIYRDNTTISSTLSISLYLT 232
Db 183 TGYIKFIENNGNTFYDMMWPAFGDKFDQSKYLMYNDNKTVDTSKSVKIEVHLTT 236

RESULT 54
ABG71369
ID ABG71369 standard; protein; 240 AA.
XX
AC ABG71369;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin SEC3-FRI913.
XX
KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC3-FRI913.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 240 /label= unknown
FT
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011619.
XX
PR 13-APR-2001; 2001US-0283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX

New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
PT immune function and as a vaccine against toxic shock syndrome or food
PT poisoning.
XX
PS Disclosure; Fig 15; 67pp; English.
XX
CC The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin

CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic response-
CC inducing activity decreased by about 100-fold in comparison to a native
CC toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents the staphylococcal enterotoxin,
CC SEC3-FRI913
XX
SQ Sequence 240 AA;

Query Match 23.6%; Score 287.5; DB 6; Length 240;
Best Local Similarity 32.5%; Pred. No. 1.7e-20;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;
QY 11 DLKKESELOQTALGNLKIYYNSKAITSS-KSADQFLTNTLLFKGFTGHPWYNDLLV 69
Db 10 DLKSSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLIYNSDKLKNYDKVKT 66
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKACMYGGVTLHDNNRLTEE 122
Db 67 ELLNEDLAKYKDEVDVYGSNYVYCYFSSKDNVGVTKGTCMYGGITKHEGNHFDNG 126
QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYD--TLRLIYRDNTTISSTLSISLYLT 232
Db 183 TGYIKFIENNGNTFYDMMWPAFGDKFDQSKYLMYNDNKTVDTSKSVKIEVHLTT 236

RESULT 55
ABG71370
ID ABG71370 standard; protein; 240 AA.
XX
AC ABG71370;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin SEC3-FRI909.
XX
KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC3-FRI909.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 240 /label= unknown
FT
XX
PN WO200283169-A1.
XX
PD 24-OCT-2002.
XX
PF 11-APR-2002; 2002WO-US011619.
XX
PR 13-APR-2001; 2001US-0283720P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX
DR WPI; 2003-058608/05.
XX
PT New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
PT immune function and as a vaccine against toxic shock syndrome or food
PT poisoning.
XX
PS Disclosure; Fig 15; 67pp; English.
XX

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FR1909
 XX
 SQ Sequence 240 AA;

Query Match 23.6%; Score 287.5; DB 6; Length 240;
 Best Local Similarity 33.3%; Pred. No. 1.7e-20;
 Matches 78; Conservative 45; Mismatches 92; Indels 19; Gaps 9;
 QY 11 DLKKESELOGTALGNLQIYYNYSKAITSE--KSADQFLNTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKKSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLDIYNINDKLNNDKVKVT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYYGQC-----AGGTENKTAACMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYDEVDVYGSNYVNCYPSSKDNVKGVTSGKTCMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKKLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQCPD--TLRIYRDNTTISSTLSISLYLT 232
 DB 183 TGVKIFIESNGNTFWYDMMPAPGDKFDQSKYLMYKDNKQKVSQVKIEVHLTT 236

RESULT 56
 AAY06256
 ID AAY06256 standard; protein; 239 AA.
 XX
 AC AAY06256;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC-4446.
 XX
 KW Enterotoxin; SEC-4446; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX

XX This protein represents the Staphylococcus aureus type C enterotoxin SEC-
 CC 4446. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the

CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06256). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while ID50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 23.2%; Score 282.5; DB 2; Length 239;
 Best Local Similarity 32.1%; Pred. No. 5.3e-20;
 Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;
 QY 11 DLKKESELOGTALGNLQIYYNYSKAITSE--KSADQFLNTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKKSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLDIYNINDKLNNDKVKVT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYYGQC-----AGGTENKTAACMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYDEVDVYGSNYVNCYPSSKDNVKGVTSGKTCMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKKLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQCPD--TLRIYRDNTTISSTLSISLYLT 232
 DB 183 TGVKIFIESNGNTFWYDMMPAPGDKFDQSKYLMYKDNKTVDSKRVKIEVHLTT 236

RESULT 57
 ABG71372
 ID ABG71372 standard; protein; 240 AA.
 XX
 AC ABG71372;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-4446.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-4446.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 XX /label= unknown
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 PS Disclosure; Fig 15; 67pp; English.

CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-4446

SQ Sequence 240 AA;
 Query Match 23.2%; Score 282.5; DB 6; Length 240;
 Best Local Similarity 32.1%; Pred. No. 5.4e-20;
 Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;
 QY 11 DLKSKSELGQALGNLQIYYNSKAITSSB-KSADQFLNTLFLKFGFTCHPWYNDLLV 69
 Db 10 DLKSSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNISDKRLKNYDKVKT 66
 QY 70 DLGSTAATSEYEGSVLDLYGAYGYQC-----AGGTPNKTAQMYGGVTLHNNRLTEE 122
 Db 67 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFLYNSDSFGKQVQ 180
 Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNTTISSTLSISLYLT 232
 Db 183 TGYIKFIENNNGTFCYDMWPAKPGDKFDQSKYLMYNDKNTVDSKRVKIEVHLT 236

RESULT 58
 AAY06255
 ID AAY06255 standard; protein; 239 AA.
 AC AAY06255;
 XX
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC-MNCopeland.
 XX
 KW Enterotoxin; SEC-MNCopeland; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins.
 PT
 PS Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C enterotoxin SEC-
 CC MNCopeland. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide loop

CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX
 SQ Sequence 239 AA;

Query Match 23.0%; Score 280.5; DB 2; Length 239;
 Best Local Similarity 31.3%; Pred. No. 8.5e-20;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;
 QY 2 EKSEINEKDLKSKSELGQALGNLQIYYNSKAITSSB-KSADQFLNTLFLKFGFTG 60
 Db 1 ESQDPTDELKHSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSVLDLYGAYGYQC-----AGGTPNKTAQMYGGVTL 113
 Db 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
 QY 114 HNNRLTER--KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFLY 171
 Db 118 HEGNHFDNGLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
 QY 172 SDSFGKQVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNTTISSTLSISLY 229
 Db 176 FNS--SPYETGYIKFIENNNGTFCYDMWPAKPGDKFDQSKYLMYNDKNTVDSKRVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 59
 ABG71371
 ID ABG71371 standard; protein; 240 AA.
 AC ABG71371;
 XX
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-MNCopeland.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-MNCopeland.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 FT /label= unknown
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX

CC New modified staphylococcal enterotoxin derived from a native disulfide
 CC loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 CC immune function and as a vaccine against toxic shock syndrome or food

PT poisoning.
 XX Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-MNCopeland
 XX
 SQ Sequence 240 AA;

Query Match 23.0%; Score 280.5; DB 6; Length 240;
 Best Local Similarity 31.3%; Pred. No. 8.6e-20;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSE-KSADQFLNTLLPKGFFTG 60
 DB 1 ESQDPPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHDLLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTAQWYGGVTL 113
 DB 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGKTCWYGITK 117
 QY 114 HDNRLTEE--KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
 DB 118 HEGHFDNGNLQNLVIRY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLLRIYRDNNTTISSTLSISLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFYQDMPPAGDKFDQSKYLMYNDNKTVDKRVKIEVH 233
 QY 230 LYT 232
 DB 234 LTT 236

RESULT 60
 AAY06252
 ID AAY06252 standard; protein; 239 AA.
 XX
 AC AAY06252;
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC2.
 XX
 KW Enterotoxin; SEC2; toxin; disulphide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN W09927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX

PT Non-toxic modified staphylococcal enterotoxins.
 XX Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin
 CC SEC2. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the
 CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06261). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 22.9%; Score 279.5; DB 2; Length 239;
 Best Local Similarity 31.3%; Pred. No. 1.1e-19;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSE-KSADQFLNTLLPKGFFTG 60
 DB 1 ESQDPPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHDLLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTAQWYGGVTL 113
 DB 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGKTCWYGITK 117
 QY 114 HDNRLTEE--KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
 DB 118 HEGHFDNGNLQNLVIRY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLLRIYRDNNTTISSTLSISLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFYQDMPPAGDKFDQSKYLMYNDNKTVDKRVKIEVH 233
 QY 230 LYT 232
 DB 234 LTT 236

RESULT 61
 ABG71368
 ID ABG71368 standard; protein; 240 AA.
 XX
 AC ABG71368;
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC2.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin; SEC2;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 XX /label= unknown
 XX
 PN W0200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PR 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX

XX WPI; 2003-058608/05.
XX
XX New modified staphylococcal enterotoxin derived from a native disulfide
XX loop-containing pyrogenic toxin, useful for non-specifically enhancing an
XX immune function and as a vaccine against toxic shock syndrome or food
XX poisoning.
XX
XX Disclosure; Fig 15; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
XX disulfide loop-containing pyrogenic toxin where the modified toxin
XX comprises a disulfide loop having no more than 10 amino acids. The
XX modified toxin has a fever-inducing activity or an ennetic response.
XX inducing activity decreased by about 100-fold in comparison to a native
XX toxin. The modified pyrogenic toxin, that is a staphylococcal
XX enterotoxin, is useful for non-specifically enhancing an immune function
XX and for vaccination against diseases such as toxic shock syndrome and
XX food poisoning. This sequence represents the staphylococcal enterotoxin,
XX SEC2
XX
XX Sequence 240 AA;

Query Match 22.9%; Score 279.5; DB 6; Length 240;
Best Local Similarity 31.3%; Pred. No. 1.1e-19;
Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNSKAITSE-KSADQFLTNTLLFKGFTG 60
Db 1 ESQDPTDEHLKSEFTGT-MGNWK--LYDDHVVSATKVMVDKFLAHLDIYNISDKK 57
QY 61 HPWYNDLAVDLSAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGVTL 113
Db 58 LKNYDKVKTLLNEDLAKKYDEVVDVYGSNYYNVCYFSSKDNVKGVTGGKTCMYGGITK 117
QY 114 HDNNRLTEE--KKYPINLWIDGKOTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFNDNGNLQNLIRYV-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
QY 172 SDSFGKQVQGLIVFHSSEGSTVSYDLFDAQGQYPD--TLIRIYRDNTTSSLSISLSY 229
Db 176 FNS--SPYETGVIKFIENNGNTFYDMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVH 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 62
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
XX AAR45016;
XX
XX 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
XX Staphylococcal enterotoxin SEC3.
XX
XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; protein A; perfusion system.
XX
XX Staphylococcus aureus.
OS
XX WO9324136-A1.
XX
XX 09-DEC-1993.
PD
XX 01-JUN-1993; 93WO-US005213.
PF
XX 01-JUN-1992; 92US-00891718.
PR
XX (TERM/) TERMAN D S.
PA

PA (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
PI
XX WPI; 1993-405418/50.
DR
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX in a patient or for the treatment of auto-immune diseases.
PT
XX
XX Disclosure; Fig 1; 90pp; English.
PS
XX
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs and homologues of them can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 238 AA;

Query Match 22.8%; Score 277.5; DB 2; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.7e-19;
Matches 76; Conservative 44; Mismatches 95; Indels 19; Gaps 9;
QY 11 DLKRSSELOGTALGNLQIYYNSKAITSE-KSADQFLTNTLLFKGFTGHPWYNDLIV 69
Db 9 ELKKSSEFTGT-MGNWK--LYDDHVVSATKVMVDKFLAHLDIYNISDKLKNYDKVKT 65
QY 70 DLGSAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGVTLHNNRLTEE 122
Db 66 ELLNEDLAKKYDEVVDVYGSNYYNVCYFSSKDNVKGVTGGKTCMYGGITKEGNHFDNG 125
QY 123 --KKYPINLWIDGKOTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 126 NLQNLIRYV-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYEFPNS--SPYE 181
QY 181 RLIVFHSSEGSTVSYDLFDAQGQYPD--TLIRIYRDNTTSSLSISLSIPLYT 232
Db 182 TGVKFIENNGNTFYDMLPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVHLT 235

RESULT 63
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
XX AAB67343;
XX
XX 23-APR-2001 (first entry)
DT
XX
XX Staphylococcus aureus enterotoxin C3 protein.
DE
XX
XX Tumour; cancer; immune; enterotoxin.
KW
XX
XX Staphylococcus aureus.
OS
XX
XX US6180097-B1.
PN
XX
XX 30-JAN-2001.
PD
XX
XX 30-OCT-1998; 98US-00183437.
PF
XX
XX 03-OCT-1989; 89US-00416530.
PR
XX 17-JAN-1990; 90US-00466577.
PR
XX 17-JAN-1991; 91WO-US000342.
PR
XX 01-JUN-1992; 92US-00891718.
PR
XX 02-MAR-1993; 93US-00025144.
PR
XX 31-JAN-1994; 94US-00189424.
PR
XX 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) TERMAN D S.
PA
XX
XX Terman DS;
PI

XX WPI; 2001-158657/16.
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 238 AA;
 SQ
 Query Match 22.6%; Score 275.5; DB 4; Length 238;
 Best Local Similarity 32.1%; Pred. No. 2.7e-19;
 Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;
 QY 11 DLKKSSELTGALGNLKOIYYNSKAITSE--KSADQELTNLLFKGFTGHPWYNDLLV 69
 DB 9 ELHKSSEFTGT-MGNMK--YLYDDHYVSATKWSVDKFLAHDLIYNSDKKLNVDKVK 65
 QY 70 DLGSTAATSEYGGSDVLYGAYGYQC-----AGTTPNKTCMYGGVTLHDNNRLTEE 122
 DB 66 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGKTCMYGGITKHEGHNFDNG 125
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 126 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEENS--SPYE 181
 QY 181 RGLIVFHSSEGTSTVSDLPDAQGVDP--TLRLRYDNTTISSTLSISLYYT 232
 DB 182 TGYIKFIENNGNTFWYDMPEAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
 RESULT 64
 ABB76239
 ID ABB76239 standard; protein; 238 AA.
 XX ABB76239;
 AC ABB76239;
 DT 09-AUG-2002 (first entry)
 XX Staphylococcus aureus enterotoxin C3.
 DE Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 XX Staphylococcus aureus.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc-difference 208
 FT /note= "given as 'O' in the specification"
 XX US2002051765-A1.
 XX 02-MAY-2002.
 XX 19-DEC-2000; 2000US-00741503.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX

PA (TERM/) Terman D S.
 XX Terman DS;
 PI WPI; 2002-415198/44.
 DR Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.
 XX The present sequence is the protein sequence of enterotoxin C3 (SEC3) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumoricidal reaction
 XX Sequence 238 AA;
 SQ
 Query Match 22.6%; Score 275.5; DB 5; Length 238;
 Best Local Similarity 32.1%; Pred. No. 2.7e-19;
 Matches 75; Conservative 44; Mismatches 96; Indels 19; Gaps 9;
 QY 11 DLKKSSELTGALGNLKOIYYNSKAITSE--KSADQELTNLLFKGFTGHPWYNDLLV 69
 DB 9 ELHKSSEFTGT-MGNMK--YLYDDHYVSATKWSVDKFLAHDLIYNSDKKLNVDKVK 65
 QY 70 DLGSTAATSEYGGSDVLYGAYGYQC-----AGTTPNKTCMYGGVTLHDNNRLTEE 122
 DB 66 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGKTCMYGGITKHEGHNFDNG 125
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 126 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEENS--SPYE 181
 QY 181 RGLIVFHSSEGTSTVSDLPDAQGVDP--TLRLRYDNTTISSTLSISLYYT 232
 DB 182 TGYIKFIENNGNTFWYDMPEAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
 RESULT 65
 AAG63856
 ID AAG63856 standard; protein; 228 AA.
 XX AAG63856;
 AC AAG63856;
 DT 29-OCT-2001 (first entry)
 XX Amino acid sequence of a modified Staphylococcal enterotoxin C1.
 DE Enterotoxin C1; SEC-SER; infectious disease; mastitis.
 KW Enterotoxin C1.
 OS Synthetic.
 OS Staphylococcus sp.
 XX WO200160851-A1.
 XX 23-AUG-2001.
 XX

Pf	31-OCT-2000; 2000WO-KR001241.
Xx	
Xx	17-FEB-2000; 2000KR-00007612.
Xx	
Pa	(GLDS) LG CHEM LTD.
Xx	
Pi	Lee H, Park Y, Han K, Chang B, Lee Y;
Xx	
Dn	WPI; 2001-522585/57.
Dn	N-PSDB; AAH74983.
Xx	
Pt	Producing stable modified Staphylococcal toxin polypeptide for treating infectious diseases, e.g. mastitis, in animals involves substituting cysteine at specified position of modified Staphylococcal toxin C1 with serine.
Xx	
Ps	Claim 1; Page 59-60; 64pp; English.
Xx	
Cc	The present sequence represents a modified Staphylococcal enterotoxin C1, designated SEC-SER. The modified toxin is characterised in that the 95th amino acid (cysteine) is substituted with serine. This results in a toxin that has improved stability. The modified enterotoxin is useful for preventing or treating infectious diseases due to microorganisms in CC animals such as cows, pigs, horses, sheep, hens, dogs and cats, e.g. mastitis in cows
Xx	
Sq	Sequence 228 AA;
	Query Match 22.5%; Score 273.5; DB 4; Length 228;
	Best Local Similarity 32.1%; Pred. No. 4.1e-19;
	Matches 76; Conservative 45; Mismatches 97; Indels 19; Gaps 9;
Qy	2 EKSEETNEKLRKSELQGTALGNLKOIY--YNSKAITSSSEKSADQFLTWLLFKGFFT 59
Db	2 ESQPDTPPELHKASFTG-LMENMKVLYDHRVS---ATKVSKVDKFLAHLINISDK 57
Qy	60 GHFWNDLLVLGSTAATSEYGSSVDLYGAYGYQCAGGTPNKTA CMYGGVTTLHDNRL 119
Db	58 KLKNYDKVKTELLINEGLAKKYDEVVDVGSNYVNCSGKT-----CMYGGITKHGHNF 112
Qy	120 TEE--KKVPINLMIDGKQTVPIDKTKSKEVTVOELDLQARHYLHGKFGLYNSDFGG 177
Db	113 DNGNLQNVLIRTV-ENKRNIIISFE-VQTDKKSVTAQELDIAKARNFLINKNLYEFNS--S 169
Qy	178 KVQRGLIVFHSSEGSTVSVDLFDAQGQYPD--TLLRIYRDNTTISSTLSISLYLT 232
Db	169 PYETGVIKTIENNNGTFWYDMMPAPGDKFDQSXYLMYNDNKTVDKSKVEVHLT 225
RESULT 66	
AAR13208	
ID	AAR13208 standard; protein; 238 AA.
XX	
AC	AAR13208;
XX	
DT	15-OCT-1991 (first entry)
XX	
DE	Staphylococcal enterotoxin C3.
XX	
Kw	SEC3; cancer treatment; pyrogen; tumouricide.
OS	Staphylococcus aureus.
XX	
FN	WO9110680-A.
XX	
PD	25-JUL-1991.
XX	
Pf	17-JAN-1990; 90US-00466577.
XX	
PR	17-JAN-1990; 90US-00466577.
XX	
PA	(TERM/) TERMAN D S.
XX	

Pf	Terman DS;
XX	
Dn	WPI; 1991-237984/32.
XX	
Pt	Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumoricidal activity as Staphylococcal protein A without potential toxic reactions.
XX	
Ps	Disclosure; Fig 1; 74pp; English.
XX	
Cc	SEC3 was isolated and purified from S.aureus. It can be used for treating cancer, activating cytokine mediators and procoagulant systems, augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be administered intravenously, optionally with ibuprofen to attenuate toxic reaction to SEC3. Synthetic polypeptides having structural homology to Staphylococcal enterotoxins are claimed, provided the homology includes statistically significant sequence homology, alignment of Cysteine residues and similar hydropathy profiles. See AAR13203-R13211
XX	
Sq	Sequence 238 AA;
	Query Match 22.4%; Score 272.5; DB 2; Length 238;
	Best Local Similarity 31.1%; Pred. No. 5.5e-19;
	Matches 76; Conservative 41; Mismatches 88; Indels 39; Gaps 8;
Qy	11 DLRKSELQGTALGNLKQIYYNSKAITSSSE-KSADQFLTNILLKGFFTGHFWNDLLV 69
Db	9 ELHKSSEFTGT-MGNMK--YLVDHYVSAIKWMSVDRFLAHLIYNISDKLNKYDKVKT 65
Qy	70 DLGSTAATSEYGSSVDLYGAYGYQC-----AGGTPNKTA CMYGGVTTLHDNN---- 117
Db	66 ELLNEDLAKKYDEVVDVGSNYVNCVFSSKDNVGKTVGGKTCMYGGITKHGSHGDNG 125
Qy	118 -----PLTEKKVPINLMIDGKQTVPIDKTKSKEVTVOELDLQARHYLHGKFGLY 170
Db	126 NLQNCLIRVENKRNITISF-----EVQTDKKSVTAQELDIAKARNFLINKNLY 173
Qy	171 NDSFEGGKVVQGLIVFHSSEGSTVSVDLFDAQGQYPD--TLLRIYRDNTTISSTLSISL 228
Db	174 EFNS--SPYETGIKFIENNNGTFWYDLMPAPGDKFDQSXYLMYNDNKTVDKSKVIEV 231
Qy	229 LYLT 232
Db	232 HLTT 235
RESULT 67	
AAR12153	
ID	AAR12153 standard; protein; 251 AA.
XX	
AC	AAR12153;
XX	
DT	04-NOV-1997 (first entry)
XX	
DE	Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
XX	
Kw	Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody;
Kw	streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
Kw	hypotension; group A streptococcal infection; myositis; fasciitis;
XX	liver damage; T cell; lymphoma; ovarian; uterine.
OS	Streptococcus pyogenes.
XX	Synthetic.
FH	Key Location/Qualifiers
Peptide	1..30 /label= sig_peptide
Peptide	31..251 /label= mat_peptide
Misc-difference 120	/note= "wild type Cys replaced by Ser"
XX	

PN WO9640930-A1.
 XX 19-DEC-1996.
 PD 07-JUN-1996; 96WO-US010252.
 XX 07-JUN-1995; 95US-00480261.
 PR (MINU) UNIV MINNESOTA.
 PA Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX WPI; 1997-099936/09.
 DR Mutant SPE-A toxin with at least one amino acid change is substantially
 PT non-lethal - used in vaccine composition for treatment of cancer and
 PT streptococcal toxic shock syndrome etc.
 XX Example 4; Page; 102pp; English.
 PS The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
 CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
 CC animals against wild type SPE-A and to treat cancer and streptococcal
 CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
 CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
 CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
 CC myositis, fascitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and uterine
 CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
 CC cell lymphoma cells. N.B. Sequence not given in the specification, but
 CC constructed using the wild type SPE-A sequence given on pages 77-79
 XX SQ Sequence 251 AA;
 Query Match 22.3%; Score 271.5; DB 2; Length 251;
 Best Local Similarity 32.5%; Pred. No. 7.5e-19;
 Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
 QY 4 SBEINEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLTNTLLFKGFTG 60
 Db 25 SQEFAQQDDPSQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN---VS 81
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYOC-AGGTPNKTCMYGGVTLHDNNRL 119
 Db 82 GPNYDKLTKELKNQEMATLFKDKNVDIYGVEYHLCYLSENAERSACIYGGVTNEGNHL 141
 QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGGKV 179
 Db 142 ETPKKIVKVSIDGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKQLYTNGP--SKY 197
 QY 180 QRGGLIVFHSSEGSTVSYDLFD----AQQYPTLLRIYRDNTTISSTLSISLYLT 232
 Db 198 ETGYIKFIPKNKESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250
 RESULT 68
 AAR13209
 ID AAR13209 standard; protein; 221 AA.
 AC AAR13209;
 XX 27-AUG-2003 (revised)
 DT 15-OCT-1991 (first entry)
 XX Streptococcal pyrogenic enterotoxin A.
 XX SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 OS Streptococcus sp.
 XX WO9110680-A.
 PN
 XX

PD 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 PR (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 PS SPE A can be used for tumoricidal treatment, esp. with a haemoiysin.
 CC Synthetic polypeptides having structural homology to Streptococcal
 CC pyrogenic exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophobic profiles. See AAR13203-R13211. (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 221 AA;
 Query Match 22.2%; Score 270.5; DB 2; Length 221;
 Best Local Similarity 33.8%; Pred. No. 7.9e-19;
 Matches 76; Conservative 42; Mismatches 88; Indels 19; Gaps 10;
 QY 16 SELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLG 72
 Db 7 SQLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN---VSGPNYDKLTKELK 63
 QY 73 STAATSEYEGSSVDLYGAYGYOC-AGGTPNKTCMYGGVTLHDNNRLTEEEKVPIINLWI 131
 Db 64 NQEMATLFKDKNVDIYGVEYHLCYLSENAERSACIYGGVTNEGNHLIPIKIVVKVSI 123
 QY 132 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQRGGLIVFHSSE 191
 Db 124 DGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
 QY 192 STVSYDLFD----AQQYPTLLRIYRDNTTISSTLSISLYLT 232
 Db 180 ESFWDLPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 220
 RESULT 69
 AAR45017
 ID AAR45017 standard; protein; 221 AA.
 AC AAR45017;
 XX 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX Staphylococcal enterotoxin SPE A.
 XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 XX autoimmune disease; toxicity; Protein A; perfusion system.
 OS Staphylococcus aureus.
 XX WO9324136-A1.
 PN 09-DEC-1993.
 PD 01-JUN-1993; 93WO-US005213.
 PF 01-JUN-1992; 92US-00891718.
 PR (TERM/) TERMAN D S.
 PA


```
AAW12154
ID AAW12154 standard; protein; 251 AA.
XX
AC AAW12154;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
protection; treatment; cancer; neutralising antibody;
XX
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
XX
KW hypotension; group A streptococcal infection; myositis; fasciitis;
liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 225
FT /note= "wild type Ser replaced by Ala"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
non-lethal - used in vaccine composition for treatment of cancer and
streptococcal toxic shock syndrome etc.
XX
PS Example 4; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
animals against wild type SPE-A and to treat cancer and streptococcal
toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
antibodies (Ab) to be produced, which may be used to ameliorate STSS
symptoms, e.g. fever, hypotension, group A streptococcal infection,
myositis, fasciitis and liver damage. The neutralising Ab is preferably
administered in conjunction with antibiotic therapy. The mutant SPE-A is
especially useful for treating T cell lymphomas, and ovarian and uterine
cancer. It is thought that mutant SPE-A can be selectively toxic to T
cell lymphoma cells. N.B. Sequence not given in the specification, but
constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;
Query Match 22.0%; Score 268.5; DB 2; Length 251;
Best Local Similarity 32.5%; Pred. No. 1.5e-18;
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
QY 4 SEEINEKDLRKKSLEQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLTNTLLFKGFTTG 60
DB 25 SQEYFAQQDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLSHLIYN--VS 81
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQC-AGTPTNKTACMGYGVILHNNRL 119
DB 82 GPNYDKLTKLKNQEMATLFKDKNVDIYGVVEYHLCYLCENAKRSACIYGGVTNHEGNHL 141
```

```
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKV 179
DB 142 ETPKKIIVKSIDGIO-SLSFD-IETNKKXVTAQELDYKVKYLTNDKQLYTNGP--SKY 197
QY 180 QRGLIVFHSSEGSTVSVDLFD---AQGYPTTLRIYRDNTTISTSTLSISLYLT 232
DB 198 ETGYIKFIPKNKESFWDFPPEFTQAKY----LWYKDNELTDSNTSQIEVYLT 250

RESULT 74
AAW12146
ID AAW12146 standard; protein; 251 AA.
XX
AC AAW12146;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
protection; treatment; cancer; neutralising antibody;
XX
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
XX
KW hypotension; group A streptococcal infection; myositis; fasciitis;
liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 187
FT /note= "wild type Lys replaced by Glu"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
non-lethal - used in vaccine composition for treatment of cancer and
streptococcal toxic shock syndrome etc.
XX
PS Claim 5; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
animals against wild type SPE-A and to treat cancer and streptococcal
toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
antibodies (Ab) to be produced, which may be used to ameliorate STSS
symptoms, e.g. fever, hypotension, group A streptococcal infection,
myositis, fasciitis and liver damage. The neutralising Ab is preferably
administered in conjunction with antibiotic therapy. The mutant SPE-A is
especially useful for treating T cell lymphomas, and ovarian and uterine
cancer. It is thought that mutant SPE-A can be selectively toxic to T
cell lymphoma cells. N.B. Sequence not given in the specification, but
constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;
Query Match 22.0%; Score 268.5; DB 2; Length 251;
Best Local Similarity 32.5%; Pred. No. 1.5e-18;
```



```

89 85.5 7.0 394 15 US-10-371-122-367 Sequence 367, App
90 85.5 7.0 394 15 US-10-373-567-71 Sequence 71, Appl
91 85.5 7.0 394 16 US-10-628-088-367 Sequence 367, App
92 85.5 7.0 638 12 US-10-282-122A-78278 Sequence 78278, A
93 84.5 6.9 313 14 US-10-311-879-32 Sequence 32, Appl
94 84.5 6.9 531 14 US-10-043-344-115 Sequence 115, App
95 84.5 6.9 232 12 US-10-282-122A-70242 Sequence 70242, A
96 83.5 6.9 250 12 US-10-412-699B-1671 Sequence 1671, Ap
97 83.5 6.9 250 15 US-10-374-780A-1645 Sequence 1645, Ap
98 83.5 6.9 250 16 US-10-437-963-162337 Sequence 162337,
99 83.5 6.9 292 12 US-10-282-122A-43929 Sequence 43929, A
100 83 6.8 226 12 US-10-282-122A-43957 Sequence 43957, A

```

ALIGNMENTS

```

RESULT 1
US-09-900-766-2
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

```

```

Query Match 100.0%; Score 1218; DB 10; Length: 233;
Best Local Similarity 100.0%; Pred. No. 3.4e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQCQYPTDLLRIYRDNTTISSTLSISLYLYTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQCQYPTDLLRIYRDNTTISSTLSISLYLYTT 233

```

```

RESULT 2
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

```

```

; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

```

```

Query Match 100.0%; Score 1218; DB 10; Length 672;
Best Local Similarity 100.0%; Pred. No. 1.5e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
DB 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 346 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405

QY 181 RGLIVFHSSEGSTVSYDLFDAQCQYPTDLLRIYRDNTTISSTLSISLYLYTT 233
DB 406 RGLIVFHSSEGSTVSYDLFDAQCQYPTDLLRIYRDNTTISSTLSISLYLYTT 458

```

```

RESULT 3
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

```

```

Query Match 92.8%; Score 1130; DB 10; Length 233;
Best Local Similarity 91.4%; Pred. No. 3.5e-107;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDANKKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

```

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233

RESULT 4

US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, PER
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPRANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P0218US0:10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 90.9%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 7.9e-105;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHNNRLT 120
DB 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233

RESULT 5

US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Foraberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,986
REFERENCE/DOCKET NUMBER: 419866/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 90.9%; Score 1107; DB 14; Length 233;
Best Local Similarity 89.7%; Pred. No. 7.9e-105;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHNNRLT 120
DB 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233

RESULT 6

US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Belognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,682
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:
 US-10-267-682-112

Query Match 90.9%; Score 1107; DB 12; Length 257;
 Best Local Similarity 89.7%; Pred. No. 9.1e-105;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKKSELGATGALGNLQIYYYNKAITSEKSAQDFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLKKSELGATGALGNLQIYYYNKAITSEKSAQDFLNTLLFKGFTG 84

QY 61 HPWYNDLLVGLGSKATNTKYKKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 DB 85 HPWYNDLLVGLGSKATNTKYKKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVHSSSEGSTVSDYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 205 RGLIVHSSSEGSTVSDYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTT 257

RESULT 7

US-10-267-748-112
 Sequence 112, Application US/10267748
 Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 Matthews, Thomas J.
 Wild, Carl T.
 Barney, Shawn O.
 Lambert, Dennis M.
 Petteway, Stephen R.
 Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,748
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:
 US-10-267-748-112

Query Match 90.9%; Score 1107; DB 12; Length 257;
 Best Local Similarity 89.7%; Pred. No. 9.1e-105;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKKSELGATGALGNLQIYYYNKAITSEKSAQDFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLKKSELGATGALGNLQIYYYNKAITSEKSAQDFLNTLLFKGFTG 84

QY 61 HPWYNDLLVGLGSKATNTKYKKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 DB 85 HPWYNDLLVGLGSKATNTKYKKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVHSSSEGSTVSDYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 205 RGLIVHSSSEGSTVSDYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLTT 257

RESULT 8

US-09-870-759-16
 Sequence 16, Application US/09870759
 Patent No. US20020177551A1

GENERAL INFORMATION:

APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 15
 LENGTH: 248

TYPE: PRT

ORGANISM: Staphylococcus aureus
 US-09-870-759-16

Query Match 88.0%; Score 1072; DB 9; Length 248;
 Best Local Similarity 90.2%; Pred. No. 3.3e-101;
 Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

```
QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 84
QY 61 HPWNDDLVLGSLGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWNDDLVLGSLGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSL 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSL 248

RESULT 9
US-09-751-708A-16
; Sequence 16, Application US/09751-708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751-708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 88.0%; Score 1072; DB 10; Length 248;
Best Local Similarity 90.2%; Pred. No. 3.3e-101;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 84
QY 61 HPWNDDLVLGSLGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWNDDLVLGSLGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSL 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSL 248

RESULT 10
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900.766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
```

```
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 77.8%; Score 948; DB 10; Length 233;
Best Local Similarity 76.4%; Pred. No. 1.5e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLTNTLLFKGFFTG 60
QY 61 HPWNDDLVLGSLGTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDFDSKQIVDKYKGGKVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSLISLYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTSLISLYLYTT 233

RESULT 11
US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Haansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41996/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
```

US-10-283-838-7

Query Match 77.8%; Score 948; DB 14; Length 233;
Best Local Similarity 76.4%; Pred. No. 1.5e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITENKESHQFLQHTLLFKGFFTD 60

QY 61 HPWYNLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
DB 61 HSWYNLLVDFDSKQIDVYKKGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120

QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 BEKKVPINLWIDGKQNTVPLETVTKNKQNTVOELDLQARRYLQSKYLYNSDVFQKQV 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKTIENSEMHIDIYLYTS 233

RESULT 12

US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match 77.8%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 1.7e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDKRKSELOGTALGNLKOIYYNEKAKTENKESHQFLQHTLLFKGFFTD 84

QY 61 HPWYNLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKQIDVYKKGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKKVPINLWIDGKQNTVPLETVTKNKQNTVOELDLQARRYLQSKYLYNSDVFQKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKTIENSEMHIDIYLYTS 257

RESULT 13

US-10-267-748-113
; Sequence 113, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113;
US-10-267-748-113

Query Match 77.8%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 1.7e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTD 84

QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVFQKVQ 204

QY 181 RGLVFSHSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 205 RGLVFTSTEPSVNYDLFGAQGYSTLLRIYRDNKNTINSENHMDIYLYTS 257

RESULT 14
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US2003020962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION DATA:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4;
US-10-354-948-4

Query Match 77.5%; Score 944; DB 12; Length 233;
Best Local Similarity 76.3%; Pred. No. 3.9e-88;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 61
Db 2 EKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTDH 61

QY 62 PWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
Db 122 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVFQKVQ 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 182 GLIVFTSTEPSVNYDLFGAQGYSTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 15
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 76.8%; Score 935; DB 9; Length 257;
Best Local Similarity 75.5%; Pred. No. 3.7e-87;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTN 84

QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVFQKVQ 204

QY 181 RGLVFSHSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 205 RGLVFTSTEPSVNYDLFGAQGYSTLLRIYRDNKNTINSENHMDIYLYTS 257

RESULT 16
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1

```

; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match          76.8%; Score 935; DB 10; Length 257;
Best Local Similarity 75.5%; Pred. No. 3.7e-87;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFN 84

QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVYKKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGFLYNSDSFGKVQ 180
Db 145 EEKKVPINLWLDGKQNTVPLETVTNKNVTVQELDLQARRYLOEKYLNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFDAQGQSNLTLLRIYRDNKNTINSENHIDIYLYTS 257

RESULT 17
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match          75.9%; Score 925; DB 14; Length 257;
Best Local Similarity 75.1%; Pred. No. 4e-86;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVYKKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGFLYNSDSFGKVQ 180
Db 145 EEKKVPINLWLDGKQNTVPLETVTNKNVTVQELDLQARRYLOEKYLNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFDAQGQSNLTLLRIYRDNKNTINSENHIDIYLYTS 257

RESULT 18
US-10-002-784A-4

```

```

; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match          75.6%; Score 921; DB 14; Length 233;
Best Local Similarity 75.0%; Pred. No. 8.8e-86;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTTG 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTDH 61

QY 62 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTE 121
Db 62 SWYNDLLVDFDSKDIDVYKKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTE 121

QY 122 EKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGFLYNSDSFGKVQ 181
Db 122 EKVPINLWLDGKQNTVPLETVTNKNVTVQELDLQARRYLOEKYLNLYNSDVDFGKVQ 181

QY 182 GLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNNTTISLSISLYLTT 233
Db 182 GLIVFHTSTEPSVNYDLFDAQGQSNLTLLRIYRDNKNTINSENHIDIYLYTS 233

RESULT 19
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-UA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match 74.5%; Score 908; DB 8; Length 257;
Best Local Similarity 74.2%; Pred. No. 2.2e-84;
Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKLGQGTALGNLQIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSEKLGQGTALGNLQIYYNEKAKTENKESHDPQROHTLLFKGFFTD 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWDGKQNTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSVDFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYSTLLRIYRDNTTINSENNHIDIYLYTS 257

RESULT 20
US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Ulrich,
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 74.1%; Score 903; DB 8; Length 233;
Best Local Similarity 73.7%; Pred. No. 6.1e-84;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSEKLGQGTALGNLQIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSEKLGQGTALGNLQIYYNEKAKTENKESHDPQROHTLLFKGFFTDH 61
QY 62 PWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 122 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKOR 181
Db 122 EEKVPINLWDGKQNTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSVDFGKVAR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSTLLRIYRDNTTINSENNHIDIYLYTS 233

RESULT 21
US-09-870-759-14
; Sequence 14, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-14

Query Match 50.2%; Score 611; DB 9; Length 258;
Best Local Similarity 51.1%; Pred. No. 5.7e-54;
Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKLGQGTALGNLQIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGQDFLENTLLYKFFTD 85
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFKSKNVDPYPIRVSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKTPINLWINGVQKESVSLDKVQTDKNVTVOELDLQARHYLHGKFGLYNSDNLGG 205
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLY 231
Db 206 RGLIEFSDSGSKVSYDLFVKGDFPEKQLRIYSNKTILSTEHLHIDIYLY 256

RESULT 22
US-09-751-708A-14
```


Db 1 SHDQFLOHTILFKGFFTHSWYNDLLVDFSDKIDVYKXKKVLDLYGAYGYQCAGTPN 60
Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82
RESULT 26
US-09-900-766-6
; Sequence 6, Application US/09900766
; Publication No. US2003009655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSEN, BOORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-6
Query March 25.3%; Score 308; DB 10; Length 217;
Best Local Similarity 33.9%; Pred. No. 4.7e-23;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;
Qy 10 KDLKKSSELQGTALGNLKQIYYNKAITGSEKSAQDQFLNTLLFKGFFTHGFWYNDLLV 69
Db 1 EDLHDKSELDTLALAN--AYQVNHPIKENIKSDEISGEKDLIFRN--QGDGSG-NDLRV 55
Qy 70 DLGSTAATSEYEGSSVDLYGAYGYQCAGTPNKTAQMYGVTLHDNNRLTEKKVPINL 129
Db 56 KFATADLAQKFNKNVDIYGASFYKCEKISNISSECLYGGTTL-NSEKLAQSERVICANV 114
Qy 130 WIDGQKQTTVPIDKTKSKVTVQELDLQARHYLHGKFLYNSDSFGKVCQRGLIVPHSS 189
Db 115 WVDGIQKETEL--IRTNKNVTLQELDIKIRKILSDKIYKIDS---EISKGLIEFDMK 169
Qy 190 EGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSLS-ISLYLT 232
Db 170 TPRDYSFDVLKGCNDYEIDKIYEDKNKTLKSDDISHDVNLVT 213
RESULT 27
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match 22.0%; Score 268.5; DB 8; Length 251;
Best Local Similarity 32.5%; Pred. No. 6.4e-19;
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
Qy 4 SEEINEKDLRKKSSELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLNTLLFKGFFTG 60
Db 25 SQEFAQQDPDPESQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN--VS 81
Qy 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTAQMYGVTLHDNNRL 119
Db 82 GPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHYLCYLCEAERASACTYGGVTNHEGNHL 141
Qy 120 TEEKKVPINLWIDGKQTTVPIDKTKSKVTVQELDLQARHYLHGKFLYNSDSFGKGV 179
Db 142 ETPKXIVVKSIDGIQ-SLSPD-IEINKMNTAQELDYKVKYKLTNDNKQLYNGP--SKY 197
Qy 180 QRGLIVFHSSEGSTVSYDLFD---AQGYPTDLLRIYRDNTTISSTLSLSLYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEPTQSKY---LMIYKDNETLDSNTSQIEVYLTT 250
RESULT 28
US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-308-830-13
Query Match 22.0%; Score 268.5; DB 12; Length 251;
Best Local Similarity 32.5%; Pred. No. 6.4e-19;

```
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
QY 4 SBEINEKDLRKSELOGTALGNLKQIYY-YNSKAIT-SSEKSAQOFTNTLLFKGFTTG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 25 SQEFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLSHLIYN--VS 81
QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-AGGTENKTACMYGGVTLHDNNRL 119
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 GPYNDKLTTELKQENWATLFDKQNDIYGVETIYHLCYLCENAEKACIYGGVTHEGNHL 141
QY 120 TBEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 EIPKKIWKVSDIGIQ-SLSFD-IETNKQWTAQELDKVKRYLTDNKQLYNGP--SKY 197
QY 180 QRLIVPHSSEGSTVSYDLFD-----AQQGYPPTLLRIYRDNTTISSTLSLSLYLT 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 ETGYIKFIPKNKESFWDFPEFPTQSKY----LMIYKONETLDSNTSQIEVLYLT 250

RESULT 29
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match 22.0%; Score 268.5; DB 9; Length 266;
Best Local Similarity 31.6%; Pred. No. 7e-19;
Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSAQOFTNTLLFKGFTTG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 AESQDPKPDDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 84
QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 LGYNDVNRVEFKNLADKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 144
QY 111 VTLHDNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 VTEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 202
QY 171 NSDSFGGKVQRLIVPHSSEGSTVSYDLFDAAQGYPD--TLRIYRDNTTISSTLSLSL 228
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV 259
QY 229 YLYT 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 260 YLYT 263

RESULT 30
US-09-751-708A-10
; Sequence 10, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-10

Query Match 22.0%; Score 267.5; DB 9; Length 239;
Best Local Similarity 31.7%; Pred. No. 7.6e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSAQOFTNTLLFKGFTTG 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ESQDPKPDDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 58
QY 62 PWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 GYNDVNRVEFKNLADKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 118
QY 112 TLDHNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 171
```

```
US-09-751-708A-10
; Sequence 10, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 22.0%; Score 267.5; DB 9; Length 239;
Best Local Similarity 31.7%; Pred. No. 7.6e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSAQOFTNTLLFKGFTTG 61
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ESQDPKPDDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 58
QY 62 PWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 GYNDVNRVEFKNLADKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 118
QY 112 TLDHNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 171
```

Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVNKKLYE 176
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 32
US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10172425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12

Query Match 22.0%; Score 267.5; DB 14; Length 239;
Best Local Similarity 31.7%; Pred. No. 7.6e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGH 61
Db 1 ESQDPKPDDELHKSFKTG-LMENMK-VLYDDNHVSAINVKSIDQFLYDLIYSIKDTKL 58
Qy 62 PWYNDLLVDLGS"AAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNRVVEFKNDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTMYGGV 118
Qy 112 TLHDNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVNKKLYE 176
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 33
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match 22.0%; Score 267.5; DB 12; Length 255;
Best Local Similarity 31.7%; Pred. No. 8.3e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGH 61
Db 17 ESQDPKPDDELHKSFKTG-LMENMK-VLYDDNHVSAINVKSIDQFLYDLIYSIKDTKL 74
Qy 62 PWYNDLLVDLGS"AAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 75 GNYDNRVVEFKNDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 134
Qy 112 TLHDNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVNKKLYE 192
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 249
Qy 230 LYT 232
Db 250 LTT 252

RESULT 34
US-08-892-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran

```
STREET: US Army MCMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 21.6%; Score 263.5; DB 8; Length 251;
Best Local Similarity 32.1%; Pred. No. 2.1e-18;
Matches 76; Conservative 45; Mismatches 97; Indels 19; Gaps 10;

QY 4 SBEINEKDLRKSELOQTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLLFKGFTG 60
Db 25 SQEVAQDPDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMYGGVTLHDNNRL 119
Db 82 GPNYDKLTKELKNQEMATLFDKKNVDIYGVEYHLCYLCEAERSACIYGGVTNHEGNHL 141

QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 179
Db 142 EIPKKIIVKVSIDGIQ-SLSFD-IETNKKQWTAQELDYKVKYLTDNKQLYTNGP--SKY 197

QY 180 QRGILVHFHSEGSTVSVDLFD----AQGOYPTLLRIYRDNTTISSTLSISLYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 35
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence

STREET: US Army MCMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/870,759
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-870-759-12

Query Match 21.6%; Score 263.5; DB 9; Length 266;
Best Local Similarity 30.6%; Pred. No. 2.3e-18;
Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYY--YNSKAITSSSEKSADQFLNTLLFKGFF 58
Db 27 AESQDPPTDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDFLAHLDLIYNISD 82

QY 59 TGHFWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 83 KKLKNYDKVKTELLNEGLAKYKDEVDVYGSYVYVNCYFSSKDNVGVKVTGGKTCMYGGI 142

QY 112 TLHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFL 169
Db 143 TKEGHNHFDNGNLQNLVIRY-ENKENT-SFE-VQTDKSVTAQELDIKARPLINKKML 200

QY 170 YNSDSFGGKVQRGILVHFHSEGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSIS 227
Db 201 YFNPS--SPYETGYIKFIEENNGTFFWDMWMPAPDFQDSKILMYNDNKTVDKSKVKIE 258

QY 228 LYLYT 232
Db 259 VHLTT 263

RESULT 37
US-09-751-708A-12
; Sequence 12, Application US/09751708A
```


Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751.708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-12

Query Match 21.6%; Score 263.5; DB 10; Length 266;
Best Local Similarity 30.6%; Pred. No. 2.3e-18;
Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;
QY 1 SEKSEINEKDLRKSELOQTALGNLKOIY--YNSKAITSSSEKSAQDFLTNTLLPKGFF 58
DB 27 AESQDPDTPDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDFKFLAHLIYINISD 82
QY 59 TGHFWYNDLLVGLGTAATSEYEGSSVDLYGAYGYOC-----AGGTENKTKACMYGGV 111
DB 83 KKLKMYDKVKTLLNEGLAKYKDEVVDVYGSNNYVNCYFSSKDNVGVKVTGGTKOMYGGI 142
QY 112 TLHNNRLTEB--KKVPINLWIDKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFG 169
DB 143 TKHEGNHFDNGLONVIRY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNL 200
QY 170 YNSDFGKQVORGLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSIS 227
DB 201 YEFNS--SPYETGYIKFIENNGNTFWYDMMPAPGDKFQSKYLMYNDNKTVDKSVKIE 258
QY 228 LYLYT 232
DB 259 YLYTT 263

RESULT 38
US-10-002-784A-6
Sequence 6, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002.784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 6
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: mutant staphylococcal enterotoxin B
US-10-002-784A-6

Query Match 21.4%; Score 260.5; DB 14; Length 266;
Best Local Similarity 30.7%; Pred. No. 4.6e-18;
Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYVNSKAITSSSEKSAQDFLTNTLLPKGFFTG 60
DB 27 AESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQSLYFDLIYSIKDTK 84

QY 61 HPWYNDLLVGLGTAATSEYEGSSVDLYGAYGYOC-----AGGTENKTKACMYGG 110
DB 85 LGYDNVRVEFKNDLADIKYKDYVDFGANYYYOCYFSKKTNDINSQTDKRTKTCMYGG 144
QY 111 VTLDHNNRLTEBKKVPINLWIDKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFG 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKQVORGLIVFHSSEGSTVSVDLFDQAQGYPD--YPTLLRIYRDNTTISSTLSISL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNVDSKDVKIEV 259
QY 229 YLYT 232
DB 260 YLYT 263

RESULT 39
US-10-151-336-8
Sequence 8, Application US/10151336
Publication No. US20030079248A1
GENERAL INFORMATION:
APPLICANT: Mason, Hugh
APPLICANT: Palmer, Kenneth
APPLICANT: Hefferon, Kathleen
APPLICANT: Mor, Tsafir
APPLICANT: Arntzen, Charles
TITLE OF INVENTION: Genini Virus Vectors for Gene Expression in Plants
FILE REFERENCE: 4869/84453
CURRENT APPLICATION NUMBER: US/10/151.336
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/09/414.276
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 266
TYPE: PRT
ORGANISM: bean yellow dwarf virus
US-10-151-336-8

Query Match 21.4%; Score 260.5; DB 14; Length 266;
Best Local Similarity 31.1%; Pred. No. 4.6e-18;
Matches 76; Conservative 44; Mismatches 105; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYVNSKAITSSSEKSAQDFLTNTLLPKGFFTG 60
DB 27 AESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQSLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVGLGTAATSEYEGSSVDLYGAYGYOC-----AGGTENKTKACMYGG 110
DB 85 LGYDNVRVEFKNDLADIKYKDYVDFGANYYYOCYFSKKTNDINSQTDKRTKTCMYGG 144
QY 111 VTLDHNNRLTEBKKVPINLWIDKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFG 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKQVORGLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSISL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFQSKYLMYNDNKNVDSKDVKIEV 259
QY 229 YLYT 232
DB 260 YLYT 263

RESULT 40
US-10-002-784A-10
Sequence 10, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.

```

; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant staphylococcal enterotoxin B cytoplasmic
; US-10-002-784A-10.

Query Match      21.0%; Score 255.5; DB 14; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.3e-17;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLRKSELOGTALGNLQKQIYYNNKAITSSSEKSDAQFLTNLLFKGFTGHPWINDLLVD 70
DB 10 ELHKSFKTG-LMENMK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNVDNRVE 67
QY 71 LGSTAATSEYEGSSVDLYGAYGYOCAGG-----TPNKTACMYGGVTLHDNRILT 120
DB 68 FKXKLADIKYKVDVFGANAYQCARSKTNDINSHQTDKRTCMYGGVTEHNGQLD 127
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHKGFLGNSDFGKQV 180
DB 128 KYRSITRVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHLYVKNKKLYEFNN--SPYE 183
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNTTISSTLSLSLYLT 232
DB 184 TGYIKFIENENS-FWYDMPAPGDFQSKYLMYNDNRQVDSKDVKIEVYLT 236

RESULT 41
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065

```

```

; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14

Query Match      21.0%; Score 255.5; DB 8; Length 266;
Best Local Similarity 30.2%; Pred. No. 1.5e-17;
Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOGTALGNLQKQIY--YNNKAITSSSEKSDAQFLTNLLFKGFF 58
DB 27 AESQDPPTDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDKFRAHDLIYNISD 82
QY 59 TGHFWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGV 111
DB 83 KKLKNYDKVKTTELLNEGLAKYKDEVDVYGSYYNVCYFSSKDNVKGVTGGKTCMYGGI 142
QY 112 TLHDNRNLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHKGFL 169
DB 143 TKHEGNHFDNGNLQNLVIRVY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKNL 200
QY 170 YNSDSFGGKVQRCGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNTTISSTLSIS 227
DB 201 YEFNS--SFVETGYIKFIENNGNTFWYDMPAPGDFQSKYLMYNDNRQVDSKSVKIE 258
QY 228 LYLTY 232
DB 259 VHLTT 263

RESULT 42
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
; US-10-002-784A-14

Query Match      21.0%; Score 255.5; DB 14; Length 266;
Best Local Similarity 30.2%; Pred. No. 1.5e-17;
Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOGTALGNLQKQIY--YNNKAITSSSEKSDAQFLTNLLFKGFF 58
DB 27 AESQDPPTDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDKFRAHDLIYNISD 82
QY 59 TGHFWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGV 111
DB 83 KKLKNYDKVKTTELLNEGLAKYKDEVDVYGSYYNVCYFSSKDNVKGVTGGKTCMYGGI 142
QY 112 TLHDNRNLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHKGFL 169
DB 143 TKHEGNHFDNGNLQNLVIRVY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKNL 200

```

QY 170 YNSDSFGKVGORGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLIS 227
Db 201 YEFNS--SFYETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMVYNDNKTVDKSKVIE 258
QY 228 LYLVT 232
Db 259 VHLT 263

RESULT 43
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 20.9%; Score 254.5; DB 8; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.6e-17;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLKRSSELOGTALGNLKOIYYNSKAITSSSEKSDQFLNTLLFKGFTTGHPPWDLVD 70
Db 10 ELHSSKFTG-KMENMK-VLYDDNHVSAINVKSIDQFRYDPLIYSIKDTKLGNVDNRVE 67
QY 71 LGSTAATSEYEGSSVDLYGAYGYCCAGG-----TPNKTCMYGGVTLHDNNRLT 120
Db 68 FKNKDLADKYDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRTCMYGVTEHNGQLD 127
QY 121 EEKVPINLWDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKVG 180
Db 128 KYRSITVRVFDGK-NLISFD-VQTNKKKVTQAQELDYLTRHYLVKDKLYEFNN--SPYE 183
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLISLYLT 232

Db 184 TGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKKVDSKVKIEVILTT 236

RESULT 44
US-10-002-784A-8
; Sequence 8, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
US-10-002-784A-8

Query Match 20.6%; Score 250.5; DB 14; Length 266;
Best Local Similarity 30.7%; Pred. No. 4.9e-17;
Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFLNTLLFKGFTT 60
Db 27 AESQDPKPEDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFRYDPLIYSIKDTK 84
QY 61 HPWYNDLLVDLSTATSEYEGSSVDLYGAYGYCCAGG-----TPNKTCMYGG 110
Db 85 LGNYDNVRVEFFNKDLADKYDKYVDVFGANAYYQCAFSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEEEKVPIINLWDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLY 170
Db 145 VTEHNGQLDKYRSITVRVFDGK-NLISFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLISL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKKVDSKVKIEV 259
QY 229 YLVT 232
Db 260 YLTT 263

RESULT 45
US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-6

Query Match 20.3%; Score 247; DB 8; Length 265;
Best Local Similarity 29.5%; Pred. No. 1.1e-16;
Matches 72; Conservative 43; Mismatches 109; Indels 20; Gaps 7;

QY 1 SEKSEINBKDLRKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFKGFTG 60
Db 27 AESQDPKPKDELHKSKF--TGIMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOC-----AGSTPNKTACMYGG 110
Db 85 LGDYDNRVFEKNKLADKYKVDVFGANYYQCYFSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEKKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNLDKYSITVRVFEDEK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTSVSYDLFDAQOQ--YPTTLRIYRDNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKF--IENQNFYDMMFAPGDKFAQSKYLMYNDNKNQVDSKDVKLEV 258
QY 229 YLYT 232
Db 259 YLTT 262

RESULT 46
US-08-882-431-8
Sequence 8, Application US/08882431
Publication No. US2003009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF INVENTIONS: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-8

Query Match 20.0%; Score 244; DB 8; Length 265;
Best Local Similarity 29.9%; Pred. No. 2.2e-16;
Matches 73; Conservative 43; Mismatches 108; Indels 20; Gaps 8;

QY 1 SEKSEINBKDLRKSELOQTALGNLKOIYYNSKAITSEKSAOQFLNTLLFKGFTG 60
Db 27 AESQDPKPKDELHKSKFTG-LMENKK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGG-----TPNKTACMYGG 110
Db 85 LGDYDNRVFEKNKLADKYKVDVFGANYYQCAFSSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEKKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNLDKYSITVRVFEDEK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTSVSYDLFDAQOQYD--TLRIYRDNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKF--IENQNFYDMMFAPGDKFDQSKYLMYNDNKNQVDSKDVKLEV 258
QY 229 YLYT 232
Db 259 YLTT 262

RESULT 47
US-10-002-784A-26
Sequence 26, Application US/10002784A
Publication No. US2003003664A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 26
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match 18.5%; Score 225.5; DB 14; Length 220;
Best Local Similarity 31.6%; Pred. No. 1.3e-14;

Matches 71; Conservative 43; Mismatches 90; Indels 21; Gaps 12;
QY 16 SELOGTAL-GNLKQIYY-YNSKAIT-SSEKADQFLNTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN--VSGPNYDKLTKTELK 64
QY 73 STAATSEYEGSSVDLYGAYGYQC-AGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWI 131
Db 65 NQEMATLFDKXNDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVI 123
QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEG 191
Db 124 DGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
QY 192 STVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 180 ESFWDFPFPEFTQSKY----LMIYKDNETLDSNT-QIEVYLTT 219
RESULT 48
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27
Query Match 18.5%; Score 225.5; DB 14; Length 468;
Best Local Similarity 31.6%; Pred. No. 4e-14;
Matches 71; Conservative 43; Mismatches 90; Indels 21; Gaps 12;
QY 16 SELOGTAL-GNLKQIYY-YNSKAIT-SSEKADQFLNTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN--VSGPNYDKLTKTELK 64
QY 73 STAATSEYEGSSVDLYGAYGYQC-AGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWI 131
Db 65 NQEMATLFDKXNDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVI 123
QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEG 191
Db 124 DGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
QY 192 STVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 180 ESFWDFPFPEFTQSKY----LMIYKDNETLDSNT-QIEVYLTT 219
RESULT 49
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20
Query Match 18.1%; Score 220; DB 9; Length 250;
Best Local Similarity 28.9%; Pred. No. 5.9e-14;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;
QY 14 KKSELQGTALGNLKQIYY-YNSKAITSSSE--KSAQOFLNTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVTKFIYFFMRVTLVTHENVKSDQLLSDHLIYN--VSGPNYDKLTKTE 91
QY 71 LGSTAATSEYEGSSVDLYGAYGYQC-AGTGNKTAACMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKQEMATLFDKXNDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVI 151
QY 130 WIDGKQT-TVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHS 188
Db 152 SIDGIQSLSFDEIQKNG---NCSRIISYTVRKYLTDNKQLYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 206 KKNESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 249
RESULT 50
US-09-751-708A-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20
Query Match 18.1%; Score 220; DB 10; Length 250;
Best Local Similarity 28.9%; Pred. No. 5.9e-14;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;
QY 14 KKSELQGTALGNLKQIYY-YNSKAITSSSE--KSAQOFLNTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVTKFIYFFMRVTLVTHENVKSDQLLSDHLIYN--VSGPNYDKLTKTE 91
QY 71 LGSTAATSEYEGSSVDLYGAYGYQC-AGTGNKTAACMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKQEMATLFDKXNDIYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVI 151
QY 130 WIDGKQT-TVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHS 188
Db 152 SIDGIQSLSFDEIQKNG---NCSRIISYTVRKYLTDNKQLYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 206 KKNESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 249
RESULT 51

```

US-10-002-784A-33
; Sequence 33, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
;
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 33
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin D
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-33

Query Match      15.9%; Score 194; DB 14; Length 82;
Best Local Similarity 45.1%; Pred. No. 5.5e-12;
Matches 37; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

QY 43 SADOFLNTLLFKGFTGHPWYNDLLVLDLSTAATSEYEGSVVDLYGAYGYQCAGGTPN 102
Db      1 TGDQFLNTLLYKFTDLINFEDLLINENSKMAQHPKKNVDYPIRYSINCYGGEID 60

QY 103 KTACMGYGVTLHDNNRLTEKK 124
Db      61 RTACTYGGVTPHEGNLKERKK 82

RESULT 52
US-09-308-829-2
; Sequence 2, Application US/09308829
; Publication No. US20020039585A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Ohlendorf, Douglas
; APPLICANT: Mitchell, David T.
; APPLICANT: Gahr, Pamela J.
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
; FILE REFERENCE: 600.347USW0
; CURRENT APPLICATION NUMBER: US/09/308,829
; CURRENT FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/US97/22125
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US 60/033,251
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-308-829-2

Query Match      12.8%; Score 155.5; DB 12; Length 235;
Best Local Similarity 24.2%; Pred. No. 2.2e-07;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLNTLLFKGFTGH-----PW-YNDLLVDLGGSTAA-----TSE 79
Db 11 FITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDYKDCRVNFSTHTLNIDTQK 70

QY 80 YEGSS-----VDLYGAYGYQCAGGTPNKTCMGYGVTLHDNNRL 119
Db 71 YRGKDYVISSEMSYEASQKFKRDDHVDVFLGYLNSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDQARHYLHGKFLYNSDS--FGG 177
Db 126 NH--KLGNLFISSGSGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS-LSLYL 230

QY 178 KVGRLIVFHSSEGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS-LSLYL 230
Db 184 RIEIG-----TKDGKEQIDLFDSPEGTRSDIFAK-YKDNRIINMKNFSHFDIYL 233

RESULT 54
US-10-002-784A-39
; Sequence 39, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
;
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
US-10-002-784A-39

Query Match      12.8%; Score 155.5; DB 12; Length 235;
Best Local Similarity 24.2%; Pred. No. 2.2e-07;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLNTLLFKGFTGH-----PW-YNDLLVDLGGSTAA-----TSE 79
Db 11 FITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDYKDCRVNFSTHTLNIDTQK 70

QY 80 YEGSS-----VDLYGAYGYQCAGGTPNKTCMGYGVTLHDNNRL 119
Db 71 YRGKDYVISSEMSYEASQKFKRDDHVDVFLGYLNSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQELDQARHYLHGKFLYNSDS--FGG 177
Db 126 NH--KLGNLFISSGSGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS-LSLYL 230

QY 178 KVGRLIVFHSSEGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS-LSLYL 230
Db 184 RIEIG-----TKDGKEQIDLFDSPEGTRSDIFAK-YKDNRIINMKNFSHFDIYL 233

```

```
; SEQ ID NO 39
; LENGTH: 79
; TYPE: PRT
; ORGANISM: streptococcal pyrogenic enterotoxin a
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-39

Query Match          9.2%; Score 112; DB 14; Length 79;
Best Local Similarity 32.1%; Pred. No. 0.0013;
Matches 25; Conservative 17; Mismatches 32; Indels 4; Gaps 2;

QY 43 SADQFLNTLTKGFTGHPWYNDLLDLGSTAATSEYEGSSVDLYGAYGYQC-AGGTP 101
Db 1 SVDQLSLDLIYN--VSGPNYDKLTKEKQEMATLFDKKNVDIYGVVEYVHLCYCENA 57

QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 55
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 35
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin B
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-35

Query Match          9.2%; Score 111.5; DB 14; Length 89;
Best Local Similarity 33.3%; Pred. No. 0.0017;
Matches 29; Conservative 15; Mismatches 32; Indels 11; Gaps 2;

QY 43 SADQFLNTLTKGFTGHPWYNDLLDLGSTAATSEYEGSSVDLYGAYGYQC----- 96
Db 1 SIDQLFLDLIYSKDTKLGNVDNRVEFNKDLADKFKDYVDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTACMYGGVTLHDNNRL 119
Db 60 NDINSHQTDKRKTCWYGGVTEHNGNQL 86

RESULT 56
US-10-424-599-264720
; Sequence 264720, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Staphylococcal enterotoxin B
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264720
```

```
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81062C.1.pap
US-10-424-599-264720

Query Match          8.5%; Score 103.5; DB 12; Length 621;
Best Local Similarity 23.0%; Pred. No. 0.18;
Matches 51; Conservative 39; Mismatches 83; Indels 49; Gaps 11;

QY 24 GNLKQIYYN---SKAITSSEKSAQDLNTLLFKGFTGHPWYNDLLVDLGSTAATSEY 80
Db 162 GNGTDVYQDGDSESLTDSSESDSSVNN--YSGFSRNGS-----DLGINRRIMEL 212

QY 81 EGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 140
Db 213 ETELREVKELWQE-----BEHA---DGSTRGRNNTEDVYTKINAY---EQELMTV 260

QY 141 -DKVTSKKEVTVQELDLQARHYLHGKFLYNSDFGGKVQGLIVPHSSEGST----- 193
Db 261 NEKLRLSEBEITKQIELQ-----KYRLFTNLEAGFESSLTKKHINEGGEAHKMLE 313

QY 194 -----VSVDLFDAGQGYPTL---LRIYRDNNTTISSTLS 225
Db 314 VEGSIDGVDKELFDQNGEI-ETLARELRITKENLKASEMQIT 347

RESULT 57
US-10-425-114-57792
; Sequence 57792, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57792
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC107B05_FLI.pap
US-10-425-114-57792

Query Match          8.5%; Score 103.5; DB 12; Length 628;
Best Local Similarity 23.0%; Pred. No. 0.19;
Matches 51; Conservative 39; Mismatches 83; Indels 49; Gaps 11;

QY 24 GNLKQIYYN---SKAITSSEKSAQDLNTLLFKGFTGHPWYNDLLVDLGSTAATSEY 80
Db 162 GNGTDVYQDGDSESLTDSSESDSSVNN--YSGFSRNGS-----DLGINRRIMEL 212

QY 81 EGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 140
Db 213 ETELREVKELWQE-----BEHA---DGSTRGRNNTEDVYTKINAY---EQELMTV 260

QY 141 -DKVTSKKEVTVQELDLQARHYLHGKFLYNSDFGGKVQGLIVPHSSEGST----- 193
Db 261 NEKLRLSEBEITKQIELQ-----KYRLFTNLEAGFESSLTKKHINEGGEAHKMLE 313

QY 194 -----VSVDLFDAGQGYPTL---LRIYRDNNTTISSTLS 225
Db 314 VEGSIDGVDKELFDQNGEI-ETLARELRITKENLKASEMQIT 354
```

```

; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-870-759-18

Query Match      8.2%; Score 100; DB 9; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

Qy 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
Db 45 NIKDLLWYSSGSDTTFNSEVLDNSLGSRIKNTDGSISLIIFPS-----PYYSAPFK 98
Qy 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NTRKTKKSQHTS---EGTVIHFIQISGVT-----NTEKLTPIEL 140
Qy 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
Db 141 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 197
Qy 183 LIVFHSSEGSTVSVDL 198
Db 198 -----NNDGSGTYQSDL 208

RESULT 60
US-09-751-708A-18
; Sequence 18, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-751-708A-18

Query Match      8.2%; Score 100; DB 10; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

Qy 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
Db 45 NIKDLLWYSSGSDTTFNSEVLDNSLGSRIKNTDGSISLIIFPS-----PYYSAPFK 98
Qy 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NTRKTKKSQHTS---EGTVIHFIQISGVT-----NTEKLTPIEL 140
Qy 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
Db 141 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 197
Qy 183 LIVFHSSEGSTVSVDL 198

RESULT 59
US-09-870-759-18
; Sequence 18, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-12

Query Match      8.4%; Score 102.5; DB 8; Length 233;
Best Local Similarity 24.5%; Pred. No. 0.058;
Matches 48; Conservative 33; Mismatches 60; Indels 55; Gaps 12;

Qy 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
Db 45 NIKDLLWYSSGSDTTFNSEVLDNSLGSRIKNTDGSISK-IIFPS-----PYYSAPFK 98
Qy 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NTRKTKKSQHTS---GTVIHFIQISGVT-----NTEKLTPIEL 139
Qy 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
Db 140 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 196
Qy 183 LIVFHSSEGSTVSVDL 198
Db 197 -----NNDGSGTYQSDL 207

RESULT 59
US-09-870-759-18
; Sequence 18, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCWR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-12
```


QY	183	LIVFHSSEGSTVSYDL	198
Db	198	-----MNDGSTYQSDL	208
RESULT 62			
US-10-267-748-111			
; Sequence 111, Application US/10267748			
; Publication No. US20040052820A1			
; GENERAL INFORMATION:			
; APPLICANT: Bolognesi, Dani P.			
; Matthews, Thomas J.			
; Wild, Carl T.			
; Barney, Shawn O.			
; Lambert, Dennis M.			
; Petteway, Stephen R.			
; Langlois, Alphonse J.			
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION			
; NUMBER OF SEQUENCES: 239			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Pennie & Edmonds			
; STREET: 1155 Avenue of the Americas			
; CITY: New York			
; STATE: New York			
; COUNTRY: USA			
; ZIP: 10036-2711			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.30			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/10/267,682			
; FILING DATE: 08-Oct-2002			
; CLASSIFICATION: <Unknown>			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US/08/484,223A			
; FILING DATE: 07-JUN-1995			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Coruzzi, Laura A.			
; REGISTRATION NUMBER: 30,742			
; REFERENCE/DOCKET NUMBER: 7872-029			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (212) 790-9090			
; TELEFAX: (212) 869-9741/8864			
; TELEX: 66141 PENNIE			
; INFORMATION FOR SEQ ID NO: 111:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 234 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: <Unknown>			
; TOPOLOGY: unknown			
; MOLECULE TYPE: protein			
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:			
US-10-267-682-111			
Query Match 8.2%; Score 100; DB 12; Length 234;			
Best Local Similarity 24.5%; Pred. No. 0.1;			
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;			
QY	25	NLKQI---YYNKAITSSE-----KSADQFLNTLLFKGFTTCHPWYNDLL--	68
Db	45	NIKDLWDVSSGSDTTNSEVLNDSLSGRMKNTDGSISLIIFPS-----PYISPAFTK	98
QY	69	---VDLGSATAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKV	125
Db	99	GEKVLD-NTRTKKSQHTS---EGTVIHFIQISGV-----NTEKLPPIEL	140
QY	126	PINLWDGKQTTPIDKVKTSKEVTVQELDLQARHYLHCKFGLY-NSDSFGG--KVQRG	182
Db	141	PLKVKVHGKDSPLKYGK-PKFDKKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGGYWKIT--	197

QY	183	LIVFHSSEGSTVSYDL	198
DB	198	-----MNDGSTYQSDDL	208
 RESULT 62			
US-10-267-748-111			
; Sequence 111, Application US/10267748			
; Publication No. US20040052820A1			
; GENERAL INFORMATION:			
APPLICANT: Bolognesi, Dani P.			
Matthews, Thomas J.			
Wild, Carl T.			
Barney, Shawn O.			
Lambert, Dennis M.			
Petteaway, Stephen R.			
Langlois, Alphonse J.			
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION			
NUMBER OF SEQUENCES: 239			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Pennie & Edmonds			
STREET: 1155 Avenue of the Americas			
CITY: New York			
STATE: New York			
COUNTRY: USA			
ZIP: 10036-2711			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/10/267,682			
FILING DATE: 08-Oct-2002			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/08/484,223A			
FILING DATE: 07-JUN-1995			
ATTORNEY/AGENT INFORMATION:			
NAME: Coruzzi, Laura A.			
REGISTRATION NUMBER: 30,742			
REFERENCE/DOCKET NUMBER: 7872-029			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (212) 790-9090			
TELEFAX: (212) 869-9741/8864			
TELEX: 66141 PENNIE			
INFORMATION FOR SEQ ID NO: 111:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 234 amino acids			
TYPE: amino acid			
STRANDEDNESS: <Unknown>			
TOPOLOGY: unknown			
MOLECULE TYPE: protein			
SEQUENCE DESCRIPTION: SEQ ID NO: 111:			
US-10-267-682-111			
Query Match	8.2%;	Score 100;	DB 12; Length 234;
Best Local Similarity	24.5%;	Pred. No. 0.1;	
Matches	48; Conservative	33; Mismatches	61; Indels 54; Gaps 12;
QY	25	NLKQI---YYNSKAITSS-----KSADQLNTLLFKGFTTCHPWYNLL--	68
DB	45	NIKDLLDWSSGGDTTNSEVLDSNGSRMKRTDGSII-SLIIFPS-----PYISPAFTK	98
QY	69	---VDLGSATAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLDHNNRLTEKKV	125
DB	99	GKVDL-NTRTKKSQHTS---EGTVIHFIQSGVT-----NTEKLPTPIEL	140
QY	126	PINLWIDGQTTPIDVKVTSKEVTVOELDLQARHYLHGCKFGLY-NSDSFGG--KVQRG	182
DB	141	PLKVKVHGKDSPUKYGP-KPDKKQLAISTLDLFIRHQLTQIHGLYRSSDKTGYSWKIT--	197

```
QY 183 LIVFHSSEGSTVSVDL 198
Db 198 -----MNDGSTYQSDL 208

RESULT 63
US-10-002-784A-12
; Sequence 12, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: toxin shock syndrome toxin-1 mutant
US-10-002-784A-12

Query Match      8.2%; Score 100; DB 14; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

QY 25 NLKQI---YYNSKATISSE-----KSADQFLTNTLLFKGFFTGHPWYNDLL-- 68
Db 45 NIKDLWDYSSGSDFTNSEVLNDSGSMRIKNTDGSI-SLIIFPS-?-PYSPATK 98

QY 69 ---VLDGSTAAATSEYSGSVVDLYGAYGYQCAGTGNKTACMYGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NIKRTKKSQHTS---EGTVIHFIQISGVT-----NTEKLPPIEL 140

QY 126 PINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQKG 182
Db 141 PLKVKVHGKDSPLKYGP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 197

QY 183 LIVFHSSEGSTVSVDL 198
Db 198 -----MNDGSTYQSDL 208

RESULT 64
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match      8.2%; Score 99.5; DB 14; Length 89;
Best Local Similarity 28.0%; Pred. No. 0.03;
Matches 23; Conservative 14; Mismatches 38; Indels 7; Gaps 1;

QY 43 SADQFLTNTLLFKGFFTGHPWYNDLLVLDGSTAAATSEYSGSVVDLYGAYGYQC----- 96
Db 1 SVDKFLADHLIYNISDKLKNYDKVKTLELNEGLAKKYKDEVVDVYGSNYNYNCYFSSKD 60

QY 97 -AGGTENKTACMYGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITKEGN 82

RESULT 65
US-09-465-714-3
; Sequence 3, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Bacterial Sequence
US-09-465-714-3

Query Match      8.0%; Score 98; DB 10; Length 194;
Best Local Similarity 24.6%; Pred. No. 0.13;
Matches 49; Conservative 33; Mismatches 57; Indels 60; Gaps 13;

QY 25 NLKQI---YYNSKATISSE-----KSADQFLTNTLLFKGFFTGHPWYNDLL-- 68
Db 5 NIKDLWDYSSGSDFTNSEVLNDSGSMRIKNTDGSI-SLIIFPS-----PYSPATK 58

QY 69 ---VLDGSTAAATSEYSGSVVDLYGAYGYQCAGTGNKTACMYGVTLHDNNRLTEKKV 125
Db 59 GEKVDL-NIKRTKKSQHTS---EGTVIHFIQISGVT-----NTEKLPPIEL 100

QY 126 PINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KV 179
Db 101 PLKVKVHGKDSPLKYWP-----KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKI 156

QY 180 QRGILVHFSSEGSTVSVDL 198
Db 157 T-----MNDGSTYQSDL 168

RESULT 66
US-10-354-948-6
; Sequence 6, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Potter, Terence A.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/354,948
APPLICATION DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-354-948-6

Query Match      8.0%; Score 98; DB 12; Length 194;
Best Local Similarity 24.6%; Pred. No. 0.13;
Matches 49; Conservative 33; Mismatches 57; Indels 60; Gaps 13;

QY 25 NLKQI---YYNSKAITSE-----KSADQFLNTLLFKGFTGHPWYNDLL-- 68
DB 5 NIKOLLDWSSGSDFTNSEVLNLSGWRINKNTDGS-I-SLIIIPS-----PYISPAFTK 58
QY 69 ---VDLGSTAATSEEGSSVDLYGAYGYQCAGT--PNTACMYGVGVTLHDNNRTEKKV 125
DB 59 GEKVDL-NTRKTKSQHTS---EGTYIHFIQSGVT-----NTEKLPTEIPL 100
QY 126 PINLWDGKQTTV---PIDKVKTSKKEVTQVQLDQAARHYLHGKFLY--NSDSFGG--KV 179
DB 101 PLKRVHGDSPKWP-----KFDKKQLAISTLDFEIRHQLTQIHGLYRSDKTKGTGWKI 156
QY 180 QRGLIVFHSSEGSTVSVDL 198
DB 157 T-----MNDGSTYQSDL 168

RESULT 67
US-10-282-122A-70243
Sequence 70243, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/354,948
APPLICATION DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-354-948-6

Query Match      8.0%; Score 98; DB 12; Length 227;
Best Local Similarity 26.4%; Pred. No. 0.16;
Matches 53; Conservative 28; Mismatches 78; Indels 42; Gaps 9;

QY 8 NEKDKRKSELQGTALGNLKOIY-YYNSKAITSEKSADQFLNTLLFKGFTGHPWYND 66
DB 33 NQKSVNKHDK-----EALYRYTGTMTWEMKNISALKHKNLRFK--FRGIKIQVL 81
QY 67 LLVDLGSTAATSEEGSSV-----DLYGAYGYQCAGT--PNTACMYGVGVTLHDNN 117
DB 82 LPGNDDKSKFQORSYEGLDVFFVQEKRDKHIFY---TVGGVIQNNKTS-----GVVSAPIL 134
QY 118 RTEKKKYPINLWDGKQTTVPIDKVKTSKKEVTQVQLDQAARHYLHGKFLYNSDSFGG 177
DB 135 NISKEK-----GEDAFVKGYPIYKKEKITLKELDYKLRKHLIERKLYGTISKOG 185
QY 178 KVQRGLIVFHSSEGSTVSVDL 198
DB 186 RVKISL-----KDGsfYNLDL 201

RESULT 68
US-10-282-122A-70390
Sequence 70390, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/207,727

```

```

RESULT 71
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
;
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:

```


; Sequence 191455, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 191455
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87772C.1.pap
US-10-437-963-191455

Query Match 7.6%; Score 92; DB 16; Length 600;
Best Local Similarity 20.5%; Pred. No. 2.6; Indels 76; Gaps 8;
Matches 45; Conservative 30; Mismatches 68; Indels 76; Gaps 8;
QY 24 GNLKQIYYNSKAITSSSEKADQFLNTLLPKGFTGHPWYNDLLVLDLGSTAAATSEYEGS 83
Db 79 GNI-PIYACSGTAISQEGSGIFLTSASLVRAFYDTEIYDNLKIEV-----RHEGN 130
QY 84 SVDLGAYGYGQAGGTENKTAACMGVTLHNNRLTEKKYPINLWDGKQTTVPIDKV 143
Db 131 EV-----YKGLAKYDLDKFNFAVY----- 150
QY 144 KTSKKEVTVOELDLQ---ARH-----YLHGKFGLYNSDSFGGKVGQRLIV--PHSSEGSTV 194
Db 151 -----TWESLDVHVVLSEHLKDRYAKKLVAVSRNKYGGILITKSVVMVGHSHNSRSEV 203
QY 195 SYD-----LFDAGQGYPTLLRIYRDNNTISS 221
Db 204 CHDISVNAEDWEGGPLDFDGRFVGMKNKFLAMDITFILS 242

RESULT 75
US-10-435-766-23
; Sequence 23, Application US/10435766
; Publication No. US20030228616A1
; GENERAL INFORMATION:
; APPLICANT: Strategene
; APPLICANT: Sorge, Joseph A
; APPLICANT: Arezi, Bahram
; APPLICANT: Hogrefe, Holly
; APPLICANT: Hansen, Connie J
; TITLE OF INVENTION: DNA Polymerase Mutants with Reverse Transcriptase Activity
; FILE REFERENCE: 25436/1565C
; CURRENT APPLICATION NUMBER: US/10/435,766
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 10/223,650
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 09/896,923
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/698,341
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,600
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/29706
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23

; LENGTH: 1634
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (382)..(382)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-435-766-23
Query Match 7.5%; Score 91; DB 15; Length 1634;
Best Local Similarity 21.6%; Pred. No. 14;
Matches 50; Conservative 36; Mismatches 79; Indels 66; Gaps 10;
QY 12 LRKSELOGTALGNLQIYYVNSKAITSSSEKADQFLNTLLPKGFTGHPWYNDLLVLDL 71
Db 614 VRRKGTGKAITLGCAKADYLLKIEEL---KNKEKYLPAAIL-RGFFEGDGVNTRRAV 669
QY 72 GSTAATSEYE-----GSSVDLYGAYGYGQAGGTENKTAACMGVTLHNNRLTEKKVP 126
Db 670 VVNGQTNVYDKIKFIASLLDLRLGKIYSP-----YTYSEERGKKLKRYV 713
QY 127 INLWIDGKQTTVPIDKVKTS-----KKEVTVOELDLQARHLYHGKFGLYNSD----- 173
Db 714 IEIFSKG-----DLIKFSILISFISRRNNLLNLEIRQKLYLKIDYGFYDLDDVCVS 766
QY 174 --SFGGKV-----QRGLIVFHSSEGS-TVSYDLFDAQGYPTLL 209
Db 767 LESYKGEVVDLTLEGRPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

Search completed: August 12, 2004, 13:46:20
Job time : 26.7742 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 9.21353 Seconds
(without alignments)
1305.563 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEXDLKXKSELOG.....RDNTTISSTLSISLXLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1107	90.9	233	4	US-08-695-692B-8
2	1107	90.9	257	3	US-08-486-099-112
3	1107	90.9	257	3	US-08-360-107A-122
4	1107	90.9	257	3	US-08-484-223B-112
5	1107	90.9	257	3	US-08-919-597-112
6	1107	90.9	257	3	US-08-475-668A-112
7	1107	90.9	257	3	US-08-485-551A-112
8	1107	90.9	257	3	US-08-471-913A-112
9	1107	90.9	257	4	US-08-474-349A-112
10	1107	90.9	257	4	US-08-470-896-112
11	1107	90.9	257	4	US-08-485-546A-112
12	1107	90.9	257	3	US-08-896-933-24
13	1040	85.4	226	3	US-08-896-933-24
14	1040	85.4	226	4	US-08-314-235-24
15	948	77.8	233	4	US-08-695-692B-7
16	948	77.8	257	3	US-08-486-099-113
17	948	77.8	257	3	US-08-360-107A-123
18	948	77.8	257	3	US-08-484-223B-113
19	948	77.8	257	3	US-08-919-597-113
20	948	77.8	257	3	US-08-475-668A-113
21	948	77.8	257	3	US-08-485-551A-113
22	948	77.8	257	3	US-08-471-913A-113
23	948	77.8	257	3	US-08-485-546A-113
24	948	77.8	257	4	US-08-474-349A-113
25	948	77.8	257	4	US-08-470-896-113
26	948	77.8	257	4	US-08-485-546A-113
27	944	77.5	233	1	US-08-446-918A-4

28	944	77.5	233	2	US-08-580-806-4	Sequence 4, Appli
29	931.5	76.5	232	3	US-08-896-933-23	Sequence 23, Appl
30	931.5	76.5	232	4	US-09-314-235-23	Sequence 23, Appl
31	925	75.9	237	4	US-09-144-776B-2	Sequence 2, Appli
32	921	75.6	233	4	US-09-144-776B-4	Sequence 4, Appli
33	605	49.7	228	3	US-08-896-933-25	Sequence 25, Appl
34	605	49.7	228	4	US-09-314-235-25	Sequence 25, Appl
35	406	33.3	82	4	US-09-144-776B-19	Sequence 19, Appl
36	362	29.7	82	4	US-09-144-776B-17	Sequence 17, Appl
37	277.5	22.8	238	3	US-08-896-933-28	Sequence 28, Appl
38	277.5	22.8	238	4	US-09-314-235-28	Sequence 28, Appl
39	270.5	22.2	221	3	US-08-896-933-29	Sequence 29, Appl
40	270.5	22.2	221	4	US-09-314-235-29	Sequence 29, Appl
41	268.5	22.0	251	4	US-08-973-391C-13	Sequence 13, Appl
42	267.5	22.0	255	1	US-08-446-918A-2	Sequence 2, Appli
43	267.5	22.0	255	2	US-08-580-806-2	Sequence 2, Appli
44	265.5	21.8	221	4	US-08-973-391C-14	Sequence 14, Appl
45	264.5	21.7	239	3	US-08-896-933-27	Sequence 27, Appl
46	264.5	21.7	239	4	US-09-314-235-27	Sequence 27, Appl
47	263.5	21.6	251	4	US-09-144-776B-16	Sequence 16, Appl
48	260.5	21.4	239	3	US-08-896-933-26	Sequence 26, Appl
49	260.5	21.4	239	4	US-09-314-235-26	Sequence 26, Appl
50	260.5	21.4	266	4	US-09-414-276-8	Sequence 8, Appli
51	260.5	21.4	266	4	US-09-144-776B-6	Sequence 6, Appli
52	255.5	21.0	239	4	US-09-144-776B-14	Sequence 10, Appl
53	255.5	21.0	266	4	US-09-144-776B-14	Sequence 14, Appl
54	250.5	20.6	266	4	US-09-144-776B-8	Sequence 8, Appli
55	225.5	18.5	239	3	US-08-896-933-21	Sequence 21, Appl
56	225.5	18.5	239	4	US-09-314-235-21	Sequence 21, Appl
57	220	18.1	220	3	US-08-896-933-20	Sequence 20, Appl
58	220	18.1	220	4	US-09-314-235-20	Sequence 20, Appl
59	194	15.9	82	4	US-09-144-776B-18	Sequence 18, Appl
60	189	15.5	45	1	US-08-220-378-1	Sequence 1, Appli
61	189	15.5	45	2	US-08-696-012-1	Sequence 1, Appli
62	150	12.3	208	3	US-08-896-933-30	Sequence 30, Appl
63	150	12.3	208	4	US-09-314-235-30	Sequence 30, Appl
64	131	10.8	27	3	US-08-896-933-34	Sequence 34, Appl
65	131	10.8	27	4	US-09-314-235-34	Sequence 34, Appl
66	127	10.4	24	3	US-08-838-413A-22	Sequence 22, Appl
67	126	10.3	23	1	US-08-220-378-5	Sequence 5, Appli
68	126	10.3	23	2	US-08-696-012-5	Sequence 5, Appli
69	124	10.2	29	1	US-08-220-378-6	Sequence 6, Appli
70	124	10.2	29	2	US-08-696-012-6	Sequence 6, Appli
71	112	9.2	79	4	US-09-144-776B-24	Sequence 24, Appl
72	111.5	9.2	89	4	US-09-144-776B-20	Sequence 20, Appl
73	110	9.0	22	1	US-08-220-378-4	Sequence 4, Appli
74	110	9.0	22	2	US-08-696-012-4	Sequence 4, Appli
75	107	8.8	28	1	US-08-220-378-2	Sequence 2, Appli
76	107	8.8	28	2	US-08-696-012-2	Sequence 2, Appli
77	106	8.7	28	1	US-08-220-378-7	Sequence 7, Appli
78	106	8.7	28	2	US-08-696-012-7	Sequence 7, Appli
79	101.5	8.3	29	1	US-08-220-378-9	Sequence 9, Appli
80	101.5	8.3	29	2	US-08-696-012-9	Sequence 9, Appli
81	100	8.2	28	1	US-08-220-378-8	Sequence 8, Appli
82	100	8.2	28	2	US-08-696-012-8	Sequence 8, Appli
83	100	8.2	234	3	US-08-486-099-111	Sequence 11, App
84	100	8.2	234	3	US-08-360-107A-121	Sequence 121, App
85	100	8.2	234	3	US-08-484-223B-111	Sequence 111, App
86	100	8.2	234	3	US-08-919-597-111	Sequence 111, App
87	100	8.2	234	3	US-08-475-668A-111	Sequence 111, App
88	100	8.2	234	3	US-08-485-546A-111	Sequence 111, App
89	100	8.2	234	3	US-08-471-913A-111	Sequence 111, App
90	100	8.2	234	4	US-08-485-546A-111	Sequence 111, App
91	100	8.2	234	4	US-08-474-349A-111	Sequence 111, App
92	100	8.2	234	4	US-08-470-896-112	Sequence 12, Appl
93	100	8.2	234	4	US-08-470-896-111	Sequence 11, App
94	100	8.2	234	4	US-08-485-546A-111	Sequence 11, App
95	99.5	8.2	89	4	US-09-144-776B-21	Sequence 21, Appl
96	99.5	8.2	193	3	US-08-896-933-31	Sequence 31, Appl
97	99.5	8.2	193	4	US-09-314-235-31	Sequence 31, Appl
98	98	8.0	194	1	US-08-446-918A-6	Sequence 6, Appli
99	98	8.0	194	2	US-08-580-806-6	Sequence 6, Appli
100	97.5	8.0	89	4	US-09-144-776B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-08-695-692B-8
 ; Sequence 8, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692B
 ; FILING DATE: August 12, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-695-692B-8

Query Match 90.9%; Score 1107; DB 4; Length 233;
 Best Local Similarity 89.7%; Pred. No. 2.5e-110; Indels 0; Gaps 0;
 Matches 209; Conservative 9; Mismatches 15;

QY 1 SEKSEINEKDLRKSELOQTALGNLQKQIYYNSKAITSEKSDAQFLNTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOQTALGNLQKQIYYNSKAITSEKSDAQFLNTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSATATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVDLGSATATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 2
 US-08-486-099-112

; Sequence 112, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,099
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cortuzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-031
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8964
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-486-099-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
 Best Local Similarity 89.7%; Pred. No. 2.9e-110; Indels 0; Gaps 0;
 Matches 209; Conservative 9; Mismatches 15;

QY 1 SEKSEINEKDLRKSELOQTALGNLQKQIYYNSKAITSEKSDAQFLNTLLFKGFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLQKQIYYNSKAITSEKSDAQFLNTLLFKGFTG 84

QY 61 HPWYNDLLVDLGSATATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HPWYNDLLVDLGSATATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 3
 US-08-360-107A-122
 ; Sequence 122, Application US/08360107A
 ; Patent No. 6017536
 ; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO.: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

```

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYYNKRAITSSSEKSADQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYYNKRAITSSSEKSADQFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGGTATSYEGSSVDLYGAYGYQCAGGTPNKTCACMGVYGLHNNRLT 120
DB 85 HPWYNLLVDLGGKDATYIKGKKVDLYGAYGYQCAGGTPNKTCACMGVYGLHNNRLT 144
QY 121 EEKVPINLWIDGQTTPIDVKVTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGQTTPIDVKVTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSSGSTVSVDLFDAGQYPTDLLRIYRONTTISSTLSISLYTT 233
DB 205 RGLIVFHSSSGSTVSVDLFDAGQYPTDLLRIYRONTTINSENHIDLYLYTT 257

RESULT 5
US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.

```

APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TITLE OF INVENTION: TRANSMISSION
 NUMBER OF SEQUENCES: 273
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/919,597

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/470,896

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-020

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-919-597-112

Query Match 90.9%; Score 1107; DB 3; Length 257;

Best Local Similarity 89.7%; Pred. No. 2.9e-110;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 60

DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 84

QY 61 HPWYNDLLVLDGSKATNKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 85 HPWYNDLLVLDGSKATNKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 180

DB 145 EEKVPINLWIDGKQTTPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 204

QY 181 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233

DB 205 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 257

RESULT 6

US-08-475-668A-112

Sequence 112, Application US/08475668A

Patent No. 6060065

GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,668A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-026

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-475-668A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;

Best Local Similarity 89.7%; Pred. No. 2.9e-110;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 60

DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 84

QY 61 HPWYNDLLVLDGSKATNKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 85 HPWYNDLLVLDGSKATNKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 180

DB 145 EEKVPINLWIDGKQTTPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 204

QY 181 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233

DB 205 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 257

RESULT 7

US-08-485-551A-112

Sequence 112, Application US/08485551A

Patent No. 6069973

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOQYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGOQYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 8
US-08-471-913A-112
Sequence 112, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOQYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGOQYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 9
US-08-485-264A-112
Sequence 112, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112

```

```

Query Match          90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQPLNTLLPKGFTG 60
   |||||
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFTG 84
   |||||

QY 61 HPWYNDLLVLDGKATNTKYGAYGYOCAGGTPNKTACWYGGVTLHDNNELT 120
   |||||
Db 85 HPWYNDLLVLDGKATNTKYGAYGYOCAGGTPNKTACWYGGVTLHDNNELT 144
   |||||

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
   |||||
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSVSYDLFDAQCYPTLLRIYRDNTTISSTLSLSLYTT 233
   |||||
Db 205 RGLIVFHSSEGSVSYDLFDAQCYPTLLRIYRDNTTISSTLSLSLYTT 257
   |||||

```

```

RESULT 10
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112

Query Match          90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQPLNTLLFKGFTG 60
   |||||
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFTG 84
   |||||

QY 61 HPWYNDLLVLDGKATNTKYGAYGYOCAGGTPNKTACWYGGVTLHDNNELT 120
   |||||
Db 85 HPWYNDLLVLDGKATNTKYGAYGYOCAGGTPNKTACWYGGVTLHDNNELT 144
   |||||

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
   |||||
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSVSYDLFDAQCYPTLLRIYRDNTTISSTLSLSLYTT 233
   |||||
Db 205 RGLIVFHSSEGSVSYDLFDAQCYPTLLRIYRDNTTISSTLSLSLYTT 257
   |||||

RESULT 11
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896

```

/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-470-896-112

Query Match 90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTG 84

Qy 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/485,546A
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-485-546A-112

Query Match 90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTG 84

Qy 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 13
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-24

Query Match 85.4%; Score 1040; DB 3; Length 226;
Best Local Similarity 85.2%; Pred. No. 3.6e-103;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

Qy 4 SEBINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTGHPW 63
Db 1 SEBINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDQFLNTLLFKGFFTGHPW 60

Qy 64 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDGSKDQATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTEB- 119

Qy 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVQGL 183
Db 120 ---VBKWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVQGL 176

QY 184 IVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 233
DB 177 IVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 226

RESULT 14

US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-09-314-235-24

Query Match 85.4%; Score 1040; DB 4; Length 226;
Best Local Similarity 85.2%; Pred. No. 3.6e-103;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;
QY 4 SEBINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLPKGFTHPW 63
DB 1 SEBINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLPKGFTHPW 60
QY 64 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEK 123
DB 61 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEK 119
QY 124 KVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 120 ---VBKWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRL 176
QY 184 IVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 233
DB 177 IVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 226

RESULT 15

US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamsen and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; FILE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston

STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692B
FILING DATE: August 12, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 77.8%; Score 948; DB 4; Length 233;
Best Local Similarity 76.4%; Pred. No. 2.6e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 120
QY 121 BEKVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQ 180
DB 121 BEKVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQ 180
QY 181 RGLIVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 233
DB 181 RGLIVFHSSEGSTVSYDLFPAQGYPTDILLRIYRNTTISSTLSISLYLTT 233

RESULT 16

US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Biognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Larois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; FILE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PATENT IN RELEASE #1.0, Version #1.30
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAOFNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAOFNTLLFKGFTTG 84
QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTISLSISLYTT 233
Db 205 RGLIVHSTSPSVNYDLFGAQGGYSNTLLRIYRDNNTTINSENHIDIYLYTS 257

RESULT 17
US-08-360-107A-123 -
Sequence 123 Application US/08360107A
Patent No. 6017336
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
PATENT IN RELEASE #1.0, Version #1.30
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAOFNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAOFNTLLFKGFTTG 84
QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTTISLSISLYTT 233
Db 205 RGLIVHSTSPSVNYDLFGAQGGYSNTLLRIYRDNNTTINSENHIDIYLYTS 257

RESULT 18
US-08-484-223B-113
Sequence 113 Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CLASSIFICATION: PRIOR APPLICATION DATA: US 08/470,896
APPLICATION NUMBER: 06-JUN-1995
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADOFINTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYNLYNSDVFQKVQ 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDILLRIYRDNTTISSTLSISLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHDIYLYTS 257

CLASSIFICATION: PRIOR APPLICATION DATA: US 08/470,896
APPLICATION NUMBER: 06-JUN-1995
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADOFINTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYNLYNSDVFQKVQ 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDILLRIYRDNTTISSTLSISLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 20
US-08-475-668A-113
Sequence 113, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

RESULT 19
US-08-919-597-113
Sequence 113, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Boicognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langleis, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:

REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 77.8%; Score 948; DB 3; Length 257;

Best Local Similarity 76.4%; Pred. No. 3.1e-93;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVYKGGKVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYSTNLLRIYRDNKTINSENHDIYLYTS 257

RESULT 21

US-08-485-551A-113

Sequence 113, Application US/08485551A

Patent No. 6068973

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 211

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,551A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-023

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 77.8%; Score 948; DB 3; Length 257;

Best Local Similarity 76.4%; Pred. No. 3.1e-93;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVYKGGKVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLYGAYGYCCAGTGNKTACMYGGVTLHNNRLT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQGYSTNLLRIYRDNKTINSENHDIYLYTS 257

RESULT 22

US-08-471-913A-113

Sequence 113, Application US/08471913A

Patent No. 6093794

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Petteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 214

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,913A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNNSKAITSEKSAOQPLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNNEKAKTENKESHQDLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTSSLSLSLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKNTINSENNHDIYLYTS 257

RESULT 23
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 628983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNNSKAITSEKSAOQPLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNNEKAKTENKESHQDLOHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTSSLSLSLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKNTINSENNHDIYLYTS 257

RESULT 24
US-08-474-349A-113
Sequence 113, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOCS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

Query Match	77.8%	Score 948	DB 4	Length 257
-------------	-------	-----------	------	------------

QY 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNSKAITSSSEKADQFLNTLTLFKGFFTG 60
 Db 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVDFDSDKIDVYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKXVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 Db 145 EEKVPINLWDGKQNTVPLETVTKNKVTVQELDLQARRYLQEKYLYNSDVFDEGKQV 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 257
 RESULT 27
 US-08-446-918A-4
 ; Sequence 4, Application US/08446918A
 ; Patent No. 5705151
 ; GENERAL INFORMATION:
 ; APPLICANT: Dow, Steve W.
 ; APPLICANT: Elmslie, Robyn E.
 ; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross & McIntosh
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado
 ; COUNTRY: U.S.A.
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,918A
 ; FILING DATE: 18-MAY-1995
 ; CLASSIFICATION: 552
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kovarik, Joseph E.
 ; REGISTRATION NUMBER: 33,005
 ; REFERENCE/DOCKET NUMBER: 2879-29
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-918A-4
 Query Match 77.5%; Score 944; DB 1; Length 233;
 Best Local Similarity 76.3%; Pred. No. 7.1e-93;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKKSELOQTALGNLQIYYNSKAITSSSEKADQFLNTLTLFKGFFTG 61
 Db 2 EKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 61
 QY 62 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVDFDSDKIDVYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWDGKQTTVPIDKVKTSKXVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
 Db 122 EKKVPINLWDGKQNTVPLETVTKNKVTVQELDLQARRYLQEKYLYNSDVFDEGKQV 181
 QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
 Db 181 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 257
 RESULT 29
 US-08-896-933-23
 ; Sequence 23, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.

QY 182 GLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 233
 RESULT 28
 US-08-580-806-4
 ; Sequence 4, Application US/08580806
 ; Patent No. 5935568
 ; GENERAL INFORMATION:
 ; APPLICANT: Dow, Steve W.
 ; APPLICANT: Elmslie, Robyn E.
 ; APPLICANT: Potter, Terence A.
 ; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross & McIntosh
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado
 ; COUNTRY: U.S.A.
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/580,806
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Connell, Gary J.
 ; REGISTRATION NUMBER: 32,020
 ; REFERENCE/DOCKET NUMBER: 2879-29-C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-580-806-4
 Query Match 77.5%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 7.1e-93;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKKSELOQTALGNLQIYYNSKAITSSSEKADQFLNTLTLFKGFFTG 61
 Db 2 EKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 61
 QY 62 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVDFDSDKIDVYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWDGKQTTVPIDKVKTSKXVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
 Db 122 EKKVPINLWDGKQNTVPLETVTKNKVTVQELDLQARRYLQEKYLYNSDVFDEGKQV 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 233
 RESULT 29
 US-08-896-933-23
 ; Sequence 23, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.

```

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match      76.5%; Score 931.5; DB 3; Length 232;
Best Local Similarity 76.0%; Pred. No. 1.5e-91;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 60
Db 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 59
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 60 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVEQDLQARHYLHGKFGLYNSDSFGKGKQV 180
Db 120 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVEQDLQARHYLHGKFGLYNSDSFGKGKQV 179
QY 181 RGLIVFHSSEGSTVSYDLFDAGQVPTDILLRIYRDNNTTISLSISLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAGQVSNLLRIYRDNNTTISLSISLYTT 232

```

```

RESULT 31
US-09-144-776B-2
; Sequence 2, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

```

```

Query Match      75.9%; Score 925; DB 4; Length 257;
Best Local Similarity 75.1%; Pred. No. 8.9e-91;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 60
Db 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNRLT 120

```

```

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match      76.5%; Score 931.5; DB 3; Length 232;
Best Local Similarity 76.0%; Pred. No. 1.5e-91;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 60
Db 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 59
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 60 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYOCAGGTPNKTAACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVEQDLQARHYLHGKFGLYNSDSFGKGKQV 180
Db 120 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVEQDLQARHYLHGKFGLYNSDSFGKGKQV 179
QY 181 RGLIVFHSSEGSTVSYDLFDAGQVPTDILLRIYRDNNTTISLSISLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAGQVSNLLRIYRDNNTTISLSISLYTT 232

```

```

RESULT 30
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-23

```

```

Query Match      76.5%; Score 931.5; DB 4; Length 232;
Best Local Similarity 76.0%; Pred. No. 1.5e-91;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTTG 60

```

Db 85 HSWNDLLVRPDSKDIDVKYKGGKVDLYGAVAGYQACGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQV 180
Db 145 EKKVPINLWIDGKQNTVPLETVKTKNKQNTVQELDLQARRYLOEKYLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKINSENHDIYLYTS 257

RESULT 32
US-09-144-7765-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 75.6%; Score 921; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 2e-90;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEENKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTTCH 61
Db 2 EKSEENKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDQFRQRTLLFKGFFTDH 61

QY 62 PWTNDDLVLGSTAATSEYEGSSVDLYGAYGQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWNDLLVRPDSKDIDVKYKGGKVDLYGAVAGYQACGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQV 181
Db 122 EKKVPINLWIDGKQNTVPLETVKTKNKQNTVQELDLQARRYLOEKYLYNSDVDFGKQV 181
QY 182 GLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKINSENHDIYLYTS 233

RESULT 33
US-08-896-933-25
; Sequence 25, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
; US-08-896-933-25

Query Match 49.7%; Score 605; DB 3; Length 228;
Best Local Similarity 52.0%; Pred. No. 1.3e-56;
Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

QY 7 INKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTTCH 66
Db 2 VKEKELHKKSELSSTALNNKHSYADKNPIGENKSTGDFLENTLLYKKFFTDLINFED 61

QY 67 LLDLGSSTAATSEYEGSSVDLYGAYGQCAGGTPNKTACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKNVDVPIRISINCYGEIDRTACTYGGVTPHEGNLKEKKIP 121

QY 127 INLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQVGLIVF 186
Db 122 INLWINGVQKEVSLDKVQTDKNVTVQELDLQARRYLOEKYLYNSDVDFGKQV 181

QY 187 HSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLY 231
Db 182 DSSDGSKSVSYDLFQVKGDFPEKQIRIYSONKTLSTEHLDIYLY 226

RESULT 34
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match 49.7%; Score 605; DB 4; Length 228;
Best Local Similarity 52.0%; Pred. No. 1.3e-56;
Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOQTALCNLKOIYYVNSKATTSSEKSAADQFLTNTLLFKGFFTGHPWYND 66
Db 2 VKKELHKKSLSSTALNNMKGSHADKNPIIGENKSTGDFLENTLLYKKFFDTDLINFED 61
QY 67 LLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNTACMYGVTLDHNNRLTEKKVP 126
Db 62 LLINFNSKEMAHQFKSKNVDPYPIRYINCYGGIBDTACTYGGVTPEHGNKLKERKKIP 121
QY 127 INLWDGKQTVVPIDKVKTSKKEVTVOELDLQARHYLHGRFGLYNSDSFGKVGQRLIVF 166
Db 122 INLWINGVQKESLDKVDKNTVQELDLQARHYLHGRFGLYNSDSFGKVGQRLIVF 166
QY 187 HSEGSTVSYDLFPAQGOYPTLLRIYRDNNTTISSTLSISLXLY 231
Db 182 DSDGSKVSYDLFVKGDFPEKQLRIYSDNKTLSLTHLHIDVLY 226

RESULT 35
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid

Query Match 29.7%; Score 362; DB 4; Length 82;
Best Local Similarity 79.3%; Pred. No. 2.8e-31;
Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 43 SADQFLTNTLLFKGFTGHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPN 102

; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19

Query Match 33.3%; Score 406; DB 4; Length 82;
Best Local Similarity 89.0%; Pred. No. 5.6e-36;
Matches 73; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 43 SADQFLTNTLLFKGFTGHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPN 102
Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDANKYNGKKVDLYGAYGQCAGGTPN 60
QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 36
US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match 29.7%; Score 362; DB 4; Length 82;
Best Local Similarity 79.3%; Pred. No. 2.8e-31;
Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 43 SADQFLTNTLLFKGFTGHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPN 102

Db

1 SHQQLQHTILFKGFTDHSWYNDLAVDFSDKIDVRYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124

Db
61 KTACMYGGVTLHDNNRLTEKK 82

RESIST 37

```

RES011 37
US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28

```

Query Match	22.8%	Score	277.5	DB 3	Length	238
Best Local Similarity	32.5%	Pred. No.	1.6e-21			
Matches	76	Conservative	44	Mismatches	95	Indels
					19	Gaps
						9

QY	11	DLRKSELEQGTALGNLKQIIVYNSKAITSS--KSADQFLTNTLLFKGFFTHGPVNDLLV	69
DB	9	ELHKSSEFTGT--GNMK--VLYDDHYVSATKMSVDKFLAHLIINISDKLKNYDKVKYT	65
QY	70	DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTGNPKTACMYGGVTLHDNNRLTEE	122
DB	66	ELLNEDIAKKYDKBWDVYGSNYVNCYFSSKDNVGGKVTGCGKITCYGGITHEGNHFDNG	125
QY	123	--KKVPLNLMTDGRQTTVPIDKVTSKETVTVQELDLOARHYLHGCKFGLYNSDSFGGKVQ	180
DB	126	NLQNWLRVY--ENKRNITISEP--VOTDKSSVTAQELDKARNELINKNLYEFNS--SPYE	181
QY	181	RGLIVFSSSEGSTVSYDLFAQCQCPD--TLARIYRDNTTISSLSISLYLT	232
DB	182	TGYIKFTEINGNTFWYDLMPAPGDKFDOSKYLMTYNDNKTVDNSKVKTEVHTTT	235

RESULT 39
US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03

```

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PaatSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: prt
; ORGANISM: Staphylococcus aureus
US-09-114-235-28

```

[illegible]


```
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match      22.2%; Score 270.5; DB 4; Length 221;
Best Local Similarity 33.8%; Pred. No. 8.1e-21;
Matches 76; Conservative 42; Mismatches 88; Indels 19; Gaps 10;

QY      16  SELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLNTLLFKGFFTHPHWYNDLLVDLG 72
DB      7  SOLHRSVLXNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGENYDKLTKELK 63

QY      73  STAATSEYEGSVLDYGAAYGYQC-AGGTPNKTACMYGGVTLHNNRLTEKKVPINLWI 131
DB      64  NQEMATLFDKKNVDIYGVVEYHLCVLCENASRSACIYGGVTNHEGHNLEIPKKIWKVSI 123

QY      132 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVFHSSEG 191
DB      124 DGIO-SLSFD-IFTNKQWVTAQELDYKVRKYLTDNKLQYTNGP--SKYETGYIKFIPNK 179

QY      192 STVSVDLPD----AQGOYPTLLRIYRDNNTTISSTLSISLYLT 232
DB      180 ESFWEDLPPEPFTQSKY----LMYKDNETLDSNTSQIEVLYLT 220

RESULT 41
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Chlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USNO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes

; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match      22.0%; Score 268.5; DB 4; Length 251;
Best Local Similarity 32.5%; Pred. No. 1.6e-20;
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;

QY      4  SBEINEKDLRKKESELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLNTLLFKGFFTHG 60
DB      25  SQEFAQQDPDPSQLHRSVLXNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VS 81

QY      61  HPWYNDLLVDLGSTAATSEYEGSVLDYGAAYGYQC-AGGTPNKTACMYGGVTLHNNRL 119
DB      82  GPNYDKLTKELKNQEMATLFDKKNVDIYGVVEYHLCVLCENASRSACIYGGVTNHEGHN 141

QY      120 TEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
DB      142 ETPKKIIVKVSIDGQIQ-SLSFD-IFTNKQWVTAQELDYKVRKYLTDNKLQYTNGP--SKY 197

QY      180 QRLGIVFHSSEGSTVSVDLPD----AQGOYPTLLRIYRDNNTTISSTLSISLYLT 232
DB      198 ETGYIKFIPKNKESFWDFPPEFTQSKY----LMYKDNETLDSNTSQIEVLYLT 250

RESULT 42
US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match      22.0%; Score 267.5; DB 1; Length 255;
Best Local Similarity 31.7%; Pred. No. 2.1e-20;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;

QY      2  EKSEINEKDLRKKESELQGTALGNLQIYYNSKAITSEKSAQDQFLNTLLFKGFFTHG 61
DB      17  ESQDPKPELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQLYDLIVSIKDTKL 74

QY      62  PWNDDLVDLGSTAATSEYEGSVLDYGAAYGYQC-----AGGTPNKTACMYGGV 111
```

Db 75 GNYDNRVRFKNDLADKYDKYVDVFGAGYNYQCYFSSKKTNDINSHQTDKKTCTMYGGV 134
QY 112 TLHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNLDKYSITVRVFDGK-NLLSFD-VQTNKKKYTAQELDYLRHYLVKNNKLYE 192
QY 172 SDSFGKVGORGLIVFHSSSGSTVSVDLFDAGQGYPD--TLRIYRDNTTISTSLISLY 229
Db 193 FNN--SPYETGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNKWDKDKVIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 43
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-2

Query Match 22.0%; Score 267.5; DB 2; Length 255;
Best Local Similarity 31.7%; Pred. No. 2.1e-20;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;

QY 2 EKSENEKDLRKSSELOGTALGNLQIYYNSKAITSEKSADQFLTNLLFKGFFTGH 61
Db 17 ESQDPKPDDELKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLFDLLIYSKOTKL 74
QY 62 PWINDLLVDLGSATSEYEGSSVDLYGAYGYQC-----AGETPNKTCMYGGV 111
Db 75 GNYDNRVRFKNDLADKYDKYVDVFGAGYNYQCYFSSKKTNDINSHQTDKKTCTMYGGV 134
QY 112 TLHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNLDKYSITVRVFDGK-NLLSFD-VQTNKKKYTAQELDYLRHYLVKNNKLYE 192
QY 172 SDSFGKVGORGLIVFHSSSGSTVSVDLFDAGQGYPD--TLRIYRDNTTISTSLISLY 229

Db 193 FNN--SPYETGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNKWDKDKVIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 44
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Orlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 21.8%; Score 265.5; DB 4; Length 221;
Best Local Similarity 33.3%; Pred. No. 2.8e-20;
Matches 75; Conservative 42; Mismatches 89; Indels 19; Gaps 10;

QY 16 SELQGTAL-GNLQIYY-YNSKAIT-SSEKSADQFLTNLLFKGFFTGHFWYNDLLVDLG 72
Db 7 SOLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN---VSGENYDKLKTCLK 63
QY 73 STATSEYEGSSVDLYGAYGYQC-AGETPNKTCMYGGVTLHNNRLTEEEKVPINLMI 131
Db 64 NOEATLFDKQNDIYGVVEYHLCYCENAEBSACIYGGVTHNEGHNHLEIPKKIYVKSVI 123
QY 132 DGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGORGLIVFHSSEG 191
Db 124 DGIQ-SLSFD-IETNKKWVTAQELDYKVKYLTLDNKQLYTNGP--SKYETGYIKFIPKKN 179
QY 192 STVSVDLFD---AQGYPTLLRIYRDNTTISTSLISLYLT 232
Db 180 ESFWDFPEPEPTQSKY----LMIYDNETLDSNTSQIEVYLT 220

RESULT 45
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-08-896-933-27

Query Match 21.7%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSBEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQPDPTDELHKASKFTG-LMENNKVLYDDHYVS---ATKVKSVDFLAHDLIYNISDK 56
 QY 60 GHPWYNDLLDLGTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCYFSSKDNVGVKVTGGKTCMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174
 QY 171 NSDSFGGKVQORGLIVFHSSEGSTSVYDLFDAQGOYPD--TLRIYRNDNTTISSTLSISL 228
 DB 175 EFNS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEV 232
 QY 229 YLYT 232
 DB 233 HLTT 236

RESULT 47
 US-09-144-776B-16
 ; Sequence 16, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Sina Bavazi
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Charles H. Harris
 ; STREET: US Army MPMC -504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 251
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-144-776B-16

Query Match 21.6%; Score 263.5; DB 4; Length 251;
 Best Local Similarity 32.1%; Pred. No. 5.5e-20;
 Matches 76; Conservative 45; Mismatches 97; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 60
 DB 25 SQSVFAQQDPDPSQLHRSSLVKLNQIYFLYEGDPVTENKSVQDLRSHDLIYN---VS 81
 QY 61 HPWYNDLLDLGTAATSEYEGSSVDLYGAYGYQC--AGGTPNKATCMYGGVTLHDNNRL 119
 DB 82 GPNYDKLTKELNQEAMATLFKDNVDIYGVYHLYCLENASERSACIIGGVTNHGNHL 141
 QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKV 179

us-09-900-766-2.ra1

US-08-896-933-27

Query Match 21.7%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSBEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQPDPTDELHKASKFTG-LMENNKVLYDDHYVS---ATKVKSVDFLAHDLIYNISDK 56
 QY 60 GHPWYNDLLDLGTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCYFSSKDNVGVKVTGGKTCMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174
 QY 171 NSDSFGGKVQORGLIVFHSSEGSTSVYDLFDAQGOYPD--TLRIYRNDNTTISSTLSISL 228
 DB 175 EFNS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEV 232
 QY 229 YLYT 232
 DB 233 HLTT 236

RESULT 46
 US-09-314-235-27
 ; Sequence 27, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-27

Query Match 21.7%; Score 264.5; DB 4; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSBEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQPDPTDELHKASKFTG-LMENNKVLYDDHYVS---ATKVKSVDFLAHDLIYNISDK 56
 QY 60 GHPWYNDLLDLGTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCYFSSKDNVGVKVTGGKTCMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174

```
Db 142 EIPKIVVKSIDG1Q-SLSFD-LEINKNMVAQELDYKVRKVLTDNKLQYNGP--SKY 197
Qy 180 ORGLIVFHSSEGTVSVDLPD---AQGGYDPTLLRIYRDNNTTISSTLSISLYVT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY---LMYKDNETLDSNTQIEVLT 250

RESULT 48
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPRANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-26

Query Match 21.4%; Score 260.5; DB 3; Length 239;
Best Local Similarity 32.0%; Pred. No. 1.1e-19;
Matches 77; Conservative 41; Mismatches 104; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTH 61
Db 1 ESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVFPKNDLADKYDKYDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYN 171
Db 119 TEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLRHYLVKNKKLYE 176
Qy 172 SDSFGKGVQRLIVFHSSEGTVSVDLPDAQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFQSKYLMYNDNMVDSKDKVIEVY 233
Qy 230 L 230
Db 234 L 234

RESULT 49
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPRANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
```

```
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match 21.4%; Score 260.5; DB 4; Length 239;
Best Local Similarity 32.0%; Pred. No. 1.1e-19;
Matches 77; Conservative 41; Mismatches 104; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTH 61
Db 1 ESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVFPKNDLADKYDKYDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYN 171
Db 119 TEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLRHYLVKNKKLYE 176
Qy 172 SDSFGKGVQRLIVFHSSEGTVSVDLPDAQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFQSKYLMYNDNMVDSKDKVIEVY 233
Qy 230 L 230
Db 234 L 234

RESULT 50
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Artzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; EARLIER FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 21.4%; Score 260.5; DB 4; Length 266;
Best Local Similarity 31.1%; Pred. No. 1.3e-19;
Matches 76; Conservative 44; Mismatches 105; Indels 19; Gaps 8;

Qy 1 EKSEINEKDLRKXSELQGTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTH 60
Db 27 AESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQSLYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 110
Db 85 LGYDNVRVFPKNDLADKYDKYDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 144
Qy 111 VTLDHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLY 170
Db 145 VTEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLRHYLVKNKKLY 202
```

QY 171 NSDSFGKQVORGLIVFHSSEGSTVSYDLFDAQOYPD--TLLRIYRDNNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFQSKYLMYNDKNQWDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 51
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 21.4%; Score 260.5; DB 4; Length 266;
Best Local Similarity 30.7%; Pred. No. 1.3e-19;
Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 7;

QY 1 SEKSEENEXDLRKSLQGTALGNLQIYYNYSKAITSEKSDAQPLNTLLFKGFFTG 60
Db 27 AESQFDPKPDELHKSRF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTR 84
QY 61 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQC-----AGGTENKTACMYG 110
Db 85 LGDYDNRVBFKNLADKYDKKVDYFGANYYYQCYFSEKKTNDINSHQTDKRTKMYG 144
QY 111 VTLDHNNRLTEKKVPINLMDGKQITVPIDKVKTSKEVTVQELDQARHYLHGKFG 170

Db 145 VTEHNGNQLDKYRSTVRVPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHVLVKNKKLY 202
QY 171 NSDSFGKQVORGLIVFHSSEGSTVSYDLFDAQO--YPTLLRIYRDNNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFQSKYLMYNDKNQWDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 52
US-09-144-776B-10
; Sequence 10, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-144-776B-10

Query Match 21.0%; Score 255.5; DB 4; Length 239;
Best Local Similarity 32.1%; Pred. No. 3.7e-19;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLRKSEIQGTALGNLQIYYNYSKAITSEKSDAQPLNTLLFKGFFTGHPWYNDLLVD 70
Db 10 ELHKSKFTG-LMENNK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDILGNYDNVRVE 67
QY 71 LGSTATSEYEGSSVDLYGAYGYQCAGG-----TENKTACMYGGVTLHDNNELT 120
Db 68 FKNKDLADKYDKKVDYFGANAYYQCAFSEKKTNDINSHQTDKRTKMYGGVTEHNGOLD 127
QY 121 BEKKVPINLWIDGKQITVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDFGKQV 180

Db 128 KYRSTVAFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHYLVNKKLYEFNN--SPYE 183
 QY 181 RGLVHSESGSTVSYDLFDAQGYPD--TLRIYRDNNTTSSLSLSLYLT 232
 Db 184 TGYIKFIENENS-FWYDMMPAGDFDQSKYLMNNDKNVDSKDVKIEVLYLT 236

RESULT 53
 US-09-144-776B-14
 ; Sequence 14, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC -504 Scott Street
 ; MCMF-JA (Charles H. Harris-patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-144-776B-14

Query Match 21.0%; Score 255.5; DB 4; Length 266;
 Best Local Similarity 30.2%; Pred. No. 4.3e-19;
 Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;
 QY 1 SEKSEINKEKDKKSELOGTALGNLKQIY--YNNKAITSEKSDADQFLNTLLFKGFF 58
 Db 27 ASQPDPTEDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDFRAHDLIYNISD 82
 QY 59 TGHFWNLLVLDLGGSTAATSEYEGSSVDLYGAYGVQC-----AGTTPNKTCMYGGV 111
 Db 83 KKLKNYDKVKTLLNEGLAKYKDEVVDYGVYNNYVYFSSKDNVKGVTGKTCMYGI 142
 QY 112 TLHNNRLTEE--KKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGL 169
 Db 143 TKHEGNHFNGLQNLVIRVY-ENKENTISFE-VQTDKKSQVTAQELDIKARNFLINKNL 200

QY 170 YNSDSEGGKVGQRLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNNTTSSLSLS 227
 Db 201 YEFNS--SPYETGYTKFIENNNGTWFYDMMPAGDFDQSKYLMNNDKNVDSKSVKIE 258
 QY 228 LYLTY 232
 Db 259 VHLTY 263

RESULT 54
 US-09-144-776B-8
 ; Sequence 8, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC -504 Scott Street
 ; MCMF-JA (Charles H. Harris-patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-144-776B-8

Query Match 20.6%; Score 250.5; DB 4; Length 266;
 Best Local Similarity 30.7%; Pred. No. 1.5e-18;
 Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 8;
 QY 1 SEKSEINKEKDKKSELOGTALGNLKQIY--YNNKAITSEKSDADQFLNTLLFKGFF 60
 Db 27 ASQPDPTEDELHKASKFTG-LMENMK-VLYDDNHVSAINVKSIDQFRFDLIYSIKDTK 84
 QY 61 HPWYNLLVLDLGGSTAATSEYEGSSVDLYGAYGVQCAGG-----TPNKTCMYGG 110
 Db 85 LGYDNRVRFKNDLADKYKVDVFGANAYYQCAFSSKKTNDINSHQTDKRTCMYGG 144
 QY 111 VTLDHNNRLTEEKKVPIINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGL 170
 Db 145 VTEHNGNQLDKYRSITVRVFEDGK-NLLSFD-VQYNNKKVTAQELDYLRHYLVNKKLY 202

```

QY 171 NSDSFGKGQVORGLIVFHSEGSTVSVDLFDAGQGYPD--TLRLRYRDNTTTSISLSLSI: 228
Db 203 EFNN--SPIETGYIKFIENENS-FWIDMMPAPGKDFQSKYLLMYNDKNVDKQVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 55
US-08-896-933-21
; Sequence 21, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-21

Query Match 18.5%; Score 225.5; DB 3; Length 239;
Best Local Similarity 30.2%; Pred. No. 6e-16;
Matches 74; Conservative 43; Mismatches 105; Indels 23; Gaps 11

QY 2 EKSEINEKDLRKKSLEOGTALGNLKQIYYYNKSAITSSSEKSADQFLTWLIFKGFPTGH 61
Db 1 ESQDPKPDDELHKSKFTG-LMENNK-VLYNNDHVSAINVKSINEPFDJYLYSINKTKL 58
QY 62 PYNLDLLVDLGSTAATSYEGSSVDLYGAYGYQC-----AGGTPNKTCAMVGG 110
Db 59 GNYDNRVFEFKQLADKADKYVDVFGANY-YQCYFSKKTNNIDSHENTKKT-CMYGG 116
QY 111 VTLDHNNRLTE-EKKVPINLMDGQTTPIDKVTSSKKEVTVQEQLDLQARHYLHGKFL 169
Db 117 VTEHGNQLDKYRSITVRVEDGK-NLLSPD-VQTNKKVTAQDLTRHYLVKNKKL 174
QY 170 YNSDSFGGKQVORGLIVFHSSGGSVSDYDLFDAGQGYPD--TLRLRYRDNTTTSISLSLS 227
Db 175 YEFNN--SPIETGYIKFIENENS-FWIDMMPAPGKDFQSKYLLMYNDKNVDKQVKIE 231
QY 228 YLYT 232
Db 232 YLTT 236

RESULT 56
US-09-314-235-21
; Sequence 21, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01

```

```

Db 122 SIDGQSLSFDIEQKNG-----NCSRISTYVRKYLTDNKLQYITNGP--SKYETGVIKFIP 175
Qy 189 SEGTSVSYDLFD-----AQGVPTDILLRIYRDNNTTISSTLSLSLYLT 232
Db 176 KNKESFWDFPEPEFTQSKY----LMIYKONETLDSNTSQIEVYLTT 219

RESULT 58
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 633845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match 18.1%; Score 220; DB 4; Length 220;
Best Local Similarity 28.9%; Pred. No. 2e-15;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;

Qy 14 KXSELOGTALGNLKIY-YNKSATTSB--KSADQFLNTLLFKGFTGHPWYNDLLVD 70
Db 5 KPSQLQRSLNLTFTKIIYFFMRVTLVTHENVKSVLDLSDIYN---VSGENYDKLKE 61
Qy 71 LGSTAATSEYEGSSVDLYGAVYGYOC--AGGTPNKTACMGYVTLHDNNRLTEKKVPINL 129
Db 62 LKNQEMATLFDKNVDIYGVYHLCYLCEAERASACLYGGVTHNEGNHLEIPKIVKV 121
Qy 130 WIDGKQT-TVPIDKVKTSKXVTVQELDLQARHYLHGKFGLYNSDSFGKVGQVGLIVPHS 188
Db 122 SIDGQSLSFDIEQKNG-----NCSRISTYVRKYLTDNKLQYITNGP--SKYETGVIKFIP 175
Qy 189 SEGTSVSYDLFD-----AQGVPTDILLRIYRDNNTTISSTLSLSLYLT 232
Db 176 KNKESFWDFPEPEFTQSKY----LMIYKONETLDSNTSQIEVYLTT 219

RESULT 59
US-09-144-776B-18
; Sequence 18, Application US/09144776B
; Patent No. 639332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Sina Bavari
; Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris

```

```

; STREET: US Army MRCM -504 Scott Street
; MCRB-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-144-776B-18

Query Match 15.9%; Score 194; DB 4; Length 82;
Best Local Similarity 45.1%; Pred. No. 2.7e-13;
Matches 37; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

Qy 43 SADQFLNTLLFKGFTGHPWYNDLLVGLGTAATSEYEGSSVDLYGAVYGYOCAGGTEN 102
Db 1 TGOQFLENTLLYKFFTDLINFEDLLINFENKEMAOHFKSKVDVYPIRYSINCYGGEID 60
Qy 103 KTACMGYVTLHDNNRLTEKK 124
Db 61 RTACTYGGVTPHEGNKLERKK 82

RESULT 60
US-08-220-378-1
; Sequence 1, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; Patent In Release #1.0, Version #1.25

```



```
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UP126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-220-378-1

Query Match 15.5%; Score 189; DB 1; Length 45;
Best Local Similarity 84.4%; Pred. No. 3.7e-13;
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SEKSEINEKDLRKXSELOQTALGNLQIYYNKSATISSEKSD 45
Db 1 SEKSEINEKDLRKXSELOQTALGNLQIYYNKSATISSEKSD 45

RESULT 61
US-08-696-012-1
/ Sequence 1, Application US/08696012
/ Patent No. 5859207
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Pontzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ TITLE OF INVENTION: Peptides
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/696,012
/ FILING DATE: 12-AUG-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UP126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-696-012-1

Query Match 15.5%; Score 189; DB 2; Length 45;
Best Local Similarity 84.4%; Pred. No. 3.7e-13;
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 SEKSEINEKDLRKXSELOQTALGNLQIYYNKSATISSEKSD 45
Db 1 SEKSEINEKDLRKXSELOQTALGNLQIYYNKSATISSEKSD 45

RESULT 62
US-08-896-933-30
/ Sequence 30, Application US/08896933
/ Patent No. 6221351
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005002
/ CURRENT APPLICATION NUMBER: US/08/896,933
/ CURRENT FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 30
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Streptococcus pyogenes
US-08-896-933-30

Query Match 12.3%; Score 150; DB 3; Length 208;
Best Local Similarity 26.3%; Pred. No. 5.8e-08;
Matches 60; Conservative 38; Mismatches 78; Indels 52; Gaps 12;

OY 33 NSKAITSEKSDQFLTNLTLPKGFHTGHPW-YNDLLVLDLGTAA---TSYEGSS--- 84
Db 1 DSKDLSNVKS-----DLLYA--YTTPDYKDCRVNFSTHTLNIDTQYRGKDYVI 51
OY 85 -----VDLYGAYGYOCAGTTPNKATCMYGGVTLHDNNRLTERKKVPI 127
Db 52 SSEMSEYASQKFKRDDHVDVGLFYILNSHTG-----EVIYGITPAQNNKYNH--KLLG 104
OY 128 NLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFLYNSDS--FGKVGRLIV 185
Db 105 NLFISGESQOONLNKILKEDIVTFQEDIDFKIRKYLMDNYKIYDATSPYVSGRIBIG--- 161
OY 186 FHSSEGSTVSYDLFDA--QGQYPTLLRIYRDNNTTISSTLS-ISLYL 230
Db 162 --TKDGKHEQIDLFDSPNEGFSDIFAK-YKDNRIINKNKFSHPDIYL 206

RESULT 63
US-09-314-235-30
/ Sequence 30, Application US/09314235
/ Patent No. 6338845
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005004
/ CURRENT APPLICATION NUMBER: US/09/314,235
/ CURRENT FILING DATE: 1999-05-18
/ EARLIER APPLICATION NUMBER: 08/896,933
/ EARLIER FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
```

```

; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-30

Query Match          12.3%; Score 150; DB 4; Length 208;
Best Local Similarity 26.3%; Pred No. 5.8e-08;
Matches 60; Conservative 38; Mismatches 78; Indels 52; Gaps 12;

QY 33 NSKAITSEKSDQFLTNLTKGFTGHPW-YNDLLVDLGSTAA-----TSEYEGSS--- 84
Db 1 DSKKDISNVKS-----DLLVA--YTTPYDKDCRVNFTHTLNIDTKYRGKDYII 51
QY 85 -----VDLYGAYGYOCAGTGNKTKACMYGVTLHDNNRLTEKKVPI 127
Db 52 SSEMSYEASQKPRDDHVDVGLFVILNSHTG-----EYIYGITPAQNNKNVH--KLLG 104
QY 128 NLWIDGKQTTVIDKVTTSKKEVTQVQLDQARHYLHGKFLGYNDS--FGKQVQRGLIV 185
Db 105 NLFISGESQONLNKILKEDIVTQEDFKIRKYLMDNYKIYDATSPVSGRIEIG-- 161
QY 186 FHSSEGSTSVYDLPA--QGVPTDLLRIYRNTTISSTLS-ISLYL 230
Db 162 --TKDGKHEQIDLFDSNEGTRSDIFAK-YKDNRIINKNFNSHFIDYL 206

```

```

RESULT 64
US-08-896-933-34
; Sequence 34, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Staphylococcal
US-08-896-933-34

Query Match          10.8%; Score 131; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 SEKSEINEKDLRKXSELOQTALGNLK 27
Db 1 SEKSEINEKDLRKXSELOQTALGNLK 27

RESULT 65
US-09-314-235-34
; Sequence 34, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

```

```

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Staphylococcal
US-09-314-235-34

```

```

Query Match          10.8%; Score 131; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOQTALGNLK 27
Db 1 SEKSEINEKDLRKXSELOQTALGNLK 27

```

```

RESULT 66
US-08-838-413A-22
; Sequence 22, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRIS, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2016-4010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

```

```
/ LENGTH: 24
/ TYPE: AMINO ACID
/ STRANDEDNESS: UNKNOWN
/ TOPOLOGY: UNKNOWN
/ MOLECULE TYPE: PEPTIDE
US-08-838-413A-22

Query Match      10.4%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 KKEVTQELDLQARHYLHGKFGLY 170
Db 1 KKEVTQELDLQARHYLHGKFGLY 24

RESULT 67
US-08-220-378-5
/ Sequence 5, Application US/08220378
/ Patent No. 5545716
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Pontzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/696,012
/ FILING DATE: 12-AUG-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UF126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-696-012-5

Query Match      10.3%; Score 126; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHNNRLTEKK 124
Db 1 NKTACMYGGVTLHNNRLTEKK 23

RESULT 69
US-08-220-378-6
/ Sequence 6, Application US/08220378
/ Patent No. 5545716
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Pontzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UF126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 23 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-220-378-5

Query Match      10.3%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHNNRLTEKK 124
Db 1 NKTACMYGGVTLHNNRLTEKK 23

RESULT 68
US-08-696-012-5
```

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-6

Query Match 10.2%; Score 124; DB 1; Length 29;
Best Local Similarity 78.6%; Pred. No. 1.7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSK 148
Db 1 EEKVPINLWDGKQNTVPLETVKTKK 28

RESULT 70
US-08-696-012-6
Sequence 6, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-6

Query Match 10.2%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 1.7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSK 148
Db 1 EEKVPINLWDGKQNTVPLETVKTKK 28

RESULT 71
US-09-144-776B-24
Sequence 24, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson,
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 79
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24

Query Match 9.2%; Score 112; DB 4; Length 79;

Best Local Similarity 32.1%; Pred. No. 0.00016;
Matches 25; Conservative 17; Mismatches 32; Indels 4; Gaps 2;

QY 43 SADQFLNTLLFKGFFTHPWNLDLLGSLTAATSEYEGSSVDLYGAYGYQC-AGTTP 101
Db 1 SVDQLSHDLIYN---VSGPNYDKLTKELKQEMATLFKXNDVIYGVETIHLCLYCENA 57

QY 102 NKTACMGYGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 72
US-09-144-776B-20
; Sequence 20, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson,
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20

Query Match 9.2%; Score 111.5; DB 4; Length 89;
Best Local Similarity 33.3%; Pred. No. 0.00021;
Matches 29; Conservative 15; Mismatches 32; Indels 11; Gaps 2;
QY 43 SADQFLNTLLFKGFFTHPWNLDLLGSLTAATSEYEGSSVDLYGAYGYQC----- 96
Db 1 SIDQFLYFDLIYSIKDKLGNVDNVRVEFKNKDLADKYDKYDVFQANY-YOCYFSKKT 59
QY 97 ----AGGTPNKTACMGYGVTLHDNNRL 119
Db 60 NDINSHQTDREKTCMGYGVTEHNGNL 86

RESULT 73
US-08-220-378-4
; Sequence 4, Application US/08220378
; Patent No. 585716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-220-378-4
Query Match 9.0%; Score 110; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.6e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 85 VDLGYGYGYQCAGGTPNKT 104
Db 3 VDKYGYGYQCAGGTPNKT 22
RESULT 74
US-08-696-012-4
; Sequence 4, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-4

Query Match 9.0%; Score 110; DB 2; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.6e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 85 VDLGYGYGYCAGGTPNKT 104
DB 3 VDKYGYGYCAGGTPNKT 22

RESULT 75
US-08-220-378-2
Sequence 2, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 8.8%; Score 107; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 0.00011;
Matches 18; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 40 SEKSADQFLTNLLFKGFTGHPWYND 66
DB 2 NKESHQFLQHTILFKGFTDHSWYND 28

Search completed: August 12, 2004, 13:34:03
Job time : 11.2135 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 7.37083 Seconds
(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEENKDLRKKSLEQG.....RDNKTINSENHIALYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1210	97.7	257	2	enterotoxin E prec
2	1037	83.8	257	2	enterotoxin A prec
3	992	80.1	260	2	enterotoxin P [imp
4	663	53.6	258	2	enterotoxin D prec
5	453.5	36.6	258	2	enterotoxin Se [i
6	380.5	30.7	260	2	enterotoxin Se [i
7	339.5	27.4	242	2	extracellular ente
8	333	26.9	240	2	extracellular ente
9	310	25.0	239	2	enterotoxin SEM [i
10	304.5	24.6	266	1	enterotoxin B prec
11	302.5	24.4	266	2	enterotoxin C3 - S
12	288.5	24.1	266	2	enterotoxin C-2 pr
13	283.5	22.9	251	1	enterotoxin type A pr
14	270.5	21.8	236	2	enterotoxin A precurs
15	270.5	21.8	266	1	enterotoxin C-1 pr
16	268.5	21.7	236	2	enterotoxin type A pr
17	263.5	21.3	236	2	enterotoxin type A pr
18	256	20.7	258	2	extracellular ente
19	234	18.9	250	1	streptococcal pyro
20	200	16.2	157	2	hypothetical prote
21	194	15.7	136	2	enterotoxin YENT2
22	175.5	14.2	235	2	enterotoxin C precurs
23	136	11.0	62	2	hypothetical prote
24	125	10.1	133	2	enterotoxin Yent1
25	105.5	8.5	234	1	toxic shock syndro
26	104.5	8.4	232	2	enterotoxin 13 [imp
27	103.5	8.4	234	2	toxic shock syndro
28	101	8.2	1634	2	DNA-directed DNA p
29	99	8.0	631	2	transferrin-bindin

30	98.5	8.0	231	2	D89807	exotoxin 11 [impor
31	97.5	7.9	232	2	E89807	exotoxin 12 [impor
32	94	7.6	227	2	G89807	exotoxin 14 [impor
33	91	7.4	411	2	A11161	flagellar hook pro
34	91	7.4	411	2	A11520	flagellar hook pro
35	89.5	7.2	194	2	AC1553	B. subtilis YJcK p
36	89	7.2	226	2	G89806	exotoxin 6 [impor
37	88.5	7.1	227	2	C89808	exotoxin 15 [impor
38	88.5	7.1	324	2	T03276	GAG protein - Yeas
39	88.5	7.1	413	2	S59650	hypothetical prote
40	88.5	7.1	816	2	C88196	protein ZK1127.7 [
41	88	7.1	203	2	C89803	hypothetical prote
42	88	7.1	617	2	E96793	hypothetical prote
43	87.5	7.1	409	2	E69886	processing protein
44	87.5	7.1	634	2	T08145	myrosinase-binding
45	87.5	7.1	956	2	T08144	myrosinase-binding
46	87.5	7.1	1014	2	H71602	protein with DnaJ
47	87	7.0	1419	1	DVZQF	multidrug resistan
48	87	7.0	2167	2	AF1489	cell wall-associat
49	86.5	7.0	614	2	D86342	hypothetical prote
50	86.5	7.0	856	2	B81399	probable periplasm
51	86.5	7.0	2971	2	T08026	hypothetical prote
52	86	6.9	853	2	G90559	trise-like protein
53	86	6.9	1090	2	AG1749	glycosidase homolo
54	85.5	6.9	291	2	G86903	cell shape determi
55	85.5	6.9	573	2	AH1793	ABC transporter, A
56	85	6.9	241	2	C89888	hypothetical prote
57	85	6.9	617	2	T10102	diphosphate-fructo
58	85	6.9	679	2	G71615	phospholipase A2-1
59	85	6.9	1014	2	T30545	major surface glyco
60	85	6.9	6486	2	T31076	tyrocidine synthet
61	84.5	6.8	573	2	AF1418	ABC transporter, A
62	84.5	6.8	637	2	S35523	El protein - human
63	84.5	6.8	593	2	A97334	type II restrictio
64	84	6.8	241	2	T07067	beta-fructofuranos
65	84	6.8	333	2	A95882	hypothetical prote
66	84	6.8	552	2	T41863	chitinase chi-A or
67	84	6.8	562	2	S01312	alpha-amylase (EC
68	84	6.8	616	1	A40457	replication protei
69	84	6.8	1902	1	B44858	lactocepin (EC 3.4
70	84	6.8	1948	2	S00485	gene 11-1 protein
71	83.5	6.7	507	2	S36595	L1 protein - human
72	83.5	6.7	547	2	S49815	transferrin-bindin
73	83.5	6.7	668	2	JQ0773	penicillin-binding
74	83.5	6.7	668	2	JQ0774	penicillin-binding
75	83.5	6.7	668	2	T44118	penicillin-binding
76	83.5	6.7	804	2	G90571	hypothetical prote
77	83	6.7	438	2	S42581	neutral metallopro
78	83	6.7	476	2	H82177	conserved hypothet
79	83	6.7	556	2	A11394	arginyl tRNA synth
80	83	6.7	631	2	S70910	transferrin-bindin
81	83	6.7	914	2	T08081	probable myrosinas
82	83	6.7	988	2	T08102	myrosinase-binding
83	83	6.7	1353	2	T27404	hypothetical prote
84	83	6.7	2910	2	T29156	DNA-directed RNA p
85	82.5	6.7	328	2	F64187	p-aminobenzoate sy
86	82.5	6.7	638	2	AH0340	putative autotransp
87	82.5	6.7	1520	2	T23620	hypothetical prote
88	82.5	6.7	2441	2	D11623	erythrocyte membra
89	82	6.6	292	2	B89807	exotoxin 9 [impor
90	82	6.6	520	2	D83845	hypothetical prote
91	82	6.6	1217	2	T21403	hypothetical prote
92	82	6.6	2380	2	E71604	hypothetical prote
93	82	6.6	5005	2	F82884	hypothetical prote
94	81.5	6.6	356	2	A69807	exotoxin 8 [impor
95	81.5	6.6	381	2	B89886	hypothetical prote
96	81.5	6.6	555	2	S71365	ovule development
97	81.5	6.6	609	2	F90160	membrane conserved
98	81.5	6.6	672	1	S73438	MG032 homolog B01
99	81.5	6.6	819	2	G89801	hypothetical prote
100	81	6.5	272	2	D86671	transposase of IS1

ALIGNMENTS

RESULT 1

A28179
 enterotoxin E precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28179
 R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
 J. Bacteriol. 170, 2954-2960, 1988
 A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
 A:Reference number: A28179; MUID:88257005; PMID:3384800
 A:Accession: A28179
 A:Molecule type: DNA
 A:Residues: 1-257 <COU>
 A:Cross-references: GB:M21319; NID:G153001; PIDN:AAA26617.1; PID:G153002
 C:Superfamily: enterotoxin B

Query Match 97.7%; Score 1210; DB 2; Length 257;
 Best Local Similarity 97.9%; Pred. No. 6e-93;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWNLLVLDGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWNLLVLDGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 2

A28664
 enterotoxin A precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28664; A29566
 R:Betley, M.J.; Mekalanos, J.J.
 J. Bacteriol. 170, 34-41, 1988
 A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
 A:Reference number: A28664; MUID:88086892; PMID:3335483
 A:Accession: A28664
 A:Molecule type: DNA
 A:Residues: 1-257 <BET>
 A:Cross-references: GB:M18970; NID:G153120; PIDN:AAA26681.1; PID:G153121
 A:Experimental source: strain FRI337
 R:Huang, I.Y.; Hughes, J.L.; Beredoll, M.S.; Schantz, E.J.
 J. Biol. Chem. 262, 7006-7013, 1987
 A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
 A:Reference number: A29566; MUID:87222293; PMID:3384106
 A:Accession: A29566
 A:Molecule type: protein
 A:Residues: 25-241, 'S', 243-257 <HUA>
 C:Genetics:
 A:Gene: entA
 A:Map position: 6
 C:Superfamily: enterotoxin B

Query Match 83.8%; Score 1037; DB 2; Length 257;
 Best Local Similarity 83.3%; Pred. No. 1.3e-78;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWNLLVLDGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWNDLLVDFSDKIDVYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 3

C89984
 enterotoxin P [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hama, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:G13701743; PIDN:BAB43036.1; GSPDS:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B

Query Match 80.1%; Score 992; DB 2; Length 260;
 Best Local Similarity 78.5%; Pred. No. 7.3e-75;
 Matches 183; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 87
 QY 61 HPWNLLVLDGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 88 HQWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 147
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 148 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 207
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 208 RGLIEFHPSSGDSVGYDLFDAQGYPTQLRIYRDNKTIKSKNMHDIYLYTT 260

RESULT 4

A33953
 enterotoxin D precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
 C:Accession: A33953
 R:Bayles, K.W.; Iandolo, J.J.
 J. Bacteriol. 171, 4799-4806, 1989
 A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
 A:Reference number: A33953; MUID:89359112; PMID:2549000
 A:Accession: A33953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <BAY>
 A:Cross-references: GB:M28521; NID:G1492109; PIDN:AAB06195.1; PID:G758691


```
C;Superfamily: enterotoxin B

Query Match      53.6%; Score 663; DB 2; Length 258;
Best Local Similarity 55.0%; Pred. No. 1.4e-47;
Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFTTG 60
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
26 NENIDSVREKELHKKSELSALANMKHSYADKPNPIIGENKSTGDFLENTLLPKGFTTD 85
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTGPKNTACMYGGVTLHDNNRLT 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
86 LINFEDLLINFSKEMAHGFKSKNDVYPIIRYSINCYGGEIDRTACTYGGVTPHEGKRLK 145
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
146 ERKKIPINLWINGVQKVSFLDKVQTDKQNVVQELDAQARYLQKDLKYNNDTLGGKIQ 205
QY 191 RGLIVFHSSESTVSVDLFDAGQGPDTLLRIYRDNKTINSNLHIALYLY 231
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
206 RGKIEFSDSGSKVSVDLFDKGFPEKQRLRIYSDNKTLSLHHLHIDYLY 256

RESULT 5
H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: H89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701618; PIDN:BAB42911.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sei
C;Superfamily: enterotoxin B

Query Match      36.6%; Score 453.5; DB 2; Length 258;
Best Local Similarity 40.8%; Pred. No. 3.2e-30;
Matches 95; Conservative 45; Mismatches 78; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOGTALGNLKOIYYNEKAIT-----ENKESDDQFLENTLLPKGFTTG 60
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32 EVDKDLKKKSDLDSSKLFNTLS--YYTD--ITWQDESNIKISTDQLLNNTIILKNIDIS 87
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTGPKNTACMYGGVTLHDNNRLT 120
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
88 VLKTSKLVFNSSSLANQFKGNIDYGLYFGNKCVCGLTEKTSCLYGGVTIHDGNQLD 147
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
148 EEKIVGNVFDKGVQCGFV--ITKRAKVYQBELDKVRFKLENLYKYNKDT--GMIQ 203
QY 181 RGLIVFHS--SEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSNLHIALYLY 231
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
204 KGCIFHSHNQDSFFYYDLNVRGSGVGAETFFQYSDNRTVSSSNHYHDVFLY 256

RESULT 6
H89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi
```

```
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: H89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701623; PIDN:BAB42916.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sei
C;Superfamily: enterotoxin B

Query Match      30.7%; Score 380.5; DB 2; Length 260;
Best Local Similarity 39.5%; Pred. No. 3.7e-24;
Matches 96; Conservative 31; Mismatches 87; Indels 29; Gaps 8;

QY 8 NEKD-----LRKSELOGTALGNLKOIYYNE-----KAITENKESDDQFLENTLLPKGFF 58
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
29 NEEDPKIESLCKKSSVDPIALHNDDYINNRFTTVKSIIVTTE---KFLDFDLFKSI- 84
QY 59 TGHFW-----YNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTGPKNTACMYGGV 111
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
85 ---NWLDDGISAEFKDLKVEFSSAISKEFLGKTVDIYGVYKAHCHGEHQVDTACTYGGV 141
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
142 TPEHNKLSPEKNIGVAVYKDNVNVNTFI--VTDDKKVTAQELDIDKVTKLNNAYKLY- 198
QY 172 SDSFGKVGORGLIVFHSSESTVS---YDLFDAGQGPDTLLRIYRDNKTINSNLHIALY 229
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
199 -DRMTSDVQKGYIKFHSSEKESFYDLYFGNLPDQYLTQYNDNKTIDSSDYHDVY 257
QY 230 LYT 232
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
258 LFT 260

RESULT 7
H89969
extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (strain N31)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi,
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: H89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701621; PIDN:BAB42914.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sei
C;Superfamily: enterotoxin B

Query Match      27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 8.5e-21;
Matches 84; Conservative 37; Mismatches 78; Indels 37; Gaps 9;

QY 8 NEKDLRKSELOGTALGNLKOIY-----YYNEKAITENKESDDQFLENTLLPKGFTTGH 62
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17 NIKDL---TYAQDDIGVGNLRFYTKHDYIDLKGVTDKNLPANOLE-----FSTG-- 64
QY 63 WYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTGPKNTACMYGGVTLHDNNRLTEE 122
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65 -TNDLISENNWDETSKFKGKLDIFGIDYNGFC-----KSKYMYGGATL--SGOYLNSA 116
```

Qy 123 KKVPIINLWIDGKOTTPIDKVKTSKEVTQVQLDQARHYLHGKGLYNSDSFG-GK--- 178
Db 117 RKIPINLWNGKHKTISTDKIATNKKLVTAQIDVKLRYLQEEYNIYGHNNITGKGEYV 176
Qy 179 -----VORGILVPHSSEGTSTVSDLDFAQQVPTDLLRIYRDNKTINSENLIHI 226
Db 177 YKSKFYGFNGKVLPHLNKESFSYDLFTYDGLPVSPLKIYEDNKIIESEKPHL 232

RESULT 8
G89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89991
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: GB:BA000018; PID:g13701803; PIDN:BAB43096.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sel
C:Superfamily: enterotoxin B

Query Match 26.9%; Score 333; DB 2; Length 240;
Best Local Similarity 35.0%; Pred. No. 2.9e-20;
Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

Qy 24 GNLKQIY---YNEKAITENKESDQFLNTLLFKGFTGHPWYND-LLVPLGSKDATN 78
Db 31 GNLNFTYKYEYVNLKNVXDKNSPESHRL-----YSKNDILYAFEDNEYITS 79
Qy 79 KYRGKKVLYGAYGYQCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTV 138
Db 80 DLKGNVDFGYSKY---GNSRT--YGVGVTKAENKLDSPRIPIINLIINGKHQTV 133
Qy 139 PIDKVTSKKEVTQVQLDQARHYLHGKGLY-----NDSFGGKVGQGLIVF 186
Db 134 TTKSVSTDKQVTAQIDVKLRYLQEEYNIYGHNDTGKGEYGTSSKPYSGFDKGVVF 193
Qy 187 HSSEGTSTVSDLDFAQQVPTDLLRIYRDNKTINSENLIHI 226
Db 194 HMDGNSFSDYDLFTYDGLPVSPLKIYEDNKIIESEKPHL 233

RESULT 9
D89969
enterotoxin SEM [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <KUR>
A:Cross-references: GB:BA000018; PID:g13701622; PIDN:BAB42915.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sem

C:Superfamily: enterotoxin B

Query Match 25.0%; Score 310; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 2.3e-18;
Matches 70; Conservative 40; Mismatches 82; Indels 26; Gaps 5;

Qy 23 LGMLKQIYYNEKAITENK--ESDDQFLNTLLFKGFTGHPWYNDLLVPLGSKDATNKY 80
Db 24 VGVNLNENYGSYPIDEDHQINPENNELSHQLVFS-----MDNSTVTAEFKVDDVKKF 77

Qy 81 KGKVDLYGAYGYQCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTVPI 140
Db 78 KNRADVIGLSYGYCL-----KKNYIYGGVTL-AGDYLEKSRRIINLWNGEHQTIST 131
Qy 141 DKVTSKKEVTQVQLDQARHYLHGKGLY-----NDSFGGKVGQGLIVFHS 188
Db 132 DKVSTNKKLVTAQIDVKLRYLQEEYNIYGHNDTGKGEYGTSSKPYSGFNAGKILPHL 191
Qy 189 SEGSTVSDYDLFAQQVPTDLLRIYRDNKTINSENLIHI 226
Db 192 NDGSSFSYDLFTYDGLPVSPLKIYEDNKIIESEKPHL 229

RESULT 10
ENSAB6
enterotoxin B precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 24-Apr-1994 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999
C:Accession: S27360; A92065; S27240; A01815
R:Jones, C.L.; Khan, S.A.
J. Bacteriol. 166, 29-33, 1986
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.
A:Reference number: S27360; MUID:86168029; PMID:3957869
A:Accession: S27360
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:Cross-references: EMBL:M1118; NID:g152999; PIDN:AAA88550.1; PID:g153000
A:Experimental source: strain S6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
A:Reference number: A92065; MUID:71007902; PMID:5470821
A:Accession: A92065
A:Molecule type: protein
A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', 1
A:Experimental source: strain S-6
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
A:Reference number: A92064; MUID:71007901; PMID:5470820
A:Contents: annotation; chymotryptic peptides
R:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
A:Reference number: A92063; MUID:71007900; PMID:5470819
A:Contents: annotation; tryptic peptides
R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunny, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792; PMID:4953912
A:Contents: annotation; biological source of protein
R:Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B.
A:Reference number: S27240; MUID:93049338; PMID:1425690
A:Accession: S27240
A:Molecule type: protein
A:Residues: 28-42, 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin B #status experimental <MAT>
F:120-140/Disulfide bonds: #status experimental

A;Residues: 1-251 <WEE>
A;Cross-references: GB:U0453; EMBL:M19350; NID:q1877426; PIDN:AAC4868.1; PID:q1877430
P;Nelson K.; Schlievert P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the *speA* gene encoded
A;Reference number: SI8782; MUID:92044323; PMID:1940804
A;Accession: SI8782
A;status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 9-244 <NBL>
A;Cross-references: EMBL:X61560; NID:q47287; PIDN:CAA43758.1; PID:q47288

A; Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18784
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-244 <NEA>
 A; Cross-references: EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID:G47292
 A; Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18785
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-244 <NEZ>
 A; Cross-references: EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID:G47294
 A; Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18791
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-244 <NEV>
 A; Cross-references: EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID:G47310
 A; Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18796
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-244 <NEO>
 A; Cross-references: EMBL:X61557; NID:G47319; PIDN:CAA43755.1; PID:G47320
 A; Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18797
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-244 <NEH>
 A; Cross-references: EMBL:X61558; NID:G47321; PIDN:CAA43756.1; PID:G47322
 A; Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A; Accession: S18800
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 9-228 <NES>
 A; Cross-references: EMBL:X61554; NID:G47327; PIDN:CAA43752.1; PID:G47328
 A; Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C; Genetics:
 A; Gene: speA1
 C; Superfamily: enterotoxin B
 C; Keywords: exotoxin
 F; 1-30/Domain: signal sequence #status predicted <SIG>
 F; 31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 22.9%; Score 283.5; DB 1; Length 251;
 Best Local Similarity 33.6%; Pred. No. 3.9e-16;
 Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

Qy 4 SEINEKDLAKKSELOQTAL-GNLKQIY--YNEKAITENKESDDQFLENTLFGKFFTG 60
 Db 25 SQEVFAQDDPNPQLHSSLSLVKLNQIYFLYEGDPVTHENVKSVDDLHSHDIYN---VS 81
 Qy 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTACMGVGVTLHNNRL 119
 Db 82 GPNYDKLTKLQKQEMATLPKDKNVDIYGEVYHLCVCLNAERSACIYGGVTVNHEGHL 141
 Qy 120 TEKKVPINLWIDKQTTVPIDKVKSKKVTQVQLDQARHYLHGKFGLYNSDSFGKV 179
 Db 142 EIPKNILVKVSDIGIQ-SLSFD-IEISKQWVTAQELDYKVRKLTDNKQLYTNGP--SKY 197
 Qy 180 QRGILVPHSSEGSFVSVDLFD---AQQVDPDLLRIYRDNKTINSNLHIALYLT 232
 Db 198 ETGYIKFIPKNSFWDFPEPEFTQSKY----LMYKDNELDSNTSQIEVLT 250

RESULT 14

S18789
 exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate California)
 N; Alternate names: scarlet fever toxin
 C; Species: Streptococcus pyogenes
 A; Variety: strain MGAS262 isolate California
 C; Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
 C; Accession: S18789
 A; Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
 J. Exp. Med. 174, 1271-1274, 1991
 A; Title: Characterization and clonal distribution of four alleles of the speA gene encoded by the nucleotide sequence of the enterotoxin A (fragment) #status predicted <SIG>
 A; Residues: 1-236 <NEL>
 A; Cross-references: EMBL:X61573; NID:G47303; PIDN:CAA43771.1; PID:G47304
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C; Genetics:
 A; Gene: speA
 C; Superfamily: enterotoxin B
 C; Keywords: exotoxin
 F; 1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F; 23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 21.8%; Score 270.5; DB 2; Length 236;
 Best Local Similarity 33.0%; Pred. No. 4.3e-15;
 Matches 75; Conservative 41; Mismatches 100; Indels 11; Gaps 7;

Qy 4 SEINEKDLAKKSELOQTAL-GNLKQIY--YNEKAITENKESDDQFLENTLFGKFFTG 60
 Db 17 SQEVFAQDDPNPQLHSSLSLVKLNQIYFLYEGDPVTHENVKSVDDLHSHDIYN---VS 73
 Qy 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTACMGVGVTLHNNRL 119
 Db 74 GLNYDKLTKLQKQEMATLPKDKNVDIYGEVYHLCVCLNAERSACIYGGVTVNHEGHL 133
 Qy 120 TEKKVPINLWIDKQTTVPIDKVKSKKVTQVQLDQARHYLHGKFGLYNSDSFGKV 179
 Db 134 EIPKNILVKVSDIGIQ-SLSFD-IEISKQWVTAQELDYKVRKLTDNKQLYTNGP--SKY 189
 Qy 180 QRGILVPHSSEGSFVSVDLFDQAGQVDPDLLRIYRDNKTINSNLHI 226
 Db 190 ETGYIKFIPKNSFWDFPEPEFTQSKY----LMYKDNELDSNTSQIEVLT 236

RESULT 15

ENSAC1
 enterotoxin C-1 precursor - Staphylococcus aureus
 C; Species: Staphylococcus aureus
 C; Date: 15-Nov-1994 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
 C; Accession: S06356; A01816
 R; Boshach, G.A.; Schlievert, P.M.
 Mol. Gen. Genet. 209, 15-20, 1987
 A; Title: Nucleotide sequence of the staphylococcal enterotoxin C-1.
 A; Reference number: S06356; MUID:8038352; PMID:2823067
 A; Accession: S06356
 A; Molecule type: DNA
 A; Residues: 1-266 <BOH>
 A; Cross-references: EMBL:X05815; NID:G46566; PIDN:CAA29260.1; PID:G46567
 R; Schmidt, J.J.; Spero, L.
 J. Biol. Chem. 258, 6300-6306, 1983
 A; Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
 A; Reference number: A01816; MUID:83213327; PMID:6189824
 A; Accession: A01816
 A; Molecule type: Protein
 A; Residues: 28-75, 117-176, N' 178-266 <SCH>
 C; Genetics:
 A; Gene: entC1
 C; Superfamily: enterotoxin B
 C; Keywords: enterotoxin
 F; 1-27/Domain: signal sequence #status predicted <SIG>
 F; 28-266/Product: enterotoxin C-1 #status experimental <MAT>
 F; 120-137/Disulfide bonds: #status experimental

A,Cross-references: EMBL:X61565; NID:g47311; PIDN:CAA43763.1.; PID:g47312
A,Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Accession: S18795
A,A>Status: nucleic acid sequence not shown; translation not shown
A,A:Molecule type: DNA
A,Residues: 1-236 <NES>
A,Cross-references: EMBL:X61566; NID:g47317; PIDN:CAA43764.1.; PID:g47318
A,Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Accession: S18799
A,A>Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-236 <NES>
A,Cross-references: EMBL:X61567; NID:g47325; PIDN:CAA43765.1.; PID:g47326
A,Experimental source: strain MGAS496 isolate Germany unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C,Genetics:
A,Gene: speA2
C,Superfamily: enterotoxin B
C,Keywords: exotoxin
C,Keywords: signal sequence (fragment) #status predicted <SIG>
F,I-22/Domain: exotoxin type A (fragment) #status predicted <MAT>
F,I-23-236/Product: exotoxin type A {fragment} #status predicted <MAT>

Query Match 21.3%; Score 263.5; DB 2; Length 236;
Best Local Similarity 32.9%; Pred. No. 1.6e-14;
Matches 76; Conservative 43; Mismatches 93; Indels 19; Gaps 10;

QY 4 SSEEINEKLRKKSEIQGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLNTLLFKGFPTG 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 17 SOEVEAQQDPDPSQLRSRSLXNLQIYFLYEGDFVTHENVKSVDQLLSHDIYN---VS 73

QY 61 HPWANDLLDLGSKDATNKYGKKVDLYCAAYGYOC-AGGTENKTACMGYGVTLHDNNRL 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 74 GPNYDKLTTELKNQEWATLFKDKNDVIYSVEYHYLCYICENAERSACIYGGVTNEGHL 133

QY 120 TEERKVPINLWDIGKQTTPVIDKVKTSKEVTVQSBLDQARHYLGKFGLYNSDSFGKV 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 134 ETPKIKIVKVISDIGIQ-SLSFD-IETNKQMTVAQELDYKVRKYLTDNKQLYTNGP--SKY 189

QY 180 QGLVLVFHSSEGSTVSYLDFD---AQOGYPDTLLRIYRDNKTINSENLIH 226
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 190 ETGYTKFIPIKNKSFWFDFPEPETQSKI----LMYIKDNELTDSNTSQI 236

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N3)
C,Species: Staphylococcus aureus
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C,Accession: G89968
R,Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc-
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A,Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A,Reference number: A89758; UID:21311952; PMID:11418146
A,Accession: G89968
A>Status: preliminary
A,Molecule type: DNA
A,Residues: 1-258 <KUR>
A,Cross-references: GB:BA000018; PID:g13701617; PIDN:BA842910.1; GSPDB:GN00149
A,Experimental source: strain N3.15
C,Genetics:
A,Gene: seg
C,Superfamily: enterotoxin B

Query Match 20.7%; Score 256; DB 2; Length 258;
Best Local Similarity 29.6%; Pred. No. 7.7e-14;
Matches 74; Conservative 50; Mismatches 84; Indels 42; Gaps 12;

QY 3 KSEINEKLRKKSELQGTLGNLKQIYY---YNEKAITENKESDDQFLNTLLFKGFPT 59
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

A;Cross-references: GB:BA000018; PID:gl3701400; PIDN:BA042694.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1430

Query Match 16.2%; Score 200; DB 2; Length 157;
Best Local Similarity 35.6%; Pred. No. 1.8e-09;
Matches 42; Conservative 20; Mismatches 54; Indels 2; Gaps 2;

QY 1 SEKSEINEKLRKSELOQTALGNLQIYYNEKAITENKESDDOLENTLLPKGFTG 60
DB 42 TNSASAIYSYDLHKKSPDKSLGNK-MSFINTQL-ENKNTNDRLLKHLDFHDMFN 99
QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNR 118
DB 100 VASKQDFKVEFENEALSKKFNKNDIYAGSYSECHGATNKQCSGGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: A89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701619; PIDN:BA042912.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: yent2

Query Match 15.7%; Score 194; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 4.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHDNRLLTEKKV--PINLW----DGKTTVPIDKVKTSKEVTVQELDL 157
DB 2 KKTCTMYGGVTEHDGNCIDKNSTDSNHLIKVYENERSLSFD-IPFNKKNITAEIDY 60
QY 158 QARHVLHGKFGLYNGDSFGKVGORGLIVFHSSEGSTVSVDLFDAGGQ--YPTDLLRIYRD 215
DB 61 KVRNILLKXKNIYFNS--SPYETGYIKFEGSGHSFWYDIMPESGKFFYTKYLLIYND 118
QY 216 NKTINSENHIALYL 230
DB 119 NKTVESKSNINVEHL 133

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-2000
C;Accession: A30509
R;Cochran, S.C.; Schlievert, P.W. Infect. Immun. 56, 2518-2520, 1988
A;Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A;Reference number: A30509; PMID:8814303; PMID:3045005
A;Accession: A30509
A;Molecule type: DNA
A;Residues: 1-235 <GCS>
A;Cross-references: GB:M35514; NID:gl53820; PIDN:AAA27017.1; PID:gl53821
C;Superfamily: enterotoxin B
C;Keywords: exotoxin

Query Match 14.2%; Score 175.5; DB 2; Length 235;
Best Local Similarity 25.4%; Pred. No. 3.2e-07;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

QY 47 FLENTLLFKGFTGH-----PWYNDLLVDLGSKDA-----TNK 79
DB 11 FITTILISTYFTYHQSDKDISNVKSDLLVAYITPYDKDCRVNFTTHTLNDITOK 70
QY 80 YGKG-----KVDLYGAYGYQCAGGTENKTACMYGGVTLHDNRLL 119
DB 71 YRGKDYIISSEMSYEASQKFRDDHVDVFGFLVILNSHTG----EYIYGITPAQNNKV 125
QY 120 TEKKVPINLWIDGKTTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDS--FG 177
DB 126 NH--KLGNLFTSGESQQNLNKKIILEKDIVTFQEIHFIRKIRYLMNDNYKIYDATSPYVG 183
QY 178 KVQORGLIVFHSSEGSTVSVDLFDG--QGVPTLLRIYRDNKTINSENHIALYL 230
DB 184 RIBIG-----TKDGKEQIDLFDSPNEGTRSDIFAK-YKDNRIINKNKFSHFDIYL 233

RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89941
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: H89941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701399; PIDN:BA042693.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1429

Query Match 11.0%; Score 136; DB 2; Length 62;
Best Local Similarity 37.5%; Pred. No. 0.00012;
Matches 21; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 176 GKVKQGLIVFHSSEGSTVSVDLFDAGGQYPTDLLRIYRDNKTINSENHIALYL 231
DB 5 GGDIVKGVYKHNDQCNVEYDFYNLNGEYGVFLKMYADNKTINRDKLHLDIYLF 60

RESULT 24
B89969
enterotoxin Yent1 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: B89969
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701620; PIDN:BA042913.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: yent1

Query Match 10.1%; Score 125; DB 2; Length 133;

QY 175 FGG--KVORGLIVFHSSRGSTVSVDL----FPAQQOYPTLLRIYRDNKTINSE 222
 Db 150 TGGYWKIT-----MNDGSTYQSDLSKKFYNTKEPINT---DEIKTIEAE 232

RESULT 28
 E64410
 DNA-directed DNA polymerase (EC 2.7.7.7) family B, intein containing precursor - Methanococcus jannaschii
 N:Contains: DNA endonuclease (EC 3.1.1.1) PI-I; DNA endonuclease (EC 3.1.1.1) PI-II; DNA
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1998
 C:Accession: E64410
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.T.; Overbeek, R.; Kirschner, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Tsao, J.D.; Sadow, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: E64410
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1634 <BUL>
 A:Cross-references: GB:U67532; GB:L77117; NID:G1591559; PID:G1591563; TIGR:MJ0885; PID:G1591563
 C:Genetics:
 A:Map position: REV816304-811400
 A:Start codon: TTG
 C:Function: <DPL>
 A:Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at th
 C:Function: <EN1>
 A:Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phospho
 C:Function: <EN2>
 A:Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phospho
 C:Superfamily: DNA-directed DNA polymerase KOD
 C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing
 F:1-425/795-882/1359-1634/Product: DNA-directed DNA polymerase family B #status predicted
 F:1-425/Domain: DNA-directed DNA polymerase family B extein 1 #status predicted <XT1>
 F:426-794/Product: DNA endonuclease PI-I (pol B extein 1) #status predicted <MAT2>
 F:795-882/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <XT2>
 F:883-1358/Product: DNA endonuclease PI-II (pol B extein 2) #status predicted <MAT3>
 F:1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <XT3>
 F:426-795/Cross-link: peptide (Arg-Ser) #status predicted
 F:882-1359/Cross-link: peptide (Arg-Ser) #status predicted

Query Match 8.2%; Score 101; DB 2; Length 1634;
 Best Local Similarity 22.9%; Pred. No. 5.5;
 Matches 53; Conservative 33; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELOGTALGNLKQIYYNEKAITENKESDQFLENTLLFKGFTTGHFWYNDLVDL 71
 Db 614 VRRKKGTKAITLGCACKDIYLIKIEILKNKE--KYLFPNAIL-RGFEGDGYVNTVRV 669

QY 72 GSKDATNKYKGGK-----VDLYGAYGYQCAGTPTNACMYGGVTLHDNNRLTEKKVP 126
 Db 670 VVNGTNNYDKIKFIASLDRLGKYSF-----YTSYSEERGGKKRYV 713

QY 127 INLWIDGKQTTVPIDKVKTS-----KREVTQELDQARHYLHGKFGLYNSD----- 173
 Db 714 IEITSGK-----DLIKFISILSIFSRKKNLLNEIRQTKLYKIGYGFYDLDVVCVS 766

QY 174 --SFGKV-----GRGLIVFHSSEGS-TVSYDLEDAQGQYDPL 209
 Db 767 LESYKGEVYDTLEGRPPYFANGILTHNSLYPSIIISYNI-----SPDIL 811

RESULT 29
 S70908
 transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
 A:Species: Haemophilus influenzae
 A:Variety: strain SB29
 C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C:Accession: S70908; S73321
 R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.B.

Mol. Microbiol. 19, 575-586, 1996
 A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
 A:Reference number: S70901; MUID:96228706; PMID:8830248
 A:Accession: S70908
 A:Molecule type: DNA
 A:Residues: 1-631 <LOO>
 A:Cross-references: EMBL:U15055
 A:Experimental source: strain SB29, clone DS-1090-3-2
 R:Loosmore, S.M.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S73320
 A:Accession: S73321
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-250, 'L', 252-349, 'RTDATTN', 357-631 <LOW>
 A:Cross-references: EMBL:U15055; NID:G1223948; PIDN:AAC43931.1; PID:G1223949
 A:Experimental source: strain SB29, clone DS-1090-3-2
 C:Genetics:
 A:Gene: tbp2
 C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 8.0%; Score 99; DB 2; Length 631;
 Best Local Similarity 21.0%; Pred. No. 2.5;
 Matches 56; Conservative 31; Mismatches 60; Indels 120; Gaps 12;

QY 14 KGELOGTALGNLKQIYYNEKAITENKESDQFLENTLLFKGFTTGHFWYNDLVDL 60
 Db 190 QRYSLFGSAFG-----AYNRRSAISDIDN----LENNLKNAGALTSEFTVNFGTKKLTG 240

QY 61 HPWYNL-----LVDLGSKDATNKYKGGK-----KVDLYGAY 91
 Db 241 KLYNERETNNKLOQRKHELVDIDDIYSNFRGKVKFTQKDSQEHFTSEGTLEGGF 300

QY 92 YGYQCAGTPTNACMYGGVTLHDNNRL-----TEKKVPINLWIDGKQTTVPID 141
 Db 301 YG-----PNCBE--LGGKFLAGDNRVGVSAXEETKDKKLSRETLDGLKLTFFKTK 351

QY 142 K-----VKTSKKEVTQVELD-----LQARHYLHG-- 165
 Db 352 KTDAKTAANAKTDENKFTKDIIPSGEADYLLIDYVFLPFEENTNDFITSRHHKVGDK 411

QY 166 -----KFGLYNSDSFGGK 178
 Db 412 TYKVEACKNLSYKFGMYEDPLNGE 438

RESULT 30
 D89807
 exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: D89807
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizukami-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; I
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: D89807
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-231 <KUR>
 A:Cross-references: GB:BA000018; PID:G13700317; PIDN:BA841615.1; GSPDB:GNO0149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: set11

Query Match 8.0%; Score 98.5; DB 2; Length 231;
 Best Local Similarity 23.6%; Pred. No. 0.77;
 Matches 55; Conservative 29; Mismatches 96; Indels 53; Gaps 10;

QY 2 EKSEINE-----KLRKSELQGTALGNL--KQIYYNEKAITENKESDDQFLENTLLFK 55
Db 32 EKQERVHLYDIKDLRYYSSEFBSKVENYNGVNVRFNQE-----QNHQLF- 85
QY 56 GFPTGHPWYNDLIVDLSKDATNKYK---GKKVDLYGAYGYQCAGGTPNKTCMYGV 111
Db 86 -----LLGKD-KDKYKGLGQNVFVVKELI-----DPNGRLSTVG 122
QY 112 TLHNNRLTEKKVPINLWIDGKQTPIDKVKTSKEVTVOELDLQARHYLHGFLYN 171
Db 123 TKNNKSSETNTHLFYK-VYGNLSDASIDSLINKKEVSLKELDFKIRKQJVEKYGLYK 181
QY 172 SDSFGGKVGORGLVPHSSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNINSNL 224
Db 182 -----GTTKVKTKITNLKDEKEVIDLGDK-----LQFERMGVDVLSKDI 221

RESULT 31
E89807
exotoxin 12 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C;Accession: E89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <KUR>
A;Cross-references: GB:BA000018; PID:g13700318; PIDN:BAB41616.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: set12
C;Superfamily: toxic shock syndrome toxin

Query Match 7.9%; Score 97.5; DB 2; Length 232;
Best Local Similarity 25.6%; Pred. No. 0.93;
Matches 63; Conservative 26; Mismatches 98; Indels 53; Gaps 11;
QY 3 KSEINEK-DLRKSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 24 ENQSVNAKGYEKMRLYDT--NKLHQYSGPSYELTNVSGSQGYDYNVLLF----- 75
QY 61 HPWYNDLVLGSKDATNKYKGGK-----VDLYGAYGYQCAGGTPNKTCMYG 109
Db 76 NQONKQFQVFLGKD-ENKYEKTHGLDPAVPELVLDGRIFS-----VS 120
QY 110 GVTLDHNNRLTEKKVPINLW----IDGQTPVPIDKVKTSKEVTVOELDLQARHYLHGK 166
Db 121 GVTGNVKSIFESLRTP-NLLVKKIDDKGFSIDFEEFKKEVSLKELDFKIRKLLIKK 179
QY 167 FGLYNSDSFGKVGORGLVPHSSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNINSNL 224
Db 180 YKLYE-----GSADKGRIVNMKNENKYEIDLSDK-----LQFERMADVINSQI 224

RESULT 32
E89807
exotoxin 14 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C;Accession: G89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89807

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: GB:BA000018; PID:g13700320; PIDN:BAB41618.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: set14
C;Superfamily: toxic shock syndrome toxin

Query Match 7.6%; Score 94; DB 2; Length 227;
Best Local Similarity 25.9%; Pred. No. 1.8;
Matches 52; Conservative 31; Mismatches 76; Indels 42; Gaps 9;
QY 8 NEKDLRKSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND 66
Db 33 NQKSVNKHDK-----EALYRYTYGKTWEMKNISALKHGSNNLRFK--PRGIKIQLV 81
QY 67 LLVDLGSKDATNKYK-----KKVDLYGAYGYQCAGG--PNKTACMYGVVTLHDNN 117
Db 82 LPGNDKSKFQORSYEGLDVFFVQEKRDKHDIFY---TVGGVIQNNKTS-----GWSAPIL 134
QY 118 RLTEKKVPINLWIDGKQTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGG 177
Db 135 NISKEK-----GDAFVGKGYPIYKKEKTLKELDYKLRKHLIEKYGLYKTSKDG 185
QY 178 KVORGLIVPHSSSEGSTVSVDL 198
Db 186 RVKISL-----KDGsfynldl 201

RESULT 33
A11161
flagellar hook protein FlgE homolog lmo0697 [imported] - Listeria monocytogenes (strain I
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: A11161
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: A51077; MUID:21537279; PMID:11679669
A;Accession: A11161
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <GLA>
A;Cross-references: GB:NC 003210; PIDN:CAC98775.1; PID:g16410086; GSPDB:GN00177
A;Experimental source: strain BGD-e
C;Genetics:
A;Gene: lmo0697

Query Match 7.4%; Score 91; DB 2; Length 411;
Best Local Similarity 20.9%; Pred. No. 6.6;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;
QY 32 YNEKAITENKESDDQFLENTLL--LFKGFFTG-HPW-----YNDLIVD--LGSKDATNK 79
Db 34 YKQSVVFN-----DLLYQNTMGSVAGGLYAGTNPMSFGSGSKIGAILTDYTAGSPSTGR 89
QY 80 YKGGKVDLYGAYGYQCAGGTPNKTCMYGVVTLHDNNRLTEK----- 123
Db 90 NKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVDNNYLLTQGGKYVMGYATDKGNVL 147
QY 124 -----KVPINLWIDGKQ-----TVPIDKVKTSKEVTVOELDLQARHYLHGKFL 169
Db 148 NGNLQP-QIPLNSAIPGEATNGSLGNIFLD---WGEKDTISSELSVY----- 193
QY 170 YNSDSFGG--KVORGLIVPHSSSEGSTVSVDL-----FDAGQGY--PD 207
Db 194 ---DNAGGKHLQVNMKAATPDASGVSYEIQMDGKALTTPVVTGTLNNAQGLNPD 250

QY 208 TLLRIYRDNKTIINSENHLIALYL 230
Db 251 ALKXNI-QINSTVNGKQVNWGLNL 272

RESULT 34
A:11520
flagellar hook protein flgE homolog lin0705 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: A11520
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourman, A.; Maok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11520
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC95937.1; PID:g16413157; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0705

Query Match 7.4%; Score 91; DB 2; Length 411;
Best Local Similarity 20.9%; Pred. No. 6.6;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;

QY 32 YNEKAIENKESDDQFLENTL-LFGFFFTG-HPW-----YNDLLVD--LGSKDATNK 79
Db 34 YKQSVVFN---DLLQNTMGVAGGLYAGTNPMPFGSGSKIGAILTDYTAGSPFSTGR 89
QY 80 YGKKKVDLYGAYGYQCAGGTPTKATCMYGGVTLHDNNRLTEK-----123
Db 90 NKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVSDNNYLLTQQGKYVMGYATDKNGNVL 147
QY 124 -----KVPINLWIDGKQF-----TVPIDKVKTSKKEVTQELDLQARHVLHGKFL 169
Db 148 NGNMLQPTQIFLNSAIPGEATKNGSLSNIPLD---WGEKDTISSELSVY-----193
QY 170 YNSDSFGG--KVQRGGLIVFHSSGGSIVSYDL-----FDAQGY--PD 207
Db 194 --DNAGGKHKLQVNMKAATPDASGNVSVEYEQMDGKALTPPVGTGLVYNAQGLTNPD 250
QY 208 TLLRIYRDNKTIINSENHLIALYL 230
Db 251 ALKXNI-QINSTVNGKQVNWGLNL 272

RESULT 35
A:11553
B. subtilis YjbK protein homolog lin0964 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C/Accession: AC1553
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourman, A.; Maok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC96195.1; PID:g16413423; GSPDB:GN00178
A:Experimental source: strain Clip11262

C;Accession: C89808
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguro, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramoto, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89808
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: GB:BA000018; PID:g13700324; PIDN:BA841622.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
C;Superfamily: toxic shock syndrome toxin

Query Match 7.1%; Score 88.5; DB 2; Length 227;
Best Local Similarity 21.9%; Pred. No. 5.1;
Matches 48; Conservative 41; Mismatches 87; Indels 43; Gaps 9;

QY 10 KDLRKXSELOQTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGPTGHPWYNDLLV 69
DB 41 QDLSEYKGRGPELTNTVGKYGKVTFFIDNSQIDVTL-----TG-----NEKLT 86
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMGVTLHDNNRLTEKKVPINL 129
DB 87 VKDDDEVN-----VDVFFVREGSKSAITTS-----IGGIT-KTNGTQHKDVTQNVNL 134
QY 130 WID---GKQTT-VPIDKVTSKKEVTQVELDLQARHYLHGKFLGYNDSFGGKVGRLIV 185
DB 135 SVSKSTGQHTTSTSEYYSIYKEISLKELDFKRLKHLIDKDLKTEPKSKIR----- 189
QY 186 FHSSEGSTVSYDLFDAGQGVPTLLRIYRDNKTINSEN 224
DB 190 ITKNGGYTFEL-----NKKLQPHRGMGTIDSRNI 220

RESULT 38
T03276
GAG protein - yeast (*Candida albicans*) retrotransposon pCal
C;Species: *Candida albicans*
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Oct-1999
C;Accession: T03276
R;Matthews, G.D.; Goodwin, T.J.D.; Butler, M.I.; Berryman, T.A.; Poulter, R.T.M.
J. Bacteriol. 179, 7118-7128, 1997
A;Title: pCal, a highly unusual *tyl*/copA retrotransposon from the pathogenic yeast *Candida albicans*.
A;Reference number: Z14877; MUID:98037512; PMID:9371461
A;Accession: T03276
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <MAT>
A;Cross-references: EMBL:AF007776; NID:G2636718; PIDN:AAC49879.1; PID:G2636720
C;Genetics:
A;Mobile element: retrotransposon pCal

Query Match 7.1%; Score 88.5; DB 2; Length 324;
Best Local Similarity 25.9%; Pred. No. 7.9;
Matches 36; Conservative 20; Mismatches 50; Indels 33; Gaps 6;

QY 14 KSELOQTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGPTGHPWYNDLLV 73
DB 40 KFNLDLPKLVAGNOKSVKDWNEE-----FKYFHVAYPDVLEFLDYNP 81
QY 74 KDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMGVTLHDNNRLTEKKVPINLWIDG 133
DB 82 KD---KFKVKKVE---GYFTGWCL-----QMLQ-----SIFDFRLIMISKPLKQK 127
QY 134 KQTTVPIDKVTSKKEVT 152
DB 128 NLKAAAYDAV-TKSKDYTI 145

RESULT 39
S59650
hypothetical protein YGL170c - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein G1654
C;Species: *Saccharomyces cerevisiae*
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 19-Apr-2002
C;Accession: S59650; S64187; S20212
R;Klima, R.; Coglievina, M.; Zaccaria, P.; Bertani, I.; Bruschi, C.V.
submitted to the EMBL Data Library, March 1995
A;Description: A putative helicase, the SUA5, PMR1, tRNA-lysl genes and four open reading
A;Reference number: S59649
A;Accession: S59650
A;Molecule type: DNA
A;Residues: 1-413 <KLI>
A;Cross-references: EMBL:X85757; NID:g971381; PIDN:CA59759.1; PID:g971383
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64183
A;Accession: S64187
A;Molecule type: DNA
A;Residues: 1-413 <BRU>
A;Cross-references: EMBL:Z72692; MIPS:YGL170c; NID:g1322771; PIDN:CAA96882.1; PID:g132277
A;Experimental source: strain S288C
R;Klima, R.; Coglievina, M.; Zaccaria, P.; Bertani, I.; Bruschi, C.V.
Yeast 12, 1033-1040, 1996
A;Title: A putative helicase, the SUA5, PMR1, tRNA(Lys1) genes and four open reading
frames *Saccharomyces cerevisiae*.
A;Reference number: S72011; MUID:97051590; PMID:8896267
A;Accession: S72012
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-413 <KLM>
A;Cross-references: EMBL:X85757; NID:g971381; PIDN:CA59759.1; PID:g971383
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
C;Genetics:
A;Gene: SGD:SPO74
A;Cross-references: SGD:S0003138
A;Map position: 7L
A;Note: YGL170c
C;Superfamily: *Saccharomyces cerevisiae* hypothetical protein YGL170c

Query Match 7.1%; Score 88.5; DB 2; Length 413;
Best Local Similarity 21.0%; Pred. No. 11;
Matches 50; Conservative 37; Mismatches 80; Indels 71; Gaps 11;

QY 1 SEKSEINEKDLRKXSELOQTALGNLQKIYYNEKAITENKESDDQFLENTLL----- 53
DB 41 SKRNSPVKQKS--QKDEKSKMGSTASNI FEN-KDIHERSEHTDDFNDGLKLPDSSPS 97
QY 54 -----FK-----GFTGH--PWY-----NDLLVDLSKDATNKYKGGKVDLY 88
DB 98 LKQCQFNWSEFWCNGTEGYTKHMQPFFHTSGLEIEKEPVNMLNI--STGPKGQR----- 151
QY 89 GAYGYQCAGTGNKTAACMGVTLHDNNRLTEKKVPINLW-----IDGKQTFPI-- 140
DB 152 -----PNSAPTEYSAAITFTKQLEVSFLKTNLLTYIKKEIDICLSSVFFD 199
QY 141 DKVTSKKEVTQVELDLQARHYLHGKFLGYNDSFGGKVGRLIVFHSSEGSTVSYDL 198
DB 200 DAVQWQKFLYDRIDLDDEYEL-----KILGELLNDLNFHMQNSLNREL 247

RESULT 40
C88196
protein ZK1127.7 [imported] - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: C88196
R;anonymouse, The C. elegans Sequencing Consortium.
Science 282, 2012-2016, 1998
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology,
A;Reference number: A75000; MUID:99069613; PMID:981916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_elegans/

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: C89196
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-816 <STO>
A;Cross-references: GB:AB93429.1; PID:AB93429.1; PID:g1330372; GSPDB:GN00020; CESP:ZK1127.
A;Note: strong similarity to DNA topoisomerase II
C;Genetics:
A;Gene: ZK1127.7
A;Map position: 2

Query Match 7.1%; Score 88.5; DB 2; Length 816;
Best Local Similarity 21.9%; Pred. No. 25;
Matches 51; Conservative 30; Mismatches 59; Indels 93; Gaps 13;

Qy 19 QGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGH-----PWNDLLVDLG 72
Db 462 QGTGTGWTNPINPRELVN-----IKRLIAGEPQKALAPWYN----- 502

Qy 73 SKDATNKYKGVLDLYGAYGYQCAGGTENKTAQMGVTLHDNNRLTEEKYPINLW-- 130
Db 503 -----FRGLIIOI-----DPSRFAC-YGEVSLDNTI-EITEPIKQWTO 541

Qy 131 -----IDG-----KOTTPIDKVKTSKKEVTVQEL-----DLQARHYLHGKFG 169
Db 542 DYKEKVLGLMESDCKSPVIVD-YKEVHTDTTVKVVKLSPGKRLERLQGLHQVF-- 598

Qy 170 YNSDSFGKVGQGLIVHSSSGSVSDYLDFAQGYQFTLIRIYRDNKNTINSE 222
Db 599 -----KLOAVI-----NTTCWVLFDAAG-----WLTQTSPEAITQE 630

RESULT 41
C89803
hypothetical protein SA0357 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: C89803
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <KUP>
A;Cross-references: GB:BA000018; PID:g13700284; PIDN:BA041582.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA0357

Query Match 7.1%; Score 88; DB 2; Length 203;
Best Local Similarity 21.1%; Pred. No. 4.9; Mismatches 34; Indels 100; Gaps 12;
Matches 50; Conservative 34

Qy 1 SEKSEINEKDLRKSLEQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 37 TONSSSVQDKLQKVEEVPNN-----SEKALVKX----- 65

Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTA-CWYGGVTLHDNNRL 119
Db 66 -----LYDRYSKDTIN-----GSKNSKRNWVYGERPLNENQ-- 96

Qy 120 TEKKVPINLWIDGQTTVPIDKVKTSKE-----VTVOELDLQARHYLHGKFG 172
Db 97 -----VRIHEGTYTVA--DRVYTPKNTLNKEVVTLKELDHIIR-FAHISYGLY-- 144

Qy 173 DSFGKVGQGLIVHSSSGSVSDYLDFAQGYQFTLIRIYRDNKNTINSENL 224
Db 145 --MGEHLPGKNIVINTKDG-----GKY--TLESKELQCKRENKINTADI 186

RESULT 42

E96793
hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Sep-2003
C;Accession: E96793
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AB005173; NID:G6642673; PIDN:AAF20253.1; GSPDB:GN00141
C;Genetics:
A;Gene: F14G6.15
A;Map position: 1
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokin

Query Match 7.1%; Score 88; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 19;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGVLDLYGAYGYQCAGGTENKTAQMGVTLHDNNRLTEE 122

Db 412 KGTG--YKGGKNAICHFFGYQARSLFSKFDYAYLVGHVCHYLAAGLNGYATVTN 469

Qy 123 KKVPIINLWIDGQTTVPIDKVKTSK 148

Db 470 LKSPVKNW--KCGAAPISAMWTVKR 492

RESULT 43

E69886
processing proteinase homolog ymxG - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: E69886; B46665; S34595
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Scoffone, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:19804033; PMID:9384377
A;Accession: E69886
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-409 <KUN>
A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13544.1; PID:g26334043
A;Experimental source: strain 168
R;Chen, N.Y.; Jiang, S.Q.; Klein, D.A.; Paulus, H.
J. Biol. Chem. 268, 9448-9465, 1993
A;Title: Organization and nucleotide sequence of the Bacillus subtilis diaminopimelate op
se.

A;Reference number: A46665; MUID:93252813; PMID:8098035
A;Accession: B46665
A;Molecule type: DNA
A;Residues: 30-269, 'LE', 272-359, 'Q', 361-409 <CHE>
A;Cross-references: EMBL:L08471; NID:g142823; PIDN:AAA2379.1; PID:g142824
C;Genetics:
A;Gene: ymxG
C;Superfamily: mitochondrial processing peptidase alpha chain

Query Match 7.1%; Score 87.5; DB 2; Length 409;
Best Local Similarity 22.4%; Pred. No. 13;
Matches 55; Conservative 43; Mismatches 79; Indels 65; Gaps 15;

QY 10 KDLRK--KSELOGTALGNLKIYYNEKAITENKESDDOFLNTLLFKGFTTGHFWYND 66
DB 198 KDVEKWFGEYAEAKGATG-LEKPEFTEK-LTRKKETQAHLL--CLGFKGLEVGHERIYD 253
QY 67 LLY--DLGSKDATNKY-----KGRKVDLYGAYGYOCAGTGNKTAACMYGGVTLHDNN 117
DB 254 LVLNNVLGSMSSRLFDQVREDKGLAYSIVSYHSSYEDSG-----MLTIYGTGANQLQ 308
QY 118 RLTEKKVPINLWIDKQTTVPIDKVTSSKE-VTVQELDLQARHYLHGKFLGNSDSFG 176
DB 309 QLSE-----TIQ-ETLTLKRDGITSKELE-NSKEQMKGSL-MLSLESTN 350
QY 177 GKVORG-----LIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENLH-IALYL 230
DB 351 SKMSRNGKHELLGKHK-----TLDEIINELNANVLERVNGLARQL 391
QY 231 YT 232
DB 392 FT 393

RESULT 44
T08145
myrosinase-binding protein 2 - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08145
R;Taipalensuu, J.; Falk, A.; Ek, B.; Rask, L.
Eur. J. Biochem. 243, 605-611, 1997
A;Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti
A;Reference number: Z16379; MUID:97210758; PMID:9057822
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-634 <TAI>
A;Cross-references: EMBL:U59444; NID:g1555825; PIDN:AAC08049.1; PID:g1555826
A;Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollinat

Query Match 7.1%; Score 87.5; DB 2; Length 634;
Best Local Similarity 22.4%; Pred. No. 22;
Matches 64; Conservative 27; Mismatches 86; Indels 109; Gaps 15;

QY 10 KDLRKSELOGTALGNLKIYYNEKAITENKESDDOFLNTLLFKG-FTTGHFWYND 66
DB 178 KDGKVEIREHGTNRGQLKFEFSDVPNDNI VAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 237
QY 67 LLVDLGSKDAT-----NKYK-----GKKVDLYGAYY--GYOCA-GGTENKTACMY 108
DB 238 PL--FGEKTGDTDFEFGENRGKLLGFHGRAGYDAIGAIFHTGSGGEGGDPK----- 290
QY 109 GGVTLHDNNRLTBEKKVPI-----NLWIDGKQ-----TTVPIDKV 143
DB 291 GG-----PKPVVPVKGPLGDRGNFNDVGDGKRVAVAADEFSVTYIKIEV 340
QY 144 KTSKKEV-----TVQELDLQ-----ARHYLH 164
DB 341 KDGKVEIREHGTNRGQLKFEFSDVPNDNI VAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 400
QY 165 GKFLYNSDSFGGKVGORG--LIVFHSSEGSTVSYDLFDAQOQYPTD 208

Db 401 PLFGEMKGTFFPKGNGEKLIGFHGRAGHAI-----DAIGAIFDT 441

RESULT 45
T08144
myrosinase-binding protein 1 - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08144
R;Taipalensuu, J.; Falk, A.; Ek, B.; Rask, L.
Eur. J. Biochem. 243, 605-611, 1997
A;Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti
A;Reference number: Z16379; MUID:97210758; PMID:9057822
A;Accession: T08144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-956 <TAI>
A;Cross-references: EMBL:U59443; NID:g1555823; PIDN:AAC08048.1; PID:g1555824
A;Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollinat

Query Match 7.1%; Score 87.5; DB 2; Length 956;
Best Local Similarity 22.4%; Pred. No. 37;
Matches 64; Conservative 27; Mismatches 86; Indels 109; Gaps 15;

QY 10 KDLRKSELOGTALGNLKIYYNEKAITENKESDDOFLNTLLFKG-FTTGHFWYND 66
DB 487 KDGKVEIREHGTNRGQLKFEFSDVPNDNI VAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 546
QY 67 LLVDLGSKDAT-----NKYK-----GKKVDLYGAYY--GYOCA-GGTENKTACMY 108
DB 547 PL--FGEKTGDTDFEFGENRGKLLGFHGRAGYDAIGAIFHTGSGGEGGDPK----- 599
QY 109 GGVTLHDNNRLTBEKKVPI-----NLWIDGKQ-----TTVPIDKV 143
DB 600 GG-----PKPVVPVKGPLGDRGNFNDVGDGKRVAVAADEFSVTYIKIEV 649
QY 144 KTSKKEV-----TVQELDLQ-----ARHYLH 164
DB 650 KDGKVEIREHGTNRGQLKFEFSDVPNDNI VAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 709
QY 165 GKFLYNSDSFGGKVGORG--LIVFHSSEGSTVSYDLFDAQOQYPTD 208
DB 710 PLFGEMKGTFFPKGNGEKLIGFHGRAGHAI-----DAIGAIFDT 750

Db 401 PLFGEMKGTFFPKGNGEKLIGFHGRAGHAI-----DAIGAIFDT 441

RESULT 46
H71602
protein with DnaJ domain (RESA-like) PFB0920w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: H71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: H71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1014 <GAR>
A;Cross-references: GB:AE001425; GB:AE001362; NID:g3845310; PIDN:AAC71973.1; PID:g3845311
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0920w
A;Superfamily: dnaJ amino-terminal homology
F:677-742/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 7.1%; Score 87.5; DB 2; Length 1014;
Best Local Similarity 23.0%; Pred. No. 40;
Matches 50; Conservative 35; Mismatches 77; Indels 55; Gaps 10;

QY 6 EINKDLRKSELOGTALGNLKIYYNEKAITENKESDDOFLNTLLFKGFTTGHFW-- 63

```

Db      218 EFVENEKEKYYLKG-----RLYKNNKFKWENKYTDE-----YPPRKKWNN 259
Qy      64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGVTLLHNNRLTEEK 123
      : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      260 YNDLIYK-GSKLEELKNKFYEWY-----KQENLNLEEVYR 294
Qy      124 KVPINLWIDGQQTVPIDKVKTKSKEVTVQELD-LQARHVLHGKFGLYNSD-SFGGKQVR 181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      295 RLVLVCRGTGWAL---YNYVENTCKEIIHSDLDIIRKKGNNKGLYNNYKNGK--- 348
Qy      182 GLIVFHSSEGSTVSVDLFDQAQGVDPDTLLRIYRDNKT 218
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      349 -NIPFNTS-SSIDNKKLYNFGKFNPMCFNYEDSLT 383
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 47
DVZQF
N:multidrug resistance protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: P-glycoprotein
C:Species: Plasmodium falciparum
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
C:Accession: S18204; A32547
R:Trigilia, T.; Foote, S.J.; Kemp, D.J.; Cowman, A.F.
Mol. Cell. Biol. 11, 5244-5250, 1991
A:Title: Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum
A:Reference number: S18204; MUID:92017800; EVID:1922044
A:Accession: S18204
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1419 <TRI>
A:Cross-references: EMBL:X56851; NID:G9935; PIDN:CAA04180.1; PID:G9936
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1990
R:Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.
Cell 57, 921-930, 1989
A:Title: Amplification of the multidrug resistance gene in some chloroquine-resistant is
A:Reference number: A32547; MUID:9288297; EVID:2701941
A:Accession: A32547
A:Molecule type: mRNA
A:Residues: 1-1419 <FOO>
A:Cross-references: GB:M29154; GB:M24322; NID:G160398; PIDN:AAA29646.1; PID:G160399
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
C:Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane ph
F:1-632,655-1276/Region: duplication
F:396-638/Domain: ATP-binding cassette homology <ABC1>
F:413-420/Region: nucleotide-binding motif A (P-loop)
F:583-587/Region: nucleotide-binding motif B
F:1144-1387/Domain: ATP-binding cassette homology <ABC2>
F:1161-1168/Region: nucleotide-binding motif A (P-loop)
F:1332-1336/Region: nucleotide-binding motif B

Query Match 7.0%; Score 87; DB 1; Length 1419;
Best Local Similarity 21.8%; Pred. No. 67;
Matches 65; Conservative 37; Mismatches 112; Indels 84; Gaps 15;
Qy      3 KSEINEKD-----LRKSELQGTALGNLQKI-----YYYN--EKAIT 38
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      955 KSKIEKKNNSSGVAFSPSDENFKDPSPFIQIAFTNMTVINYGLDYFCNLIEAK 1014
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      39 -ENKESDDQLFENTLLFKGFTGHP-----WYNDLLVDLGS-----KDA-----T 77
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1015 YKNGQKRRIIIVNAALW-GFQSQAQLFINSPAYFGSFLIKRGITILVDVDFWKSLETFIT 1073
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      78 NKYKGVKVDLYG-----AYYQCA-----GGTPNKTAQMGVGLHP-NN 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1074 GSYAGKMLSLGSDSENAKLSPEKYPLMIRKSNIDVRDDGGRINKRLIKGVDIKDNWF 1133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      118 RLTEKKVPI---NLWIDGQQTVPIDKVKTSK---EVTVELDLQASHYL-----HGK 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1134 RYISRPNVPIYKNI-SFTCDSKTTIAYGEIGSGKSTFWNLLRPYDLKNDHILKNDWTN 1193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      167 FGLYNSDSFGKVGKVRGLIVFHSSEGSTVSVDLFDQAQGVDPDTLLRIYRDNKTINSENL 224
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1194 QDYQNNNNSLVLKNNVEFNFGSQAEDYTVFNNGE-----ILLDDINI CYNL 1244
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 48
AF1489 cell wall-associated protein precursor wapA (B. subtilis) homolog lin0454 [imported] - Lj
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: AF1489
R/Glaser, P.; Franjeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Dominguez-Bernal, G.; Duchaud, E.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat Ok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A/Reference numbers: AB1077; MUID:21537279; PMID:11679663
A/Accession: AF1489
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2167 <GLA>
A/Cross-references: GB:ALU592022; PIDN:CA095686.1; PID:gl61412895; GSPDB:GN00178
A/Experimental source: strain Cl1p1262
C/Genetics:
A/Gene: lin0454

	Query Match	7.0%;	Score 87;	DB 2;	Length 2167;
	Best Local Similarity	24.0%;	Pred. No. 1.le+02;		
	Matches 56; Conservative	27;	Mismatches 86;	Indels 64;	Gaps 14;
Qy	30 YYNKEAITENKSDDOFLENTLFFGFFFTGHP- -WYNDL- ---LVDLGSKDATNKY- KG 82	:	:	:	:
Db	1671 YTYKDPTKNKGKTDKVGE- VAINHGDIYAKSYTYNDLDRTRVNDGSKNAYFEDEF 1729	:	:	:	:
Qy	83 KKYDLY- - -GAYGYQCAGTPNKTCMYGGVTLHDNRUTE- --EKVPINLMIDGK 134	:	:	:	:
Db	1730 GNIINVYTAGNGTAANYTDSYTKVTNAATSSASGTQILDENITYDYDAASNRTSIDNKODGK 1789	:	:	:	:
Qy	135 QTTVPIDKVKTSKEVTNVQSLD;-QARHYLHKGKFLXNSDSFGKKVGORGLTVFHSSEGSTV 194	:	:	:	:
Db	1790 -TTYEYDAVNQLIKE-TLPD- -----GTWKATYDFGNRTO- --VAISGSEFKTI 1834	:	:	:	:
Qy	195 --SYD-----LFDAQGVDPDTLLR;YRDNKNTINSNLHIALXYLT 232	:	:	:	:
b	1835 DASVNDGNOLVSNNGEALTYDANG-----NRTSDGK-----TYT 1869	:	:	:	:

RESULT 49

D96342
hypothetical protein F9H16.6 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Sep-2003
C:Accession: D96342
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chir, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Manser, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, C.A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schaffner, S.; Schwart, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Xie, M.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A96141; MUID:21016719; PMID:11130712

A:Residues: 1-614 <STO>
A:Cross-references: GB:AE005172; NID:G9836893; PIDN:AAD30536.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type, 6-phospho-
Query Match 7.0%; Score 86.5; DB 2; Length 614;


```
Db 390 -----KRSSIIIFINK--STNKKDLIKLQNE-----NIKVANLINIKINCL 428
QY 231 YT 232
Db 429 YT 430

RESULT 53
AG1749
Glycosidase homolog lin2540 [imported] - Listeria innocua (strain Cl1p11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1749
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1749
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1090 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97767.1; PID:gl6415062; GSPDB:GN00178
A:Experimental source: strain Cl1p11262
C:Genetics:
A:Gene: lin2540

Query Match 6.9%; Score 86; DB 2; Length 1090;
Best Local Similarity 22.5%; Pred. No. 58;
Matches 47; Conservative 35; Mismatches 61; Indels 66; Gaps 14;

QY 33 NEKAITENKESDDOFLNTLLFKGFF---TGHP-----WY-NDLLVDLGSKDATNKY 80
Db 491 DDNTVYGEORNDY----MSQVSADDTGAGYRVPASQWFGNLLDFTNKDANWV 546
QY 81 KGKK-----VDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWID 132
Db 547 TSQREYLLTDVGID-----GFKTDGG---EMVWGRDITTFSGEKGQENR----- 587
QY 133 GKQTVIPIDKVKT---SKKEVTVELDLOARHYLHG--KFGLYNS-----DSFGKQV 180
Db 588 ---NRYPTDYSSVDFPAKSNPEAVSF--SRSGTGAQKSGIYWSGDTTFDSFQASVX 643
QY 181 RGLIVFHSSEGSTVSY---DLFDAQGOVP 206
Db 644 AGL---SASTSGVSYWANDMAGFTGNYP 668

RESULT 54
G86903
cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: G86903
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: AG6625; MUID:21235186; PMID:11337471
A:Accession: G86903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: GB:AE005176; PID:gl2725299; PIDN:AAK06329.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: mreC

Query Match 6.9%; Score 85.5; DB 2; Length 291;
Best Local Similarity 20.0%; Pred. No. 12;
Matches 46; Conservative 26; Mismatches 67; Indels 91; Gaps 8;
```

```
QY 23 LGNLKOIYYNEKAIT-----ENK-----ESDDOFLNTLLFKGFFTGH----- 61
Db 69 LSNLMDTYOQNSLKTQLAKSKDDDNKLSGSEENKELKALKLOETLTDYQTVAANVIT 128
QY 62 ----PWYNDLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNN 117
Db 129 REPSSWNTLVIDSGKD-----GLTGMVWANGGV-----G 162
QY 118 RLTE-----EKKVPINLWIDGKQTVIPIDKVKTSKKEVTVOELDLQAR 160
Db 163 RVTQVNNKSSKVALSSXGIDNKIPVIESDGSPIYGILSSYDSQOEAYVVKNIQSQ-- 220
QY 161 HYLHGKFLYNSDFSGKQVQGLIVFHSSEGSVSYVDLFDAGQGYDPTLL 210
Db 221 -----GKFGNSDVSFTSLGLTNSG-----SQGTPSGLL 249

RESULT 55
AH1793
ABC transporter, ATP-binding protein homolog lin2894 [imported] - Listeria innocua (stra
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1793
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1793
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC98120.1; PID:gl6415429; GSPDB:GN00178
A:Experimental source: strain Cl1p11262
C:Genetics:
A:Gene: lin2894
C:Superfamily: Ischerichia coli ABC transporter mdla; ATP-binding cassette homology

Query Match 6.9%; Score 85.5; DB 2; Length 573;
Best Local Similarity 23.8%; Pred. No. 29;
Matches 46; Conservative 29; Mismatches 81; Indels 37; Gaps 8;

QY 22 ALGNLKKQI--YYNEKAITENKESDDOFLNTLLFKGF---FTGH--PWYNDLLVD---- 70
Db 298 ALISLARITEVLETPDIYENAPEQDLEGVFRNVSFKYDGDTPALEDISFKANVG 357
QY 71 --LGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPIN 128
Db 358 EMVGIVGATGSGKSTLAQLIPLY-----DPTGEVIGGTNLKDKINKTLRSTVSFV 410
QY 129 LMTDGGQTVIPIDKVKTSKKEVTVOELD-----LQARHYLHGKFLYNS-----DSFG 177
Db 411 LQRAILFSTIADNLNHHKKQATIDEMEHASKIAQKPIDKQAKLYEAFVSERGNFSG 470
QY 178 -----KVQRGLT 184
Db 471 GQKQRLSITRGVI 483

RESULT 56
C89888
hypothetical protein SA1011 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89888
R:Kuroda, M.; Onca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
```

A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: C89888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <KUR>
A;Cross-references: GB:BA000018; PID:gi3700967; PIDN:BA842263.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
C;Superfamily: toxic shock syndrome toxin

Query Match 6.9%; Score 85; DB 2; Length 241;
Best Local Similarity 23.9%; Pred. No. 11;
Matches 44; Conservative 31; Mismatches 63; Indels 46; Gaps 10;
QY 63 WYNDLLVGLSKD--ATNKYKGGKVDLYG-----AYGYQ--CAGGTNKTACMYG 109
Db 84 WSHIQV-FGSESWGNINQLRNKYVDIFGTKDIEDVGEYWTYDETFTGGVTPAAT----- 137
QY 110 GVTLDHNNRLTEKKVPINLWIDGKQTV--PIDKVKTSKEVTVQELDLQARHYLHGKF 167
Db 138 -----SSDKPYRLFLKYSKQQTIGGHEFYKGNKPVLTLEKELDFRIQTLINKK 187
QY 168 GLYNSDFGKVGQGLIVFHSSEGSTSVSYDLFDAQOQYDPTLLRIYRDNKT--NSENLI 226
Db 188 KLYN-----GEFNKGQIKI-TADGNNTIDL-----SKKLKLTDTNRYVKNPNAQI 233
QY 227 ALYL 230
Db 234 EVIL 237

RESULT 57

T10102
diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor
N;Alternate names: 6-phosphofructokinase (pyrophosphate)
C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2003
C;Accession: T10102
R;Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
Gene 152, 181-186, 1995

A;Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophosphatase
A;Reference number: Z16949; MUID:95137384; PMID:7835697

A;Accession: T10102
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-617 <TOD>
A;Cross-references: EMBL:Z32849; NID:G483546; PIDN:CAA83682.1; PID:G483547
C;Genetics:
A;Introns: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 373/3
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfFB type; 6-phosphofructokinase
C;Keywords: phosphotransferase

Query Match 6.9%; Score 85; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 35;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

QY 74 KDATNKYKGGKVDLYGAYGYQCAGGTNKTACMYGGVT-----LHNNRLTEE 122
Db 412 KEGT--YKGGKFNACIFFGQARGSLPSKFDYAYVLGHICYHVLAAGLNGYMATATN 469
QY 123 KKVPIINLWIDGKQTVPIDKVKTSKK 148
Db 470 LKPNVKNWRCG---AAPIAAMTVKR 492

RESULT 58

G71615
phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (*Plasmodium falciparum*)
C;Species: *Plasmodium falciparum*
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: G71615

R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; ; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
A;Reference number: A71600; MUID:99021743; PMID:9804551

A;Accession: G71615
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-679 <GAR>
A;Cross-references: GB:AE001393; GB:AE001362; NID:G3845175; PIDN:AACT71871.1; PID:G384517;
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0410c

Query Match 6.9%; Score 85; DB 2; Length 679;
Best Local Similarity 19.3%; Pred. No. 39;
Matches 50; Conservative 35; Mismatches 112; Indels 62; Gaps 7;

QY 3 KSEINEKDLRKSELOQTALGNLKOIYYNEXAITEKESDDQFLENTLLFKGFFTHP 62
Db 185 KNEITSNYSNLANNEINKICKYNLDQTDILLDSNSERRENSKFKIKNTNYDNLQNK 244
QY 63 WYNDLLV-DLGSKDATNKY-----KQKVDLYGAYGYQCAGGTNKTAC 106
Db 245 YTNSILYDDDDDKNNTETCTFTKEDQIRVPSQKKKIYLYNKY-----DNATL- 294
QY 107 MYGVTLDHNNRLTEKKVPINLWIDGKQTVPIDKVKTSKEVTVQELD-----L 157
Db 295 ---DLNVHTYNSLQMSILCKYSLLYCCKYNHIIIPDPTPKKPVLSLDGGILITSL 351
QY 158 QARHYLHGK-----FGLYNSDFGKVGQGLIVFHSSEGSTSVSYDLFDAQ 202
Db 352 LVLNLEALRKEIGSDDIKLIDCFDMVCGTSAGLISALL-----REIDLQDVS 402
QY 203 GOYDPTLLRIYRDNKTINS 221
Db 403 NMWPSTIKKVFEGNRNIIS 421

RESULT 59

T30545
major surface glycoprotein - *Pneumocystis carinii* (fragment)

C;Species: *Pneumocystis carinii*
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C;Accession: T30545

R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A. Infect. Immun. 66, 4268-4273, 1998

A;Title: Characterization of major surface glycoprotein genes of human *Pneumocystis carinii*.
A;Reference number: Z17905; MUID:98380374; PMID:9712777

A;Accession: T30545

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1014 <MEI>

A;Cross-references: EMBL:AF038556; NID:G3560524; PID:G3560525; PIDN:AACT34980.1

A;Experimental source: f.sp. hominis

C;Genetics:

A;Gene: msg1

C;Superfamily: *Pneumocystis carinii* major surface glycoprotein MSG100

Query Match 6.9%; Score 85; DB 2; Length 1014;
Best Local Similarity 26.3%; Pred. No. 64;
Matches 45; Conservative 27; Mismatches 63; Indels 36; Gaps 9;

QY 2 EKSEINE---KDLRKSELOQTALGNLKOIYYN-----EKAITEKESDDQFLENT 51
Db 328 EKCKKILEDKCKNLKEHDIING-----LCEDYNANKDKKKCEELSTDIETCKFFISKT 382

QY 52 LLFKGFFTGH-----PWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTNPK-- 103

Db 383 LMIHFFDGGNKNDDGIKAGN-LSTFLENKDKT-----KLESLYCEKSCRSSETACKNI 435

QY 104 -TACMYGQVTLHNNRLTEKKVPIN---LWIDGKQTVPIDKVKTSKKE 149

Db 436 RAACYKRGDLTIANEVLQKEMRGLHGSNKTWLSGFQKKL-IEVCKVKYKE 485

RESULT 60

T31076

tyrocidine synthetase 3 - Brevibacillus brevis

C:Species: Brevibacillus brevis

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000

C:Accession: T31076

R:Mootz, H.D.; Marahiel, M.A.

J. Bacteriol. 179, 6843-6850, 1997

A:Title: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequence

A:Reference number: Z20969; MUID:98012987; PMID:9352938

A:Accession: T31076

A:Status: preliminary

A:Superfamily: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6486 <MOO>

A:Cross-references: EMBL:AF004835; NID:G2623770; PID:G2623773; PIDN:AA045930.1

C:Genetics:

A:Gene: tycC

C:Function:

A:Pathway: tyrocidine biosynthesis

C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology

C:Keywords: carrier protein; phosphopantetheine; phosphoprotein

F:510-950/Domain: acetate-CoA ligase homology <ACLI>

F:968-1036/Domain: acyl carrier protein homology <ACPI>

F:1546-1987/Domain: acetate-CoA ligase homology <ACLI2>

F:2005-2073/Domain: acyl carrier protein homology <ACPI2>

F:2583-3025/Domain: acetate-CoA ligase homology <ACPI3>

F:3043-3111/Domain: acyl carrier protein homology <ACPI3>

F:3621-4060/Domain: acetate-CoA ligase homology <ACPI3>

F:4078-4146/Domain: acyl carrier protein homology <ACPI4>

F:4636-5104/Domain: acetate-CoA ligase homology <ACLI5>

F:5122-5190/Domain: acyl carrier protein homology <ACPI5>

F:5702-6147/Domain: acetate-CoA ligase homology <ACPI6>

F:6165-6233/Domain: acyl carrier protein homology <ACPI6>

F:1000, 2037, 3075, 4110, 5154, 6197/Binding site: phosphopantetheine (Ser) (covalent)

Query Match 6.9%; Score 85; DB 2; Length 6486;

Best Local Similarity 20.5%; Pred. No. 6.6e+02;

Matches 50; Conservative 42; Mismatches 76; Indels 76; Gaps 12;

Qy 16 SELOQTALGNLKQIY-----YYNEKAITENKESDDQFLENTLLFKGFTHG--PWY 64

Db 789 ASMPVPVGSIGEMVIAGDGVAKYFNPELTKEKFDINPRPCTKYR---TGLAKWL 845

Qy 65 NDLLVD-LGSKDATNKYKGVLDYGYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123

Db 846 PDGMEVAGRDYQVKIRHRIEM-----GBI-----ETRLTQHE 880

Qy 124 KVPINLWIDGKQTTVPIDKVKT-----SKKEVTVOELDLQARHYLHGKFLYNSD 173

Db 891 AV-----KEAVVIVEKESGQNVLYALVSRERETVAEL-----REFLGRILPSYMP 928

Qy 174 SF-----GKQVORGLIVFHSSEGSTVSYDLDLFA-QGQVPDILLRTYRDNKTINS 221

Db 929 SFFIRLAPILTANGKVERKEL--PKPAGAVVTGTAVAPQNEIAKLAEIWOQVLGISQ 986

Qy 222 ENLH 225

Db 987 VGIH 990

RESULT 61

AF1418

ABC transporter, ATP-binding protein homolog lmc2751 [imported] - Listeria monocytogenes

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AF1418

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karsst, U.

Science 294, 849-852, 2001

A:Authors: Krefth, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-573 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAD00964.1; PID:G16412251; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmc2751

C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology

Query Match 6.8%; Score 84.5; DB 2; Length 573;

Best Local Similarity 23.8%; Pred. No. 35;

Matches 46; Conservative 29; Mismatches 81; Indels 37; Gaps 8;

Qy 22 ALGNLKOI--YYNEKAITENKESDDQFLENTLLFKGF---FTGH--PWYNDLLVD---- 70

Db 298 ALISLKRITETLETPDITYNENAPQDLEGTVEFRNVSFKYDGDTPALEDISFKASVG 357

Qy 71 --LGSKDATNKYKGVLDYGYGYQCAGTGNKTACMYGGVTLHDNNRLTEKKVPIIN 128

Db 358 EMGIVGATGSGKSTLAQLIPRLY-----DPTGEVIIGTGNLKDINKTLRSTVSFV 410

Qy 129 LWIDGKQTTVPIDKVKTSKEVTVOELD-----LQARHYLHGKFLYNS-----DSFGG 177

Db 411 LQRAILFSGTIADNLRHGKDATAEEMHASKIAQAKFEIDQAKLYEAPVSEGGNFSG 470

Qy 178 -----KVORGLI 184

Db 471 GQKQLSITRGVI 483

RESULT 62

S36523

E1 protein - human papillomavirus type 35H

C:Species: human papillomavirus type 35H

C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999

C:Accession: S36523

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36523

A:Molecule type: DNA

A:Residues: 1-637

A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52563.1; PID:G397000

A:Experimental source: strain 35H

C:Superfamily: papillomavirus E1 protein

C:Keywords: early protein; nucleus

Query Match 6.8%; Score 84.5; DB 2; Length 637;

Best Local Similarity 20.9%; Pred. No. 40;

Matches 53; Conservative 41; Mismatches 91; Indels 69; Gaps 11;

Qy 21 TALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTHGFWYNDLLVDLGSKATNKY 80

Db 310 TAMSNISEV-----DGETPEWIRQTVLQHSF-----NDALFDL-SEMVQWAY 351

Qy 81 KKKVDLYGAYGYQCAGTGNKTACMY-----GGVTLHDNNRLTEKKVPIINL 129

Db 352 DNDFDIDSDIAKYQALET--NSNACAFKLSQAKIVKDCATMCRHYKAEKREMTMSQ 410

Qy 130 WIDGKQTTVPID-KVTSKEVTVOELDLQA-----RHYLHGK-----FGLYNSDSF 175

Db 411 WIKRRCRKVDDGDRDVRFLRYQQVDFAFLSKNLFHGVPKNCILLYCAPNT--- 467

Qy 176 GKQVQGLVFEHSSEGSTVSY-----DLFDAQ-----GQVPTLLRIYR 214

Db 468 -GKSLFGLMFLQCAILSYVNSKSHFWLQPLYDAKIAMLDDATSPCWAYIDQYLRLAL 526

QY 215 DNKTINSENHIAL 228
DB 527 DGNPISLDVKGKAL 540

RESULT 63
A97334
type II restriction enzyme, methylase chain [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: A97334
R: Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A97334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-993 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81460.1; PID:G15026629; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC3535

Query Match 6.8%; Score 84.5; DB 2; Length 993;
Best Local Similarity 22.9%; Pred. No. 69;
Matches 47; Conservative 33; Mismatches 62; Indels 63; Gaps 11;

QY 14 KXSELOGTALGNLKOYYNNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLLVDLGS 73
DB 663 KRKVSVSSVGNLFW-----ALVANK--DD-----MSLVK 690

QY 74 KDATNKYK-GKKYVDLYGAYGYQCAGGTENKTCACMYGGVTLHNNRLTEKKVP-INLWID 132
DB 691 KMYRNSVKGKEVELN---GIOTSAERP-----PIYFSDKEILESELYFKIKKK 739

QY 133 GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGELNSDSFGKGVQRLVIF-HSSEG 191
DB 740 DKQYIIEKILKRYFVKLVKKEKNL-----GSYDIFDTNKP-----IIFPINHEG 784

QY 192 STVSYDLFDAQQGYPTLLRIYRDN 216
DB 785 KL--YDLNTMETEYPNT-LRYLMDN 806

RESULT 64
T07067
beta-fructofuranosidase (EC 3.2.1.26) LIN5 - tomato (fragment)
N:Alternate names: invertase
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
C:Accession: T07067
R: Godt, D.E.; Roitsch, P.
Plant Physiol. 115, 273-282, 1997
A:Title: Regulation and tissue-specific distribution of mRNAs for three extracellular inulinases in tomato
A:Reference number: Z15997; MUID:97451780; PMID:9306701
A:Accession: T07067
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-241 <OOD>
A:Cross-references: EMBL:X91389; NID:G1771149; PIDN:CAA62734.1; PID:G1771150
A:Experimental source: cultivar MoneyMaker; leaf
C:Genetics:
A:Gene: LIN5
C:Superfamily: beta-fructofuranosidase
C:Keywords: cell wall; glycosidase; hydrolase

Query Match 6.8%; Score 84; DB 2; Length 241;
Best Local Similarity 21.2%; Pred. No. 13;
Matches 55; Conservative 28; Mismatches 76; Indels 100; Gaps 13;

QY 26 LKQIYYNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLLVDLGSKDAIN----- 78

DB 1 LHLFYQYNPK-----GSWGNIIWAHSVSKDLINWIHLEPA 36
QY 79 KYGKKVDLYGAYGYQCAGGT-NKTACMYGGVTLHNNRLTEKKVPINL-----W 130
DB 37 IYFSKKFDKYGTSWGSSTI--LPNKPVIITGVDSYNNQV-QNYAIPANLSDPFLRKW 93
QY 131 I--DGKQTTVPIDKV-KTSKKEVTVOELD-----L 157
DB 94 IKPNNPLIYVDSINSINRTEPRDPTTAMWGQGLWRILIASMRKRGWALLYRSRDFMKWI 153
QY 158 QARHYLHGKGLYN---SDSFGKGVQRLVIFHSSEGSTVSVDLFDACQGYPTLLRIYR 214
DB 154 KAQHPLHSSNTNGWECDFDP-----VLFNSTINGLDVSY-----K 191
QY 215 DNKTINSENHIALYLYTT 233
DB 192 NVKYLKNSLDVAREFYTT 210

RESULT 65
A99582
hypothetical protein MYPV 5610 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: A99582
R: Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: A99582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KUR>
A:Cross-references: GB:AL445566; PID:G14089976; PIDN:CAC13734.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPV 5610
A:Genetic code: SGC3
C:Superfamily: DNA-directed RNA polymerase alpha chain

Query Match 6.8%; Score 84; DB 2; Length 333;
Best Local Similarity 23.5%; Pred. No. 19;
Matches 38; Conservative 24; Mismatches 38; Indels 62; Gaps 9;

QY 25 NLKOIY-YNNEKAITENK-----BDDQFLENTLLFKGFTTGHFWYNDLLV 69
DB 82 NVKNHLYVDENIFEDNKIYRGVIETKNEKITSSDLKFPENP-----EI 125

QY 70 DLGSKD---ATNKYKGGKVDLYGAY---GYCAGGTENKTCACMYGGVTLHNNRLTEE 122
DB 126 EIVNKDLEIATN--NGOKPFVMEVYFHVGRGY-----ISFENKKLIEE 167

QY 123 KKVPIINLWID-GKQTTV-----PIDKVTSKKEVTVOELDLQ 158
DB 168 KVALINSTIKRGFLAIDSFSPVERKVKVQVEINSSSLNIE 209

RESULT 66
T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41863
R: Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>

RHOICK, A.; NAES, H.
J. Gen. Microbiol. 138, 1353-1364, 1992

RHOICK, A.; NAES, H.
J. Gen. Microbiol. 138, 1353-1364, 1992

A>Title: Cloning, sequencing and expression of the gene encoding the cell-envelope-associated protein A:Reference number: A44858; MUID:92381481; PMID:1512565
A:Accession: B44858
A:Molecule type: DNA
A:Residues: 1-1902 <HOL1>
A:Cross-references: GB:M3946; NID:G149580; PID:AAA25248.1; PID:G149582
A:Note: sequence extracted from NCBI backbone (NCBIN:112261, NCBI:P112263)
A:Note: the source is designated as Lactobacillus paracasei subsp. paracasei
A:Accession: C44858
A:Molecule type: protein
A:Residues: 189-196 <HOL2>
E:Naes, H.; Nissen-Meyer, J.
J. Gen. Microbiol. 138, 313-318, 1992
A>Title: Purification and N-terminal amino acid sequence determination of the cell-wall-associated protein A:Reference number: A44850; MUID:92226694; PMID:1564442
A:Accession: A44850
A>Status: preliminary
A:Molecule type: protein
A:Residues: 189-196 <NA2>
A:Cross-references: PID:AA22052.1; PID:G248666
A:Experimental source: strain NCDO 151
A:Note: sequence extracted from NCBI backbone (NCBI:P94706)
C:Genetics:
A:Gene: prpP
C:Superfamily: lactocepin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:23-187/Domain: propeptide #status predicted <PRO>
F:188-1902/Product: serine proteinase, cell-envelope-associated #status experimental <M2>
F:208-634/Domain: subtilisin homology #status atypical <SBT>

Query Match 6.8%; Score 84; DB 1; Length 1902;
Best Local Similarity 25.8%; Pred. No. 1.7e+02;
Matches 51; Conservative 12; Mismatches 69; Indels 66; Gaps 8;

QY 46 QFLENTLLFK-----GFFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYYG 93
DB 805 QFVEGLNFKSGDGRNLNLYMGFFGD--WND-----GKIVDSLNG-IT 845

QY 94 YQAGGTPNTACVGGVTLHNNRTEKKVPINWIDGKQTVIPIDKVKTSKEVTVO 153
DB 846 YSPAGN-----YGTVPILLTNKTHGYGGMVTDADGKQT----- 881

QY 154 ELDLQARHLYHGKFLGNSDFGKVGQGLVPHSSEGSTVSVDLFDAGQYPTDLLRIY 213
DB 882 -VDDQAIASFSDKKNALVINDISMOYLLRNI-----SNVQVLDGGGNKVTLLSS-- 930

QY 214 RDNKTINSENHIALYLY 231
DB 931 STNQTKTYDAHSQKXIY 948

RESULT 70
S00485
gene 11-1 protein precursor - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000
C:Accession: S00485
E:Scherf, A.; Hilbich, C.; Sieg, K.; Mattei, D.; Mercereau-Pujalon, O.; Mueller-Hill, E.
EMBO J. 7, 1129-1137, 1988
A>Title: The 11-1 gene of Plasmodium falciparum codes for distinct fast evolving repeats
A:Reference number: S00485; MUID:88296416; PMID:2841111
A:Accession: S00485
A:Molecule type: DNA
A:Residues: 1-1315;1316-1486;1486-1657;1658-1729;1730-1948 <SCH>
A:Cross-references: EMBL:X07453
C:Comment: This protein is associated with the membrane of red blood cells at the schizont stage.
C:Genetics:
A:Gene: 11-1
A:Introns: 71/73
C:Keywords: tandem repeat
F:1-71/Domain: signal sequence #status predicted <SIG>
F:72-1948/Product: gene 11-1 protein (fragments) #status predicted <MAT>

Query Match 6.8%; Score 84; DB 2; Length 1948;
Best Local Similarity 21.5%; Pred. No. 1.8e+02;
Matches 59; Conservative 36; Mismatches 75; Indels 104; Gaps 13;

QY 8 NEKLRKSEK-----QQTALGNLKQ-----IYYNEK-----AITENKESD 44
DB 15 NGSDKKKSFEVFKIKNGTDLKDTKDIRPHFYFIVKIIILSLLIWTVIYNNCSN 74

QY 45 DQF-----LENTLLFKGF-----FTGHPWYNDLLV-----DLGSKDATNKYKGVLD 86
DB 75 GRYKSTLYIVGNHURFRGFRILAENEYEMTKYKTLWVNIIDNDLGRKGNKKRPHHKKVE 134

QY 87 LYGAYYGYQAGGTPNKTACVGGVTLHNN-----RLTEKKVPINL-----WIDGK 134
DB 135 -----INLNDNNLSNESKSKSRKKVKVNLKDNLEKREGK 170

QY 135 QTTVPIDKVKTSKEVTVOELDLQARHLYHGKFLGNSDFGKVGQGLVPHSSEGSTV 194
DB 171 MK-----RNNKKEKRRKKNKNLKLK-----REYKESYLLDNKSDMDVI 213

QY 195 SYDLFDAGQYPTDLLRIYRDNKTINSEN--LHI 226
DB 214 RNDKF-----SYFTLYKKNLFPNSNNYFLHM 239

RESULT 71
S36595
L1 protein - human papillomavirus type 9
C:Species: human papillomavirus type 9
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36595
E:DeLius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36595
A:Molecule type: DNA
A:Residues: 1-507
A:Cross-references: EMBL:X74464; NID:G397068; PID:CAA52488.1; PID:G397076
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match 6.7%; Score 83.5; DB 2; Length 507;
Best Local Similarity 20.3%; Pred. No. 36;
Matches 49; Conservative 38; Mismatches 69; Indels 85; Gaps 14;

QY 42 ESDQFLENTLLF-----KGFTGHPWYNDLLVLDLGSKD-----ATNKYKGVLD 86
DB 23 QSTDEYVERTINIFVHAISDRLLTVGHPY-----DVRSGDQRIEVPKVGSGNQYAPRIS 77

QY 87 -----LYGAYYGYQAGGTP-----NKTACMYG 109

DB 78 LPDPNRFALADMSVYNPDKRLVWACRGIEGRGQPLGVTSGHPLNPKVDRDTENSNYQ 137

QY 110 GVTLDHNNRTEKKVPINWIDGKQTVPI-----DKVTSKKEVTVOELDL-----QAR 160

DB 138 GTTWDDQNTSFDPK-QVQNFIIQ--CIPCLGEHWDKAKVCEKDN-NOLGICPFIELR 192

QY 161 HYLHGKFLGNSYSGF---GKVGQGLVPHSSEGSTVSVDLFDAGQYPTLLR---IYR 214
DB 193 NTV-----IEDGMDFICFGNINKLSFNKSD---VSLDIVDETCKYPTFLTWANDVYG 244

QY 215 D 215
DB 245 D 245

RESULT 72
S49815
transferrin-binding protein - Actinobacillus pleuropneumoniae
C:Species: Actinobacillus pleuropneumoniae
C>Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S49815
 R:Bunka, S.; Potter, A.; Gerlach, G.
 submitted to the EMBL Data Library, November 1994
 A:Description: Cloning and sequencing of the transferrin-binding protein genes of *Actinobacillus*
 A:Reference number: S49814
 A:Accession: S49815
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-547 <BUN>
 A:Cross-references: EMBL:Z46775; NID:G577528; PIDN:CAA86730.1; PID:G577529
 C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a

Query Match 6.7%; Score 83.5; DB 2; Length 547;
 Best Local Similarity 24.4%; Pred. No. 40;
 Matches 57; Conservative 31; Mismatches 105; Indels 41; Gaps 11;

Qy 3 KSEINERDLKRSLOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHP 62
 Db 46 KDVEAKKEKEQLGELMPEALGVYVKV----PVSSFENKKYDIDIS--VITGNLDDVP 99
 Qy 63 W-----YNLLVLGSKDANKY-----KGGKDLVYGYVYQAGGTP-NKT 104
 Db 100 YKANSSKYNIL--DIKTDSLSQVYRSGYVIDGHSNGEKGYVYKGNSPAELPVNQL 157
 Qy 105 ACYGGVTLHDNRLTEKKVPINLWID-----GKQTTVPIDKVKTSKKEVTQV-ELDL 157
 Db 158 LTYGSDFTSNANLNNEGRPNYNDYYTKFKRGVLGVSGDAKLAKHKYTSQFEVDF 217
 Qy 158 QARHYLHGKFG-----LY--NSDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQ 204
 Db 218 -ATKMTGKLSKKEKTIYTVNADIRGNFTGAATASDNKKGESYNPFSSADSQ 270

RESULT 73
 JQ0773
 penicillin-binding protein mecaA, low-affinity - Staphylococcus aureus
 N:Alternate names: MRSA PBP; penicillin-binding protein 2'
 C:Species: Staphylococcus aureus
 C:Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 26-May-2000
 C:Accession: JQ0773; S00092; S20574
 R:Ryffel, C.; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser, F.
 Gene 94, 137-138, 1990
 A:Title: Sequence comparison of meca genes isolated from methicillin-resistant *Staphylococcus aureus*
 A:Reference number: JQ0773; MUID:91033056; PMID:2227446
 A:Accession: JQ0773
 A:Molecule type: DNA
 A:Residues: 1-668 <RYF>
 A:Cross-references: GB:X52593; NID:G46610; PIDN:CAA36829.1; PID:G46611
 R:Song, M.D.; Wachi, M.; Doi, M.; Ishino, F.; Matsunashi, M.
 FEBS Lett. 221, 167-171, 1987
 A:Title: Evolution of an inducible penicillin-target protein in methicillin-resistant *Staphylococcus aureus*
 A:Reference number: S00092; MUID:87304805; PMID:3305073
 A:Accession: S00092
 A:Molecule type: DNA
 A:Residues: 1-245, 'G', 247-302, 'RV', 303-609, 'T', 611-668 <SON>
 A:Cross-references: EMBL:X63598; NID:G46612; PIDN:CAA45141.1; PID:G46613
 R:Hitamatsu, K.; Asada, K.; Suzuki, E.; Okonogi, K.; Yokota, T.
 FEBS Lett. 298, 133-136, 1992
 A:Title: Molecular cloning and nucleotide sequence determination of the regulator region
 A:Reference number: S20574; MUID:92183847; PMID:1544435
 A:Accession: S20574
 A>Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-41 <HIR>
 A:Cross-references: EMBL:X63598; NID:G46612; PIDN:CAA45141.1; PID:G46613
 C:Comment: Enzymes involved in cell wall synthesis are the primary target of beta-lactam
 resistant *Staphylococcus aureus* (MRSA) has a very low affinity to beta-lactam antibiotics
 C:Genetics:
 A:Gene: meca
 A>Note: the gene for this protein contains a penicillin-inducible promoter, resulting in
 illin binding proteins from *E. coli*. The sequence Ser-X-X-Lys, conserved in penicillin b

e penicillin binding protein part is neither from *S. aureus* nor from *E. coli*
 C:Superfamily: penicillin-binding protein 2B
 C:Keywords: antibiotic resistance; cell wall synthesis
 F:403/Active site: Ser #status predicted

Query Match 6.7%; Score 83.5; DB 2; Length 668;
 Best Local Similarity 20.4%; Pred. No. 51;
 Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;

Qy 7 INEKDLRKSELOG-----TALGNLKOIYYNEK-----AITENK 41
 Db 259 INSEELKQK-EYKGYKDDAVIGKKLEKLYDKKLQHEGVRVTVIVDNDNSNTIAHTLEKK 317
 Qy 42 ESDQFLENTLLFKGFTGHPWYNLLVLGSKDATNKYKGGKVDL-----YGAYYGYQC 96
 Db 318 KDGKDIQTLIDAK---VQKSIYNNKNDYGSGETAHPQTGELLALVSTPSYDVY----- 369
 Qy 97 AGGTPNKTCMYGGVTLHDNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVTQV 153
 Db 370 -----PFMY-GMSNEEYKLTEDKPELNKF---QITSPSGTQKLTAMIGLNKK 417
 Qy 154 ELQARHYLHGKFGLYNSDSFG-----GO-----YPTLLRIY- 213
 Db 418 TLDDKTSYKIDGK-GWQDKSGWGVNTRYEVVNGNIDLKQAISSDNIFFARVALELGS 476
 Qy 178 -KYQGLIVFHSSEGSTVSVDLFDAG-----GO-----YPTLLRIY- 213
 Db 477 KFEKGGKLVGVEDIPSDYPPFNAQISKNLNDNEILLADSGVGGQELINPVOILSIYS 536
 Qy 214 --RDNKTINSEN 224
 Db 537 ALENNGNINAPHL 549

RESULT 74
 JQ0774
 penicillin-binding protein mecaA, low-affinity - Staphylococcus epidermidis
 N:Alternate names: penicillin-binding protein 2'
 C:Species: Staphylococcus epidermidis
 C:Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 26-May-2000
 C:Accession: JQ0774
 R:Ryffel, C.; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser, F.
 Gene 94, 137-138, 1990
 A:Title: Sequence comparison of meca genes isolated from methicillin-resistant *Staphylococcus aureus*
 A:Reference number: JQ0773; MUID:91033056; PMID:2227446
 A:Accession: JQ0774
 A:Molecule type: DNA
 A:Residues: 1-668 <RYF>
 A:Cross-references: GB:X52592; NID:G46993; PIDN:CAA36828.1; PID:G46994
 A:Experimental source: strain WT55
 C:Genetics:
 A:Gene: meca
 C:Superfamily: penicillin-binding protein 2B
 F:403/Active site: Ser #status predicted

Query Match 6.7%; Score 83.5; DB 2; Length 668;
 Best Local Similarity 20.4%; Pred. No. 51;
 Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;

Qy 7 INEKDLRKSELOG-----TALGNLKOIYYNEK-----AITENK 41
 Db 259 INSEELKQK-EYKGYKDDAVIGKKLEKLYDKKLQHEGVRVTVIVDNDNSNTIAHTLEKK 317
 Qy 42 ESDQFLENTLLFKGFTGHPWYNLLVLGSKDATNKYKGGKVDL-----YGAYYGYQC 96
 Db 318 KDGKDIQTLIDAK---VQKSIYNNKNDYGSGETAHPQTGELLALVSTPSYDVY----- 369
 Qy 97 AGGTPNKTCMYGGVTLHDNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVTQV 153
 Db 370 -----PFMY-GMSNEEYKLTEDKPELNKF---QITSPSGTQKLTAMIGLNKK 417
 Qy 154 ELQARHYLHGKFGLYNSDSFG-----GO-----YPTLLRIY- 213

```
Db      418  TLDDKTSYKIDGK-GWQKDKSGGVNTRYEVVNGNIDLKQAISSDNIFPARVALELGS 476
QY      178  -KVQRLIVFHSSEGSTVSDLFDAQ-----GO-----YPTLLRIY- 213
Db      477  KFEKGMKKLGVEDIPSDYFFYNAQISNKNLDNEILLADSGYGQGEILINPVQILSIYS 536
QY      214  --RDNKTINSEN 224
Db      537  ALENGNGINAPHL 549

RESULT 75
T44118
penicillin-binding protein 2 [imported] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 26-May-2000
C:Accession: T44118
R:Itô, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth
A:Reference number: Z22733; MUID:99278010; PMID:10348769
A:Accession: T44118
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-668 <IFO>
A:Cross-references: EMBL:D86934; PIDN:BAA82220.1
A:Experimental source: strain N315
C:Genetics:
A:Note: mecA
C:Superfamily: penicillin-binding protein 2B

Query Match      6.7%; Score 83.5; DB 2; Length 668;
Best Local Similarity 20.4%; Pred. No. 51;
Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;

QY      7  INEKDLRKSELOG---TALGNLKOIYYNEK-----ALTENK 41
Db      259  INSEELKQK-EYKGKDDAVIGKKGLEKLYDKLQKHEDGRTVIIVDDNSNTIAHLIEKK 317
QY      42  ESDDQFLENTLLPKGFTGHPWYNDLLDLGSKDATNKYKGGKVDL-----YCAYYGYQC 96
Db      318  KKGDKDIQLTIDAK---VQKSIYNNMKNVDYSGTATHPQTGELLALVSTPSYDVY----- 369
QY      97  AGGTPNKTAGCMYGGVTLHDNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVTVQ 153
Db      370  -----PFMY-GMSNEEYNKLTEDKKEPLLNKF---QITTSFGSTQKILTAMIGLNKK 417
QY      154  ELDLQARHYLHGKFGLYNSDSFGG----- 177
Db      418  TLDDKTSYKIDGK-GWQKDKSGGVNTRYEVVNGNIDLKQAISSDNIFPARVALELGS 476
QY      178  -KVQRLIVFHSSEGSTVSDLFDAQ-----GO-----YPTLLRIY- 213
Db      477  KFEKGMKKLGVEDIPSDYFFYNAQISNKNLDNEILLADSGYGQGEILINPVQILSIYS 536
QY      214  --RDNKTINSEN 224
Db      537  ALENGNGINAPHL 549

Search completed: August 12, 2004, 13:33:13
Job time : 11.3708 secs
```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:22:49 ; Search time 5.11863 Seconds
(without alignments)
2370.233 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238
Sequence: 1 SEKSEENRDLRKKSBLQ.....RDKNKTINSENIHALYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210	97.7	257	1	ETXK STAAU
2	1037	83.8	257	1	ETXA STAAW
3	663	53.6	258	1	ETXD STAAU
4	360	29.1	241	1	ETXH STAAW
5	304.5	24.6	266	1	ETXB STAAU
6	302.5	24.4	266	1	ETXC STAAU
7	298.5	24.1	266	1	ETC2 STAAU
8	283.5	22.9	251	1	SEPA STREY
9	270.5	21.8	258	1	ETCL STAAU
10	256	20.7	258	1	ETXG STAAU
11	209	16.9	234	1	SPEG STREY
12	191	15.4	236	1	SPEH STREY
13	171.5	13.9	235	1	SPEC STREY
14	105.5	8.5	234	1	TSST STAAU
15	101	8.2	1634	1	DROL METJA
16	95.5	7.7	150	1	R19E THEVO
17	88.5	7.1	150	1	R19E THEAC
18	88.5	7.1	413	1	SP74 YEAST
19	87.5	7.1	409	1	YMKG BACSU
20	87	7.0	1419	1	MDR FLAPF
21	86.5	7.0	2971	1	YXG5 CHLEP
22	86	6.9	171	1	LACB STARP
23	85	6.9	617	1	PPFA RICCO
24	85	6.9	6486	1	TYCC BREPA
25	84.5	6.8	419	1	PEXA PICPA
26	84.5	6.8	637	1	VE1 HPV35
27	84	6.8	333	1	RPCA MYCPU
28	84	6.8	562	1	AMY2 DICTH
29	84	6.8	616	1	RFAI HUMAN
30	84	6.8	1902	1	P2P LACPA
31	83.5	6.7	507	1	VLI HPV09
32	83	6.7	438	1	SHPI STAHY
33	83	6.7	556	1	SVR LISMO

ALIGNMENTS

RESULT 1

34	82.5	6.7	314	1	RPOR LACPL
35	82.5	6.7	328	1	YB70 HAEIN
36	82.5	6.7	670	1	PBP STAAU
37	82.5	6.7	1520	1	TOP2 CAEEL
38	81.5	6.6	1720	1	YA42 MYCPN
39	81	6.5	492	1	GLPK AQUAE
40	81	6.5	556	1	SYR LISIN
41	81	6.5	616	1	PPFA SOLTU
42	80.5	6.5	243	1	MPGP PYRHO
43	80.5	6.5	1151	1	ITAL HUMAN
44	80.5	6.5	1312	1	DPOL PYRSD
45	80	6.5	416	1	PGK GLOMO
46	80	6.5	447	1	LEC PARPC
47	80	6.5	509	1	YF08 MYCPN
48	79.5	6.4	324	1	YE64 PASMU
49	79.5	6.4	1211	1	DPJA HELPY
50	79	6.4	1156	1	PHYB SOYBN
51	79	6.4	1902	1	P2P LACLC
52	78.5	6.3	467	1	YJEA BACSU
53	78.5	6.3	509	1	CLSI BACAA
54	78.5	6.3	635	1	ETFL YABAM
55	78.5	6.3	802	1	CSD2 SCOLI
56	78.5	6.3	1018	1	FNBA STAAU
57	78	6.3	485	1	COBQ METNA
58	78	6.3	819	1	CSD1 ECOLI
59	78	6.3	1902	1	P1P LACLC
60	77.5	6.3	692	1	Y650 METJA
61	77.5	6.3	817	1	RNRI LACLA
62	77.5	6.3	1604	1	UB32 HUMAN
63	77.5	6.3	3206	1	POLG PSBMV
64	77	6.2	303	1	V212 FOWPV
65	77	6.2	419	1	TYPH MYCPI
66	77	6.2	429	1	K1C1 XENLA
67	77	6.2	440	1	MURD BUCAP
68	77	6.2	443	1	Y314 MYCGE
69	77	6.2	512	1	IBMP FNWD
70	76.5	6.2	425	1	YNN6 YEAST
71	76.5	6.2	455	1	YWAD BACSU
72	76.5	6.2	549	1	YQ29 BACAN
73	76.5	6.2	665	1	SYGB RICPR
74	76.5	6.2	884	1	SYA RALSO
75	76.5	6.2	1002	1	TAGA VIBCH
76	76.5	6.2	1325	1	Y309 MYCPN
77	76.5	6.2	1365	1	LTFS STRDO
78	76	6.1	212	1	LIP BACSU
79	76	6.1	282	1	AROK METJA
80	76	6.1	343	1	FEN FVRHO
81	76	6.1	378	1	AROC METJA
82	76	6.1	663	1	RGPI YEAST
83	76	6.1	704	1	NEUL HUMAN
84	76	6.1	762	1	SLAP ACEKI
85	76	6.1	875	1	UE3A HUMAN
86	76	6.1	876	1	SYA STAAU
87	76	6.1	876	1	SYA STAAU
88	76	6.1	1388	1	HRF3 SCHPO
89	75.5	6.1	120	1	CYBS YEAST
90	75.5	6.1	358	1	YC07 KLEPN
91	75.5	6.1	377	1	MTC3 CHVN1
92	75.5	6.1	420	1	ALAU HUMAN
93	75.5	6.1	423	1	PUR6 CAEEL
94	75.5	6.1	722	1	Y174 RICPR
95	75.5	6.1	3649	1	ACVS NOCLA
96	75	6.1	254	1	Y653 HAEIN
97	75	6.1	349	1	FEN SULSO
98	75	6.1	386	1	YA66 METJA
99	75	6.1	395	1	Y164 METJA
100	75	6.1	406	1	PNCB METMA

RESULT 1

ETX STAAU STANDARD; PRT; 257 AA.
 ID ETX STAAU STANDARD; PRT; 257 AA.
 AC P12993;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type E precursor (SEE).
 GN ENTE.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN=MJB285;
 RX MEDLINE=88257005; PubMed=3384800;
 RA Couch J.L., Solits M.T., Betley M.J.;
 RT "Cloning and nucleotide sequence of the type E staphylococcal
 enterotoxin gene";
 RL J. Bacteriol. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 CC staphylococcal food poisoning syndrome. The illness characterized
 CC by high fever, hypotension, diarrhea, shock, and in some cases
 CC death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC ENBL; M21319; AAA26617.1; -.
 DR PIR; A28179; A28179.
 DR PDB; 1SEE; 15-OCT-95.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR02279; BACTRLOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure.
 FT CHAIN 1 27 ENTEROTOXIN TYPE E.
 FT METAL 28 257 ZINC (BY SIMILARITY).
 FT METAL 211 211 ZINC (BY SIMILARITY).
 FT METAL 249 249 ZINC (BY SIMILARITY).
 FT METAL 251 251 ZINC (BY SIMILARITY).
 FT HELIX 33 35
 FT HELIX 39 41
 FT STRAND 42 42
 FT TURN 46 47
 FT TURN 48 51
 FT HELIX 52 54
 FT STRAND 59 64
 FT TURN 66 67
 FT STRAND 69 69

FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 84
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 115 116
 FT TURN 118 119
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 142
 FT STRAND 152 152
 FT STRAND 154 155
 FT TURN 156 157
 FT STRAND 163 163
 FT STRAND 171 171
 FT STRAND 173 175
 FT HELIX 176 190
 FT TURN 191 191
 FT STRAND 203 211
 FT STRAND 219 221
 FT STRAND 227 227
 FT HELIX 234 239
 FT STRAND 242 244
 FT TURN 245 247
 FT STRAND 249 257
 SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;
 Query Match 97.7%; Score 1210; DB 1; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.4e-95;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKFEENEKDLKKSELQGTALGNLKOIYYNEKATTEKESDDQPLENTLLFKGFFTG 60
 DB 25 SEKFEENEKDLKKSELQGTALGNLKOIYYNEKATTEKESDDQPLENTLLFKGFFTG 84
 QY 61 HPWYNLLVLDLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
 DB 85 HPWYNLLVLDLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
 QY 121 BEKVPINLWDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKGLYNSDSFGKQV 180
 DB 145 BEKVPINLWDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKGLYNSDSFGKQV 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 2

ETX STAAU STANDARD; PRT; 257 AA.
 ID ETX STAAU STANDARD; PRT; 257 AA.
 AC P13153;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN ENTA OR MW1889.
 OS Staphylococcus aureus (strain MW2), and
 OC Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";

RL Lancet 359:1819-1827(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FR1337;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Betley M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
 RL J. Bacteriol. 170:34-41(1988).
 RN [3]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354548; PubMed=7628431;
 RA Schach E.M., Zaitsev I., Zaitsev V.N., Dohlsien M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 type A";
 RL EMBO J. 14:3292-3301(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schach E., Dohlsien M.,
 RA Abrahamson L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding.";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [7]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schach E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 staphylococcal food poisoning syndrome. The illness characterized
 by high fever, hypotension, diarrhea, shock, and in some cases
 death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AP004828; BAB95754.1; --
 DR EMBL; M18970; AAZ26681.1; --
 DR FIR; A28664; A28664.
 DR PDB; 1ESF; 11-JUL-96.
 DR PDB; 1SXT; 19-NOV-97.
 DR PDB; 1DYQ; 21-FEB-02.
 DR PDB; 1I4G; 21-MAR-01.

DR PDB; 1I4H; 21-MAR-01.
 DR PDB; 1LOS; 18-DEC-02.
 DR PDB; 1SEA; 15-OCT-95.
 DR InterPro; IPR008992; Bact endotox.
 DR InterPro; IPR006177; Bct1 tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006136; Staph/Strep tox.
 DR InterPro; IPR006173; Staph_tox_05.
 DR Pfam; PF02876; Staph_strp_tox; 1.
 DR Pfam; PF01123; Staph_strp_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 3).
 FT HELIX 28 31
 FT TURN 32 33
 FT HELIX 39 41
 FT TURN 44 45
 FT HELIX 46 55
 FT TURN 56 56
 FT STRAND 59 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 79 80
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 116
 FT TURN 118 119
 FT TURN 125 126
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 149
 FT STRAND 151 155
 FT TURN 156 157
 FT STRAND 158 160
 FT HELIX 164 166
 FT STRAND 167 171
 FT STRAND 173 175
 FT HELIX 176 191
 FT TURN 193 194
 FT HELIX 197 199
 FT TURN 200 200
 FT STRAND 205 212
 FT STRAND 218 221
 FT TURN 222 223
 FT HELIX 230 233
 FT TURN 234 237
 FT TURN 238 239
 FT STRAND 242 244
 FT STRAND 248 255
 SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCALP14677 CRC64;

Query Match 83.8%; Score 1037; DB 1; Length 257;
 Best Local Similarity 83.3%; Pred. No. 2.8e-80;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOGTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTC 60
 Db 25 SEKSEINEKDLRKKSSELOGTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTC 84
 QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYCYQCAGTGNKTCMYGGVTLHDNNRLT 120

Db 85 HSWYNDLLVDFDSKDIDVYKYGKKVDLYGAYGYGACGGTGNKTACMGVGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTPIDPKVYKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKRVQ 180
 Db 145 EEKVPINLWIDGKQTTPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVFQKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHTSTEPSVYNDVYDLFDAQOQYNTLLRIYRDNKTINSENMHDIYLYTS 257

RESULT 3
 EYXH STAAW STANDARD; PRT; 258 AA.
 ID EYXH STAAW STANDARD; PRT; 258 AA.
 AC P20723; 1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type D precursor (SED).
 GN EYXH
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359112; PubMed=2549000;
 RA Bayless K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D";
 RL J. Bacteriol. 171:4799-4806 (1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN=ATCC 23235;
 RX MEDLINE=97157473; PubMed=9003758;
 RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W., Dohlisten M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization";
 RL EMBO J. 15:6832-6840 (1996).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -!- SUBUNIT: Homodimer; zinc-dependent.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M28521; AAB06195.1; -
 CC PIR; A33953; A33953.
 CC HSP; P13163; ISXT.
 CC InterPro; IPR008992; Bact_endotox.
 CC InterPro; IPR006177; Bctrl_tox.
 CC InterPro; IPR006123; Staph/Strep_toxin.
 CC InterPro; IPR006126; Staph/Strep_tox.
 CC Pfam; PF02876; Staph_Strep_tox_C; 1.
 CC Pfam; PF01123; Staph_Strep_toxin; 1.
 CC PRINTS; PR00279; BACTRLTOXIN.
 CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 CC Enterotoxin; Toxin; Signal; Superantigen; Zinc.
 CC SIGNAL 1 25 ENTEROTOXIN TYPE D.
 CC CHAIN 26 258
 CC METAL 212 212 ZINC.

FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT VARIANT 114 F -> A (IN STRAIN ATCC 23235).
 SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
 Query Match 53.6%; Score 663; DB 1; Length 258;
 Best Local Similarity 55.0%; Pred. No. 9.2e-49;
 Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;
 QY 1 SEKSEENEDLRKKSELOQTALGNLKOIYYINEKAITENKESDDQPLENTLLFKGFFTC 60
 Db 26 NENIDSVKEKELHKKSELSSTALNMMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYGACGGTGNKTACMGVGVTLHNNRLT 120
 Db 86 LINFEDLLINPNSKEMAQHFYSKKNVDVPIRYINCYGGEDIDTACTYGGVTTHEGNKX 145
 QY 121 EEKVPINLWIDGKQTTPIDPKVYKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKRVQ 180
 Db 146 ERKKIPINLWINGVQKESVLDKQVTDKKNVTVOELDLQARRYLQKDLKLYNNDTLGKIQ 205
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLY 231
 Db 206 RGKIEFDSGSKVSYDLFVKGDFPEKQRIYSDNKTSLTEHLHIDYLY 256

RESULT 4
 EYXH STAAW STANDARD; PRT; 241 AA.
 ID EYXH STAAW STANDARD; PRT; 241 AA.
 AC Q53585;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type H precursor (SEH).
 GN ENTH OR SEH OR MW0051.
 OS Staphylococcus aureus (strain MW2), and Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620, 1280;
 RN [1]
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION. STRAIN=DA508.
 RX MEDLINE=95053699; PubMed=7964453;
 RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C., Fischetti V.A., Zabriske J.B.;
 RT "Characterization and biological properties of a new staphylococcal exotoxin";
 RL J. Exp. Med. 180:1675-1683 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-acquired MRSA";
 RL Lancet 359:1819-1827 (2002).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).
 RX MEDLINE=20444256; PubMed=10986116;
 RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P., Antonsson P., Svensson L.A.;
 RT "The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TCR molecules";
 RL J. Mol. Biol. 302:527-537 (2000).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
 CC -!- SUBCELLULAR LOCATION: Secreted.

RT aureus." ;
Pl. J. Bacteriol. 166:20-33 (1996)

[2] SEQUENCE OF 40-91 FROM N.A.
 RP MEDLINE=8529825; PubMed=3980073;
 RX Ranelli D.M., Jores C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RA "Molecular cloning of staphylococcal enterotoxin B gene in
 RT *Escherichia coli* and *Staphylococcus aureus*";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RL [3]

SEQUENCE OF 28-266 (S-6).
MEDLINE=71007902; PubMed=5470821;
Huang I.-Y., Bergdoll M.S.;
"The primary structure of staphylococcal enterotoxin B. 3. The
cyanogen bromide peptides of reduced and aminoethylated enterotoxin
B, and the complete amino acid sequence.";
J. Biol. Chem. 245:3518-3525(1970).
[4]
X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
MEDLINE=93063291; PubMed=1436059;
Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
"Crystal structure of staphylococcal enterotoxin B, a superantigen."
Nature 359:801-806(1992).
[5]
X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
MEDLINE=94203282; PubMed=8152483;
Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
Chli Y.I., Stauffer C.B., Strominger J.L., Wiley D.C.;
"Three-dimensional structure of a human class II histocompatibility
molecule complexed with superantigen."
Nature 368:711-718(1994).
[6]
X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
MEDLINE=99036298; PubMed=9881971;

RA Li H., Liera A., Teuchiya D., Leder L., Yseern X., Schlievert P.M.,
RA Karjalainen K., Marzuza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B";
RL Immunity 9:807-816(1998).
EN [7].
EP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998)".
CC -I- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.

CC EMBL; M1118; AAA89550.1; -
DR PIR; S27360; ENSAB6.
DR DRB; LSEB; 20-JUN-96.
DR DRB; LSEB; 28-JAN-98.
DR DRB; 3SEB; 27-MAY-98.
DR DRB; 3SEB; 28-JAN-98.
DR DRB; LSE3; 16-JUN-97.
DR DRB; LSE4; 15-OCT-97.
DR DRB; LSEB; 04-MAR-99.
DR DRB; 1DSW; 14-MAR-01.
DR DRB; 1DSX; 28-JUN-00.

```

DR PDB; 1D52; 28-JUN-00.
DR PDB; 1D6E; 28-JUN-00.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_cox.
DR InterPro; IPR006173; Staph_cox_ob.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure.
FT SIGNAL 1
FT CHAIN 28 266
FT DISULFID 120 140
FT CONFLICT 56 58
FT CONFLICT 69 77
FT CONFLICT 118 118
FT CONFLICT 128 130
FT CONFLICT 133 135
FT CONFLICT 149 150
FT CONFLICT 156 156
FT CONFLICT 185 186
FT CONFLICT 233 233
FT CONFLICT 246 247
FT STRAND 29 29
FT HELIX 41 43
FT TURN 44 44
FT TURN 48 48
FT HELIX 49 52
FT HELIX 53 55
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT TURN 83 85
FT STRAND 90 94
FT STRAND 98 104
FT TURN 105 105
FT STRAND 108 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 127 128
FT STRAND 138 142
FT STRAND 145 147
FT TURN 149 150
FT STRAND 152 165
FT TURN 166 167
FT STRAND 168 179
FT STRAND 181 183
FT STRAND 184 199
FT STRAND 209 218
FT TURN 219 220
FT STRAND 221 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 255 263
SQ SEQUENCE 266 AA; 66D417F61CF018B0 CRC64;

Query Match 24.6%; Score 304.5; DB 1; Length 266;
Best Local Similarity 34.4%; Pred. No. 1.5e-18;
Matches 84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLKKSSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 27 AEGQDPKPKDLKSSKFTG-LMENMKVLYDDNRHVSAL-NKSIDQFLFDLIYSIKDTK 84
QY 61 HPWTNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKATCMYGG 110

```

RESULT 6

ID	ETC3_STAAM	STANDARD;	PRT;	266 AA.
AC	P23313;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Enterotoxin type C-3 precursor (SEC3).			
GN	ENTC3 OR SAV2009 OR SA1817.			
OS	Staphylococcus aureus (strain Mu50 / ATCC 700699),			
OS	Staphylococcus aureus (strain N315), and			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=158878, 158879, 1280;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Mu50 / ATCC 700699, and N315;			
RA	MEDLINE=21311952; PubMed=1418146;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,			
RA	Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,			
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yoshino C., Shiba T.,			
RA	Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,			
RA	Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;			
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus			
RT	aureus".			
RL	Lancet 357:1225-1240(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=9020508; PubMed=2325627;			
RA	Hovde C.J., Hackett S.P., Bohach G.A.;			
RT	"Nucleotide sequence of the staphylococcal enterotoxin C3 gene:			
RT	sequence comparison of all three type C staphylococcal			
RT	enterotoxins".			
RL	Mol. Gen. Genet. 220:329-333(1990).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.			
RC	MEDLINE=97064178; PubMed=8906797;			
RA	Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffacher C.V.,			
RA	Schlievert P.M., Karjalainen K., Mariuzza R.A.;			
RT	"Crystal structure of a T-cell receptor beta-chain complexed with a			
RT	superantigen".			
RL	Nature 384:188-192(1996).			
CC	!- FUNCTION: Staphylococcal enterotoxins cause the intoxication			
CC	staphylococcal food poisoning syndrome. The illness characterized			
CC	by high fever, hypotension, diarrhea, shock, and in some cases			
CC	death.			
CC	!- SUBCELLULAR LOCATION: Secreted.			
CC	!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin			
CC	family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)			

RT: Structure 3.769-779 (1995)

[3] X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).

RP MEDLINE=96022987; PubMed=7552730;

RX Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;

RA "Residues defining V beta specificity in staphylococcal

RT enterotoxins.";

RT Nat. Struct. Biol. 2:680-686(1995).

[4]

RP COMPARISON OF STRUCTURE OF SEA AND SEC2.

RP MEDLINE=97334373; PubMed=9191070;

RX Schad E.M., Papagorgiou A.C., Svensson L.A., Acharya K.R.;

RA "A structural and functional comparison of staphylococcal

RT enterotoxins A and C2 reveals remarkable similarity and

RT dissimilarity.";

RT J. Mol. Biol. 269:270-280(1997).

CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication

CC staphylococcal food poisoning syndrome. The illness characterized

CC by high fever, hypotension, diarrhea, shock, and in some cases

CC death.

CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary

CC for the toxin interaction with MHC class II.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin

CC family.

DR PIR; A60114; A60114.

DR PDB; 1STE; 23-DEC-96.

DR PDB; 1SE2; 08-MAR-96.

DR PDB; 1CQV; 19-SEP-01.

DR PDB; 1I42; 19-SEP-01.

DR PDB; 1I4Q; 19-SEP-01.

DR PDB; 1I4R; 19-SEP-01.

DR PDB; 1I4X; 19-SEP-01.

DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bctrl_tox.

DR InterPro; IPR006123; Staph/Strep_toxin.

DR InterPro; IPR006126; Staph/Strept_tox.

DR InterPro; IPR006173; Staph_tox_08.

DR Pfam; PF02876; Stap_strp_box_C1.

DR Pfam; PF01123; Stap_strp_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;

KW 3D-STRUCTURE.

ENTEROTOXIN TYPE C-2.		
FT	CHAIN	28
FT	DISULFID	120
FT	METAL	36
FT	METAL	110
FT	METAL	145
FT	METAL	149
FT	HELIX	35
FT	HELIX	41
FT	STRAND	44
FT	TURN	48
FT	HELIX	49
FT	STRAND	60
FT	STRAND	69
FT	TURN	73
FT	STRAND	75
FT	TURN	83
FT	STRAND	90
FT	HELIX	98
FT	TURN	105
FT	STRAND	109
FT	STRAND	116
FT	TURN	118
FT	TURN	128
FT	STRAND	136
FT	STRAND	142
FT	TURN	146
FT	STRAND	149

FT HELIX 36 38
FT HELIX 42 44
FT TURN 48 48
FT HELIX 49 56
FT STRAND 60 66
FT STRAND 69 69
FT TURN 72 74
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 101
FT TURN 102 103
FT STRAND 105 110
FT STRAND 113 113
FT TURN 115 116
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 187
FT STRAND 199 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 249
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBPC3 CRC64;

Query Match 22.9%; Score 283.5; DB 1; Length 251;
Best Local Similarity 33.8%; Pred. No. 8.4e-17;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDQPLENTLLFKGFTG 60
Db 25 SQEVAQDDPPSQLRSSLVKNQNIYFLYEGDPVTHENYKVSQDLSHDLIYN--VS 81

QY 61 HPVNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQC-AGGTPNKTCACVGGVTLHDNNRL 119
Db 82 GPNYDKLTELKNQEMATLPKDKNDVIGVYHYHLCYLCAENASACIYGGVTHNENHNL 141

QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 BIPKIVVKSIDGTQ-SLSFD-IETNKKMVTAGELDYKVRKYLTDNKKLYTNGP--SKY 197

QY 180 QRGVLVHSSSEGSVSYDLFD----AGQGYPTLLRIYRDNKTNSENLHIALVLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMYKDNELDSNTSQIEVYLT 250

RESULT 9
ETC1 STAAU STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A.; Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and

relatedness to other pyrogenic toxins."; Mol. Gen. Genet. 209:15-20(1987).
[2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J.; Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1."; J. Biol. Chem. 258:6300-6306(1983).
RL J. Biol. Chem. 258:6300-6306(1983).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC
CC EMBL: X05815; CAA329260.1; --
DR PIR; S06356; ENSACL.
DR HSP; P34071; ISE2.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bct_t1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;

Query Match 21.8%; Score 270.5; DB 1; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.1e-15;
Matches 76; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQDPPTDELHKASKFTG-LMENKVLVDDHYVSATKVK-SVDKFLAHLIYINISDKK 84

QY 61 HPVNDLLVDLGSKDQATNKYKGGKVDLYGAYGYQC-----AGTTPNKTCACVGGVTL 113
Db 85 LKNYDKVKTLELNEGLAKYKDEVDVYGSNYVANCYFSSKDNVGVKVTGGKTCMYGITK 144

QY 114 HDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFNDGNLQNLIRVY-ENKRWITISFE-VQTKSVTAQELDIKARFLINKQLYE 202

QY 172 SDSFGKVGQRLIVFHSSSEGSVSYDLFDQAQGYPD--TLRIYRDNKTNSENLHIALY 229
Db 203 FNS--SPYETGVYKFIENNGNTFWYDMMAPGDKFDQSKYLMWYNDNKTVDKSKVIEVH 260

QY 230 LYT 232
Db 261 LTT 263

RESULT 10
ETXG STAAU STANDARD; PRT; 258 AA.
ID ETXG STAAU
AC 085382;

Query Match 20.7%; Score 256; DB 1; Length 258;
Best Local Similarity 29.6%; Pred. No. 1.8e-14;
Matches 74; Conservative 50; Mismatches 84; Indels 42; Gaps 12;

DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF02876; Staph_strep_tox_C7_1.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 16.9%; Score 209; DB 1; Length 234;
Best Local Similarity 32.6%; Pred. No. 1.5e-10;
Matches 56; Conservative 31; Mismatches 71; Indels 14; Gaps 6;

QY 64 YNDLLVLDGSKDATNKKYKGVLDLYGAYGYOCAGGTENKTCMYGGVTLHNNRLTEEK 123
DB 73 YDVSIVSLGITD--QPIKDKVDVFLGPNF-----SPFYVDNIYGGIVKSHNOGKSLQ 125

QY 124 KVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQVGL 183
DB 126 FVGI-LNQGKETYLPSEAVRIKKQFTLQEFDFKIRKFLMEKYNIDSES---RYTSGS 181

QY 184 IVFHSSEGSTVSYDLPDAGQY--PDTLLRIYRDNKTINSENL-HIALYLYT 232
DB 182 LFLATKDSKHVEYDLFNKDKLLSRDSFFRYKDKNFSEISHFIDYLYKT 233

RESULT 12
SPEC_STRPY
ID SPEC_STRPY STANDARD; PRT; 236 AA.
AC Q9X5C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type H precursor (SPE H).
GN SPEH OR SPY1008.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=M15;
RX MEDLINE=99093428; PubMed=9874566;
RA Prott T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from Streptococcus pyogenes."
RL J. Exp. Med. 189:89-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta chain.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC

CC EMBL; AF124500; AAD30989.1; -
DR EMBL; AE006546; AAK33907.1; -
DR PDB; 1ET9; 24-MAY-00.
DR PDB; 1EU4; 24-MAY-00.
DR InterPro: IPR008992; Bact endotox.
DR InterPro: IPR006123; Staph7Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C7_1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome; 3D-structure.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 236 EXOTOXIN TYPE H.
SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 15.4%; Score 191; DB 1; Length 236;
Best Local Similarity 26.1%; Pred. No. 4.9e-09;
Matches 55; Conservative 44; Mismatches 82; Indels 30; Gaps 9;

QY 25 NLKQIYYNEKAITEN--KESDDQFLENTLLFK-----GFTGHPWYNDDLVDLGSKDA 76
DB 42 NLESYKXHDNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDW-----I 89

QY 77 TNKYKGGKVDLYGAYGYOCAGGTENKTCMYGGVTLHNNRLTEEKVPINLWIDGKQT 136
DB 90 SQEFKDEVDIYALSQEVCE--CPGKRYEAFGGITLTNSEK--KEIKVPVNVWDKSKQQ 145

QY 137 TVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQVGLIVFHSSEGSTVS 196
DB 146 --PMEFITVANKPKVTAQEVDIKVKLLIKYDIYNNRE--QKYSKGTVTLDLNSGKDIFV 201

QY 197 DL-FDAQGQYPTDLLRIYRDNKTINSENLHI 226
DB 202 DLYYFGNGDF-NSMLKIYSNNERIDSTQPHV 231

RESULT 13
SPEC_STRPY
ID SPEC_STRPY STANDARD; PRT; 235 AA.
AC P13380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1] SEQUENCE FROM N.A. AND SEQUENCE OF 28-52.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=88314303; PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C";
RL Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=92363541; PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Molecular population genetic evidence of horizontal spread of two alleles of the pyrogenic exotoxin C gene (speC) among pathogenic clones of Streptococcus pyogenes";
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus
RT Pyogenes."; *Proc. Natl. Acad. Sci. U.S.A.* 98:4658-4663 (2001).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
RX MEDLINE=97397352; PubMed=9253413;
RA Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
RT "Crystal structure of the streptococcal superantigen SPE-C:
RT dimerization and zinc binding suggest a novel mode of interaction
RT with MHC class II molecules."; *Nat. Struct. Biol.* 4:635-643 (1997).
RL Nat. Struct. Biol. 4:635-643 (1997).
CC -I- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -I- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -I- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M35514; AAB27017.1; ALT_SEQ.
DR EMBL; M97156; AAB59091.1; --
DR EMBL; M97157; AAB59092.1; --
DR EMBL; AE006523; AAK33664.1; --
DR PIR; A30509; A30509.
DR PIR; A44799; A44799.
DR PUB; IAN8; 29-APR-88.
DR PUB; IATK; 07-JUN-02.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_Ob-
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 235 EXOTOXIN TYPE C.
FT CONFLICT 53 53 N -> D (IN REF. 1).
FT HELIX 33 44
FT STRAND 49 59
FT STRAND 63 67
FT STRAND 69 72
FT TURN 74 75
FT STRAND 77 81
FT HELIX 84 87
FT TURN 88 89
FT TURN 92 93
FT STRAND 95 100
FT TURN 108 109
FT STRAND 110 114
FT STRAND 117 119
FT STRAND 127 128
FT STRAND 131 135
FT TURN 136 137
FT STRAND 141 142
FT TURN 144 145
FT STRAND 148 149

FT STRAND 153 155
FT HELIX 156 171
FT TURN 173 174
FT TURN 176 177
FT STRAND 182 189
FT TURN 190 191
FT STRAND 194 198
FT TURN 204 205
FT HELIX 208 212
FT HELIX 213 217
FT STRAND 220 222
FT HELIX 223 225
FT STRAND 226 235
SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
Query Match 13.98; Score 171.5; DB 1; Length 235;
Best Local Similarity 26.3%; Pred. No. 2.1e-07;
Matches 59; Conservative 42; Mismatches 78; Indels 45; Gaps 11;
QY 37 ITENKESDDQFLENTLLFKGFFFTGHPW-VNDLLVLDGSKDA-----TNKYKGK----- 83
DB 25 IKSDSKDISNVKSDLLYA--YITPYDKNCRVNPFSTHTLNIDTKYRGKDYISSEM 82
QY 84 -----KVDLYGAIYQOCAGGTGNTKACMYGGVTLHDNNELTEKKVPINLWI 131
DB 83 SYEASQKFKRDDHVDVDFGLFVILNSHTG-----EYIYGITPAQNNKVNH--KLLGNLFI 135
QY 132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHLGKFGLYNSDS--FGGKVGQGLIVFHSS 189
DB 136 SGESQQLNNKILKIDVIFQELDKIRKYLMDNYKIYDTSFYVSGRIEIG-----TK 190
QY 190 EGSTVSYDLFDA--QGYPDTLLRIYEDNKNTINSENL-HIALYL 230
DB 191 DGKEQIDLFDSNEGTRSDIFAK-YKDNRIINMKNFSDIYL 233
RESULT 14
ID TSST STAAU STANDARD; PRT; 234 AA.
AC P06856;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Toxic shock syndrome toxin-1 precursor (TSST-1).
GN TSST.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87057222; PubMed=3782090;
RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
RA Schlievert P.M.;
RT "The nucleotide and partial amino acid sequence of toxic shock
RT syndrome toxin-1."; *J. Biol. Chem.* 261:15783-15786 (1986).
RL [2]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94150598; PubMed=8107781;
RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
RA Brehm R.D., Tranter H.S.;
RT "Structural basis of superantigen action inferred from crystal
RT structure of toxic-shock syndrome toxin-1."; *Nature* 367:94-97 (1994).
RL [3]
RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=94092653; PubMed=8268150;
RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlievert P.M.,
RA Ohlendorf D.H.;
RT "Structure of toxic shock syndrome toxin 1."; *Biochemistry* 32:13761-13766 (1993).
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
RP

RX MEDLINE=96319751; PubMed=8759320;
RA Papegeorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RT Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RT 2.07-A resolution.";
RN J. Mol. Biol. 260:553-569(1996).
[5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=97337442; PubMed=9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dinges M.N., Cook W.J., Schlivert P.M., Ohlendorf D.H.;
RT "Refined structures of three crystal forms of toxic shock syndrome
RT toxin-1 and of a tetramutant with reduced activity.";
RL Protein Sci. 6:1220-1227(1997).
[6]
RN X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE=98254504; PubMed=9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlivert P.M., Ohlendorf D.H.;
RT "Structures of five mutants of toxic shock syndrome toxin-1 with
RT reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
CC -!- FUNCTION: Responsible for the symptoms of toxic shock syndrome.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announcements/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J02615; AAA26682.1; -;
DR PIR: A24606; XCSAS1.
DR PDB: 2TSS; 24-DEC-97.
DR PDB: 3TSS; 24-DEC-97.
DR PDB: 4TSS; 24-DEC-97.
DR PDB: 5TSS; 24-DEC-97.
DR PDB: 1QIL; 12-AUG-97.
DR PDB: 2QIL; 12-AUG-97.
DR PDB: 1AW7; 18-NOV-98.
DR PDB: 1TS2; 16-DEC-98.
DR PDB: 1TS3; 16-DEC-98.
DR PDB: 1TS4; 16-DEC-98.
DR PDB: 1TS5; 16-DEC-98.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph_exotoxin.
DR InterPro: IPR006173; Staph_tox OB.
DR InterPro: IPR006125; Staph_toxin.
DR Pfam: PF02876; Staph_Strep_tox C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR01800; STAPHSTOXIN.
DR PRINTS: PR01501; TOXICSTOXIN.
DR PROSITE: PS00277; STAPH STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH STREP_TOXIN_2; 1.
KW Toxin; Superantigen; Signal; 3D-structure.
FT SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
FT HELIX 46 54
FT STRAND 58 69
FT TURN 70 71
FT STRAND 72 76
FT TURN 78 79
FT STRAND 82 86
FT TURN 90 91
FT TURN 98 99
FT STRAND 101 108
FT STRAND 113 114

FT TURN 116 117
FT STRAND 120 125
FT STRAND 128 129
FT STRAND 133 138
FT STRAND 142 146
FT TURN 147 148
FT STRAND 149 151
FT STRAND 159 161
FT STRAND 163 164
FT HELIX 166 181
FT TURN 183 185
FT TURN 187 188
FT STRAND 192 198
FT TURN 199 200
FT STRAND 203 207
FT TURN 208 209
FT HELIX 214 226
FT STRAND 221 222
FT HELIX 223 225
FT STRAND 226 234
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
Query Match 8.5%; Score 105.5; DB 1; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.077;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;
QY 11 DLKKSELQCTALGNLQIYYVYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
DB 58 DFTNSEVLDSLSGVR-----IKYTDGSI--SLIIFPS-----EYISPAFT- 97
QY 71 LGSKDATNYKKGKVDL-----YGAYGYQCAGTPTNKTKACMGVGTLLHNNR 118
DB 98 -----KGEKVDLNTKTKKSQHTSEGYIHFQISGVT-----NTEK 133
QY 119 LTBEKKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLY-NSDSFGG 177
DB 134 LPTPIELPKVKGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQHLVRSSDKTGG 192
QY 178 --KVQRGLIVFHSSEGSTVSVDL---FDAQGYPTLLFIYRDNKTINSE 222
DB 193 YWKIT-----MNDGSTVQSLSKKFEYNTKPPINI---DEIKTIEAE 232
RESULT 15
DPOL METJA STANDARD; PRT; 1634 AA.
AC Q58295;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
DE intein].
DE POL OR M70885.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OC NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Stutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

```

CC + {DNA} (N).
CC -!- PTM: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the intervening region (intron)
CC followed by peptide ligation (Potential).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67533; AAB9889.1; -.
CC HSP; P56689; ITGO.
CC TIGR; MJ0885; -.
CC InterPro: IPR006172; DNA_pol_B.
CC InterPro: IPR006134; DNA_pol_B_dom.
CC InterPro: IPR006133; DNA_pol_B_exo.
CC InterPro: IPR003587; Hedgehog_hint_N.
CC InterPro: IPR003586; Hedgehog_hint_C.
CC InterPro: IPR006142; INTIN.
CC InterPro: IPR004042; Intein_endonuc.
CC InterPro: IPR006141; Intein_S.
CC InterPro: IPR004578; Pol2.
CC Pfam; PF00136; DNA_pol_B; 3.
CC Pfam; PF03104; DNA_pol_B_exo; 1.
CC PRINTS; PR00379; INTEIN.
CC SMART; SM00305; HintC; 2.
CC SMART; SM00306; HintN; 2.
CC SMART; SM00486; POLBC; 1.
CC TIGRams; TIGR01443; intein_Cterm; 2.
CC TIGRams; TIGR01445; intein_Nterm; 2.
CC TIGRams; TIGR00592; pol2; 1.
CC PROSITE; PS00116; DNA_POLYMERASE_B; 1.
CC PROSITE; PS00818; INTEIN_CTER; 2.
CC PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
CC PROSITE; PS00817; INTEIN_NTER; 2.
CC Transferrase; DNA-directed DNA polymerase; DNA replication;
CC DNA-binding; Autocatalytic cleavage; Protein splicing;
CC Complete proteome.
CC -----
CC CHAIN 1 425 POL, 1ST PART (POTENTIAL).
CC CHAIN 426 794 MJA_POL-1 INTEIN (POTENTIAL).
CC CHAIN 795 882 POL, 2ND PART (POTENTIAL).
CC CHAIN 883 1358 MJA_POL-2 INTEIN (POTENTIAL).
CC CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
CC SEQUENCE 1634 AA; 191708 MW; 84A1FAFAB1F97DDD CRC64;
CC -----
Query Match 8.2%; Score 101; DB 1; Length 1634;
Best Local Similarity 22.9%; Pred. No. 1.9;
Matches 53; Conservative 33; Mismatches 79; Indels 66; Gaps 10;
QY 12 LRKSELOGTALGNLQIYVYNEKATENKESDDQFLENTLFGKFFTCGHPYNDLLVDL 71
DB 614 VREKKGTAITLGCACKDLYLKIEELKKNK---KYLPAAIL-RGFFEGDGVNTVRRAV 669
QY 72 GSKDANKYKGGK-----VDLYGAYGYCAGGTENKTKACMYGGVTLHDNNRLTEKKVP 126
DB 670 VVNGGINNVDKIFIASLDRLGKISF-----YTSVEERGKGLKRVV 713
QY 127 INWIGKQTTVPIDKVTES-----KKEVTVQELDQARHYLHGKFLGNSD----- 173
DB 714 IEIFSKG-----DLIKFSILSFISRRKNNLLNEIRQKTLXIGDYGFDLDDVCVS 766
QY 174 --SFGKKV-----QRGLVHFSSSEGS-TVSYDLFDAQGYPDTL 209
DB 767 LESYKGEVDLTLEGRPYFANGILHNSLYSIISYNI-----SPDTL 811
-----
RESULT 16
R19E THEVO
ID_R19E_THEVO STANDARD; PRT; 150 AA.

```

```

AC Q97CU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DN 30S ribosomal protein S19E.
GN RPS19E OR TV0007 OR TVG0008143.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=1121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium";
RL Proc Natl Acad Sci U.S.A. 97:14257-14262(2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP000991; BAB59149.1; -.
CC InterPro: IPR001266; Ribosomal_S19E.
CC Pfam; PF01030; Ribosomal_S19E; 1.
CC ProDom; PD003854; Ribosomal_S19E; 1.
CC PROSITE; PS00628; RIBOSOMAL_S19E; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 150 AA; 17063 MW; FD5881CF684EB415 CRC64;
-----
Query Match 7.7%; Score 95.5; DB 1; Length 150;
Best Local Similarity 29.5%; Pred. No. 0.31;
Matches 23; Conservative 17; Mismatches 37; Indels 1; Gaps 1;
QY 116 NNRLETKKVPINLWIDGKQTTVPIDKVTESKEVTVQELDQARHYLHGKFLGYN-SDS 174
DB 17 SGKLKEEKIKPEPNVFKVTGSKPKPLQDDWIYVRAASMLRKLKLYINGYLGRMSSE 76
QY 175 FGGKVQRLVHFSSSEGS 192
DB 77 YGGKVDGRGSKRYHAASGS 94
-----
RESULT 17
R19E THEAC
ID_R19E_THEAC STANDARD; PRT; 150 AA.
AC Q9EMZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DN 30S ribosomal protein S19E.
GN RPS19E OR TA0050.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum";
RL Nature 407:508-513(2000).

```


DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical zinc protease ymxG (EC 3.4.99.-) (ORFP).
 GN ymxG OR BSU16710
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / 8G5;
 RA Bolhuis A., Vehmmanpera J., Venema G., Bron S., van Dijk J.M.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Chim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kashara Y., Kleier-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardiniois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portecelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 30-409 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=9352813; PubMed=8098035;
 RA Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.;
 RT "Organization and nucleotide sequence of the Bacillus subtilis
 RT diaminopimelate operon, a cluster of genes encoding the first three
 RT enzymes of diaminopimelate synthesis and dipicolinate synthase".
 RL J. Biol. Chem. 268:9448-9465(1993).
 CC -!- COPACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M16.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U27560; AAA73485.1; -;
 CC EMBL; Z99112; CAB13544.1; -;
 CC EMBL; L08471; AAA22379.1; -;
 CC PIR; E69886; E69886.
 CC MEROPS; M16.UPS; -;

DR Subtilist; BG10779; ymxG.
 DR InterPro; IPR001431; Peptidase_M16.
 DR InterPro; IPR007863; Peptidase_M16_C.
 DR Pfam; PF00675; Peptidase_M16; 1.
 DR Pfam; PF05193; Peptidase_M16_C; 1.
 DR PROSITE; PS00143; INSULINASE; 1.
 KW Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
 KW Complete Proteome.
 FT METAL 46 46 ZINC (BY SIMILARITY).
 FT ACT_SITE 49 49 BY SIMILARITY.
 FT METAL 50 50 ZINC (BY SIMILARITY).
 FT METAL 126 126 ZINC (BY SIMILARITY).
 FT CONFLICT 270 271 FO -> LE (IN REF. 3).
 FT CONFLICT 360 360 E -> Q (IN REF. 3).
 SQ SEQUENCE 409 AA; 45963 MW; EA9CF00EBD57563 CRC64;
 Query Match 7.1%; Score 87.5; DB 1; Length 409;
 Best Local Similarity 22.7%; Pred. No. 5;
 Matches 55; Conservative 43; Mismatches 79; Indels 65; Gaps 15;
 QY 10 KDLRK---XSELOGTALGNLKQIYYNKAITENKESDDQFLENTLLPKGFFTHGHWYND 66
 DB 198 KQVEKWFSGYEAKGKATG-LERPEFTEK-LTRKKEIQOHL--CLGFKGLEVGHERIYD 253
 QY 67 LLV---DLGSKDQATNKY-----KGRKVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNN 117
 DB 254 LIVLNVNVLGSSMSRLFDVREDKGLAYSIVSYHSHYSDSG-----MLTIYGGTGANQLQ 308
 QY 118 RLTEKKVPINLWDGQKTPIDKVTSKKE-VTVQELDLQARHVLHGKFGLYNSDSFG 176
 DB 309 QLSE-----TIQ-ETLATLRDGTISKELE-NSKEQMKGSL-MLSLESTN 350
 QY 177 GKVORG-----LIVFHSSESGSTVSDLPDAQGYPTLIRIYRDNKTINSENLH-IALYL 230
 DB 351 SKMSRNGKELLGKHK-----TLDEIINELNVLNLRVNGLARGQL 391
 QY 231 YT 232
 DB 392 FT 393
 RESULT 20
 MDR PLAFF
 ID MDR PLAFF STANDARD; PRT; 1419 AA.
 AC P33568;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DE Multidrug resistance protein (Chloroquine resistance protein).
 GN MDR1.
 OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
 OX Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5837;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89288297; PubMed=2701941;
 RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
 RT "Amplification of the multidrug resistance gene in some chloroquine-
 RT resistant isolates of P. falciparum".
 RL Cell 57:921-930(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92017800; PubMed=1922044;
 RA Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
 RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium
 RT falciparum has arisen as multiple independent events".
 RL Mol. Cell. Biol. 11:5244-5250(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93149200; PubMed=8426608;
 RA Wilson C.M., Volkman S.K., Thaitong S., Martin R.K., Kyle D.E.,
 RA Milhous W.K., Wirth D.F.;
 RT "Amplification of pfmdr 1 associated with mefloquine and halofantrine

resistance in Plasmodium falciparum from Thailand.";
RL Mol. Biochem. Parasitol. 57:151-160(1993).
CC -!- FUNCTION: Energy-dependent efflux pump responsible for decreased
CC drug accumulation in multidrug-resistant cells.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: P.falciparum resistant to the drug chloroquine
CC have multiple copies of the gene coding for MDR.
CC -!- SIMILARITY: Belongs to the ABC transporter family, MDR subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M29154; AAA29646.1; -;
DR EMBL; X56851; CAA40180.1; -;
DR EMBL; S53996; AAD13870.1; -;
DR PIR; S18204; DVZQF.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_Transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOVAIN 1 55
FT TRANSMEM 56 82
FT TRANSMEM 91 116
FT TRANSMEM 160 188
FT TRANSMEM 194 212
FT TRANSMEM 279 298
FT TRANSMEM 314 338
FT TRANSMEM 339 788
FT DOVAIN 789 807
FT TRANSMEM 825 846
FT TRANSMEM 908 928
FT TRANSMEM 1028 1048
FT TRANSMEM 1063 1083
FT DOVAIN 1084 1419
FT DOVAIN 1419 1419
FT NP_BIND 413 420
FT NP_BIND 1161 1168
FT REPEAT 1 721
FT REPEAT 722 1419
FT CARBOHYD 228 228
FT CARBOHYD 258 258
FT CARBOHYD 964 964
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 1419;
Best Local Similarity 21.8%; Pred. No. 24;
Matches 65; Conservative 37; Mismatches 112; Indels 84; Gaps 15;

Qy 3 KSEINEKD-----LRKSELOQTALGNLKOI-----YYYN--EKAIT 38
Db 955 KSKIEKENSSGVFAFPSSDDEMFKDPFLIQEAFYNMHTVINYLEDYFCNLIEKAID 1014

Qy 39 -ENKESDDQFLENTLLFKGFTGHP-----WYNDLLVDLGS-----KCA-----T 77
Db 1015 YKNGQKRIIVNAALW-GFSQSQLFINSFAYWFGSLIKRGFTLLVDWPKSLFTPTFT 1073

Qy 78 NKYGGKVDLYG-----AYGYQCA-----GTFPKNTACMYGGVTLHD--NN 117
Db 1074 GSYAGKLSLKGSDENAKLSPEKYPLMIRKSNIDVRDDGIRINKNLKGVKIDVNF 1133

Qy 118 RLTEKKVPI-----NLWIDGQTTVPIDKVKTSKK---EVTVQELDLQARHYL-----HGK 166

Db 1134 RVISRENVPIYKNLSPTCDSKTKTAIVGTSGKSTFVNLRLRYDLKNDHILKNDMTN 1193
Qy 167 FGLYNSDSGGKQVORGLIVFHSSEGSTVSYDLDFAQGGYDPTLLRLRYRDKNTINSEN 224
Db 1194 FQDYQNNNNNSLVKKNVNEFSNQSQAEDYTVFNNGE-----ILLDDINICDYNL 1244

RESULT 21
YCX9 CHLRE STANDARD; PRT; 2971 AA.
AC Q32065; Q95635;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 341.7 kDa protein in psbd-psbC intergenic region
DE (ORF2971) (ORPB).
OS Chlamydomonas reinhardtii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137c / CC-125;
RA Watson A.T., Purton S.;
RT "Unidentified open reading frame ORF2971 (ORPB) from the chloroplast
RT genome of Chlamydomonas reinhardtii.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 2635-2971 FROM N.A.
RC STRAIN=137c / CC-125;
RX MEDLINE=89305500; PubMed=2663467;
RA Rochaix J.D., Kuchka M., Mayfield S., Schirmer Rahire M.,
RA Girard Bascou J., Bemmoun P.;
RT "Nuclear and chloroplast mutations affect the synthesis or stability
RT of the chloroplast psbc gene product in chlamydomonas reinhardtii.";
RL EMBL J. 8:1013-1021(1989).
RN [3]
RP COMPLETE PLASTID GENOME.
RX MEDLINE=2305394; PubMed=12417694;
RA Maul J.E., Lilly J.W., Cui L., dePamphilis C.W., Miller W.,
RA Harris E.H., Stern D.B.;
RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
RT a sea of repeats.";
RL Plant Cell 14:2659-2679(2002).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U62943; AAB05800.1; -;
DR EMBL; X13879; CAA32083.1; -;
DR EMBL; BX000554; DAA00965.1; -;
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF00004; AAA; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 2971 AA; 341663 MW; 3BE294AF2248348A CRC64;

Query Match 7.0%; Score 86.5; DB 1; Length 2971;
Best Local Similarity 21.5%; Pred. No. 66;
Matches 47; Conservative 34; Mismatches 65; Indels 73; Gaps 9;

Qy 4 SEINEKDLRKSELOQT-ALGNLKOIYYYNKAITENKESDDQFLENTLLFKGFTGHP 62
Db 2453 SKKLKELNVKSLIGSNGTVSQGNVDQLGVFAQIVNKKKSLQQLPNS-----2501

Qy 63 WYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTENKACMYGGVTLHD--NNRLT 120

```

Db 2502 -----KKSFKKXKDKALIYEV-----GKFLNYFLNNQLT 2533
Qy 121 EKKVPINLWIDGKQTTVIDKVKTSKEVTV---QELDLQARHYLHGKFGLYNSDS--- 174
Db 2534 QSSIDPKPSVTKQPT-----NDITFGNDFLNLTINYL-----SLYNSKNKIL 2578
Qy 175 -----FGKVORGL-----IVFHSBEGSVSYVDLFDAG 203
Db 2579 LQMLIFGGKISOLLSSKNLVSLSKQASINSYWEESG 2617

RESULT 22
LACB_STAEP STANDARD; PRT; 171 AA.
AC Q8CRJ3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26).
GN LACB OR SE1786.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RX PubMed=12950922;
RA Zhang Y.-O., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
  Qin Z.-O., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
  Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
  Genome-based analysis of virulence genes in a non-biofilm-forming
  RT Staphylococcus epidermidis strain (ATCC 12228).;
  RL Mol. Microbiol. 49:1577-1593(2003).
CC -!- CATALYTIC ACTIVITY: D-galactose 6-phosphate = D-tagatose 6-
  phosphate.
CC -!- PATHWAY: Tagatose 6-phosphate pathway of lactose catabolism.
CC -!- SUBUNIT: Heteromultimeric protein consisting of lacA and lacB.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE016750; AAC05427.1; -.
CC InterPro; IPR003500; Rib/Gal isomerase.
CC Pfam; PF02502; LacAB_rpiB; 1.
CC TIGRfam; TIGR00689; rpiB_lacA_lacB; 1.
CC Lactose metabolism; Isomerase; Complete proteome.
CC SQ SEQUENCE 171 AA; 18903 MW; 0CF3B0A594208477 CRC64;

Query Match 6.9%; Score 86; DB 1; Length 171;
Best Local Similarity 23.1%; Pred. No. 2.3;
Matches 45; Conservative 28; Mismatches 56; Indels 66; Gaps 11;

Qy 37 ITENKESDQFLNTLLFKGFTGHPWYNDLLVDLGSKDATKYGKKVDLYGAYGYQC 96
Db 11 VTDTRKEVSHLS-----QGHE-----VIDGVTYDFTTH-----YPIYGGKVGSKV 53
Qy 97 AGGTENKTKCMYG-GVTLHNNRLTEBEKVPINLWIDGKQTTVIDKVKTSKEVTVQ 153
Db 54 ASGEADLVGVCIGTGVGIGN-----AANKVP-----GVRTALVDMTSLYSKEELNA- 101
Qy 154 ELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSBEGSVSYVDLFDG---QQQYPTDLR 211
Db 102 -----NVVSFGKGAGELFTF-----DIVDAFIEAEYKPT--- 131
Qy 212 IYRDNKNTINSENLIH 226
Db 132 --EENKLIAKINHL 144

```

RESULT 23

```

PPPA_RICCO STANDARD; PRT; 617 AA.
AC Q41140;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha subunit
  (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent)
DE (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPI-PFK).
GN PFP-ALPHA.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
  OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;
  OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95137384; PubMed=7835697;
RA Todd J.F., Blakeley S.D., Dennis D.T.;
  "Structure of the genes encoding the alpha- and beta-subunits of
  RT castor pyrophosphate-dependent phosphofructokinase.";
  RL Gene 152:181-186(1995).
CC -!- FUNCTION: The alpha subunit may be involved in the regulation of
  PFP by Fru-2,6-P (By similarity).
CC -!- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
  phosphate + D-fructose 1,6-bisphosphate.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
  similarity).
CC -!- MISCELLANEOUS: The active site might be on the beta subunit.
CC -!- SIMILARITY: HIGH, TO POTATO PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-
  PHOSPHOTRANSFERASE ALPHA SUBUNIT.
CC -!- SIMILARITY: TO OTHER PLANT ALPHA SUBUNITS AND ALSO, TO THE
  BETA SUBUNITS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z32849; CAA83682.1; -.
CC PIR; T10102; T10102.
CC InterPro; IPR000023; Ppfuckinase.
CC Pfam; PF00365; PFK; 1.
CC ProDom; PD000707; Ppfuckinase; 1.
CC Transferase; Kinase; Allosteric enzyme.
CC SQ SEQUENCE 617 AA; 67360 MW; 1C9B2A0AF11FF3F0 CRC64;

Query Match 6.9%; Score 85; DB 1; Length 617;
Best Local Similarity 30.2%; Pred. No. 13;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGVLDYGYGYGVCAGGTENKTKCMYGCVT-----LHNNRLTEE 122
Db 412 REGT--YKGRKFNACCHFFGQARGSLPSKFDGCDYAVLGHICYHVAAGLNGYMATATN 469
Qy 123 KKVPINLWIDGKQTTVIDKVKTSKK 148
Db 470 LKQPVNKRRCG---AAPIAAMTVKR 492

RESULT 24
TYCC_BREPA STANDARD; PRT; 6486 AA.
AC O30409;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

Tyrosine synthase III [Includes: ATP-dependent asparagine adenylase (AsnA) (Asparagine activase); ATP-dependent glutamine adenylase (GlnA) (Glutamine activase); ATP-dependent tyrosine adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent ornithine adenylase (OrnA) (Ornithine activase); ATP-dependent leucine adenylase (LeuA) (Leucine activase)].

GN TYCC.

OS Brevibacillus parabrevis.

OS Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.

OX NCBI_TaxID=54914;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=ATCC 8185 / IAM 1031 / IFO 3331 / NCD0 717 / NCIB 8598;

RX MEDLINE=98012987; PubMed=9352938;

RA Mootz H.D., Marahiel M.A.;

RT "The tyrosine biosynthesis operon of Bacillus brevis: complete nucleotide sequence and biochemical characterization of functional internal adenylase domains.";

RI J. Bacteriol. 179:6843-6850(1997).

CC -!- FUNCTION: INCORPORATES SIX AMINO ACIDS. (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE PEPTIDE PRODUCT.

CC -!- COPACTOR: Contains 6 covalently bound phosphopantetheines (By similarity).

CC -!- PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.

CC -!- SUBUNIT: LARGE MULTIMERIC COMPLEX OF TYCA, TYCB AND TYCC.

CC -!- DOMAIN: CONSISTS OF SIX MODULES, AND HARBOURS A PUTATIVE THIOESTERASE DOMAIN AT ITS C-TERMINAL END. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLEATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION (OPTIONAL).

CC -!- MISCELLANEOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSITIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.

CC -!- SIMILARITY: Belongs to the ATP-dependent AYP-binding enzyme family.

CC -!- SIMILARITY: Contains 6 acyl carrier domains.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AF004835; AAC45930.1; --

PDB; 1DNY; 17-MAY-00.

DR InterPro; IPR000873; AMP-bind.

DR InterPro; IPR001242; Condensatn.

DR InterPro; IPR006163; PP bind.

DR InterPro; IPR006162; Ppanine S.

DR InterPro; IPR000379; Ser setrs.

DR InterPro; IPR001031; Thioesterase.

DR Pfam; PF00501; AMP-binding; 6.

DR Pfam; PF00668; Condensation; 6.

DR Pfam; PF00550; pp-binding; 6.

DR Pfam; PF00975; Thioesterase; 1.

DR PRINTS; PR00154; AMPBINDING.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 6.

DR PROSITE; PS00455; AMP BINDING; 6.

DR PROSITE; PS00075; ACP_DOMAIN; 6.

KW Ligase; Antibiotic biosynthesis; Phosphopantetheine; Multifunctional enzyme; Repeat; 3D-structure.

KW REPEAT 466 1038 DOMAIN 1 (ASPARAGINE-ACTIVATING).

FT REPEAT 1521 2070 DOMAIN 2 (GLUTAMINE-ACTIVATING).

FT REPEAT 2536 3113 DOMAIN 3 (TYROSINE-ACTIVATING).

FT REPEAT 3590 4149 DOMAIN 4 (VALINE-ACTIVATING).

FT REPEAT 4606 5203 DOMAIN 5 (ORNITHINE-ACTIVATING).

FT REPEAT 5658 6245 DOMAIN 6 (LEUCINE-ACTIVATING).

FT DOMAIN 970 1037 ACYL CARRIER (ACP) 1.

FT DOMAIN 2007 2074 ACYL CARRIER (ACP) 2.

FT DOMAIN 3045 3112 ACYL CARRIER (ACP) 3.

FT DOMAIN 4080 4147 ACYL CARRIER (ACP) 4.

FT DOMAIN 5124 5191 ACYL CARRIER (ACP) 5.

FT DOMAIN 6167 6234 ACYL CARRIER (ACP) 6.

FT BINDING 1000 1000 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 2037 2037 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 3075 3075 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 4110 4110 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 5154 5154 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 6197 6197 PHOSPHOPANTHETHEINE (BY SIMILARITY).

SQ SEQUENCE 6486 AA; 724011 MW; 4934900AF07DF786 CRC64;

Query Match 6.9%; Score 85; DB 1; Length 6486;

Best Local Similarity 20.5%; Pred. No. 2.2e-02;

Matches 50; Conservative 42; Mismatches 76; Indels 76; Gaps 12;

QY 16 SEIQGTALGNLQIY-----YNEKAITENKESDDQFLENTLLFKGFTGH--PWY 64

Db 789 ASMQPVPVSGSLGEMVIAGDVAKGVFNRLPTELKFKFIDNPFPGTKMVR---TGDLAKWL 845

QY 65 NDLLVD-LGSKDATNKYKGGKVDLYGAYVGYCAGCTPNKTCMYGVTLDHNNRLTEEK 123

Db 846 PDGNEYAGRMVYQVKIRHREM-----GEI-----ETRLTQHE 880

QY 124 KVPINLWIDGKQTVIPIDVKVT-----SKKEVTYQELDLQARHYLHGKFGLYNSD 173

Db 881 AV-----KEAVIVKDESGQNVLYAVLVSERELTVAEL-----REFLGRTLPSYMP 928

QY 174 SP-----GGKVGRLIVFHSSEGSTVSYSYDLFDA-QCQYPTDLLRIYRDKNKTS 221

Db 929 SFPIRLAEPLTANGKVERKKL--PKPAGAVVTGTAYAAPONEIEAKLAEIQVVLGISQ 986

QY 222 ENLH 225

Db 987 VGIIH 990

RESULT 25

PEXA_PICPA STANDARD; PRT; 419 AA.

ID PEXA_PICPA

AC Q32265;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Peroxisome assembly protein PAS7 (Peroxin-10).

GN PEX10 OR PAS7.

OS Pichia pastoris (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI_TaxID=4922;

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE=96026021; PubMed=7565793;

RX Kalish J.E., Theda C., Morrell J.C., Berg J.M., Gould S.J.;

RA "Formation of the peroxisome lumen is abolished by loss of Pichia pastoris Pas7p, a zinc-binding integral membrane protein of the peroxisome.";

RT peroxisome.";

RL Mol. Cell. Biol. 15:6406-6419(1995).

CC -!- FUNCTION: Necessary for peroxisome assembly, essential for import of both PTS1 and PTS2 proteins, and required for the establishment of the peroxisome lumen.

CC -!- SUBCELLULAR LOCATION: Peroxisomal; membrane-associated.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>;
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U70066; AAB09086.1; -;
DR InterPro; IPR006845; Pex2_Pex12.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF04757; Pex2_Pex12; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
KW Peroxisome; Zinc-finger; Membrane.
FT ZN_FING 298 360 RING-TYPE.
FT MUTAGEN 313 313 C->S: LOSS OF ACTIVITY.
FT MUTAGEN 315 315 H->W: LOSS OF ACTIVITY.
FT MUTAGEN 316 316 C->S: NO LOSS OF ACTIVITY.
FT MUTAGEN 318 318 C->S: LOSS OF ACTIVITY.
FT MUTAGEN 318 318 C->S: LOSS OF ACTIVITY.
SQ SEQUENCE 419 AA; 47948 MW; 8D073E48A956AB85 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 419;
Best Local Similarity 22.6%; Pred. No. 9.1;
Matches 65; Conservative 34; Mismatches 87; Indels 101; Gaps 16;

QY 4 SEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQF-----LENTL-LFK 55
DB 4 SEIKURAVSPRDFKANYL-----EFANAPAIVRANQDSYFTVLRDLKQNVIQIFK 57

QY 56 G--FFTGHP-----WYNDLVDLGSKDATNKY-----RGKVDLYGAYGYQC 96
DB 58 GQGFTHTEBIGVAAKALYSLTLLGKTLGEEVVDLYVSRDGRKIPRYLAGAGIF 117

QY 97 A-----GGTNKACMGYGGVTLHDNRLTEE-----KKVPINLWIDGQT 136
DB 118 AVAILPYFLTRFLRLKSSSTP-----KQEVTEKINKELPISLRIEKYLS 163

QY 137 TVPIDKVKTSKEVTVOELDLQARHYLHGKFLGYNSD-----SFGKVKOR----- 181
DB 164 NMSYKVL-----TIMLHI-AVFYFSQF--YNIKSFPSMRVAFGHKINKERTPNGN 215

QY 182 -----GLIVFH-----SSEGSTVSYLFDAGQYPTLRIYRDNNTI 219
DB 216 YELGGLIVLQVWKSGLGFGKLGISFTGNDHDSNLR--ANNKDI 260

RESULT 26
VE1 HPV35 STANDARD; PRT; 637 AA.
AC P27220;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Replication protein El.
GN El.
OS Human papillomavirus type 35.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10587;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124733; PubMed=1310198;
RA Marich J.E., Ponteler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
RT "The phylogenetic relationship and complete nucleotide sequence of
RT human papillomavirus type 35";
RL Virology 186:770-776(1992).
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>;
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74477; CAA52563.1; -;
DR EMBL; M74117; AAA46968.1; -;
DR PIR; A40824; WIML35.
DR PIR; S36523; S36523.
DR InterPro; IPR001177; Papillom_E1.
DR Pfam; PF00519; E1; 1.
DR Pfam; PF00524; E1_N; 1.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 463 470 ATP (POTENTIAL).
FT CONFLICT 31 34 DPVS -> SSV (IN REF. 2).
FT CONFLICT 142 143 QQ -> HE (IN REF. 2).
FT CONFLICT 235 258 ESLTKIKPYCLYHIQCLSCSWG ->
FT CONFLICT 269 281 NFKHTVYIYVVRVHGA (IN REF. 2).
FT CONFLICT 417 418 EAKNRTIEKLS -> VEKREQLKTIDA (IN REF. 2).
FT CONFLICT 418 418 EK -> AQ (IN REF. 2).
FT CONFLICT 515 552 WAYIDQYLRNLDGNPISLDVVKHALVQLKCPPLITS ->
FT CONFLICT 587 587 GYRPIFKKTRWKSYSIFRCALSIHIMPTFTYI (IN
FT CONFLICT 613 613 REF. 2).
FT CONFLICT 587 587 V -> E (IN REF. 2).
FT CONFLICT 613 613 D -> V (IN REF. 2).
SQ SEQUENCE 637 AA; 72122 MW; 3C694D4451791003 CRC64;

Query Match 6.8%; Score 84.5; DB 1; Length 637;
Best Local Similarity 20.9%; Pred. No. 15;
Matches 53; Conservative 41; Mismatches 91; Indels 69; Gaps 11;

QY 21 TALGNLKOIYYNEKAITENKESDDQFLENTLFGKFTGHPWYNLLVLDLGSKDATNKY 80
DB 310 TAMSNISEV-----DGETPEWIQRTVLQHSF-----NDAIFDL-SEWQWAY 351

QY 81 KGKVDLYGAYGYQCAGTPEKNTACWY-----GGVTLHDNRLTEKVPINL 129
DB 352 DNDFIDSDIAYKVAQLAET-NSNACAFKLSNQAKIVKDCATMCRHYKAEKREMTSQ 410

QY 130 WIDGKQTTVPID-KVYTSKEVTVQELDLOA-----RHYLHGK-----FGLYNSDSF 175
DB 411 WIKRCEKVDGDDGWRDIVRFRLYQVDFVAFSALKNFLHGVKKNCLLYGAPNT--- 467

QY 176 GGVQVQGLIVFHSSEGSTVSY-----DLFDAQ-----GOYPTLLRIYR 214
DB 468 -GKSLFGMSLMHFLQGAISIYVNSKSHFWLOPLYDAKIAMLDATSPCWAYIDQYLRNAL 526

QY 215 DNKTINSENLIHAL 228
DB 527 DGNPISLDVVKHAL 540

RESULT 27
RPOA MYCFU STANDARD; PRT; 333 AA.
ID RPOA MYCFU
AC Q98Q08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (ENAP alpha
DE subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit).
GN RPOA OR MYPU 5610.
OS Mycoplasma plimonis.
OC Bacteria; Firmicutes;
OX NCBI_TaxID=2107;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chabaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski K., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 CC !- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC !- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC !- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1
 CC beta, 1 beta', and 1 omega subunit (By similarity).
 CC !- DOMAIN: The N-terminal domain is essential for RNAP assembly and
 CC basal transcription, whereas the C-terminal domain is involved in
 CC interaction with transcriptional regulators and with upstream
 CC promoter elements (By similarity).
 CC !- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AL445565; CAC13734.1; -
 CC PIR; A99582; A99582; -
 CC MYPULIST; MYPU 5610; -
 CC HAKAP; MF_00059; -; 1.
 CC InterPro; IPR009025; RNP1-like_RNAPo.
 CC InterPro; IPR001700; RNA_pola_bac_org.
 CC Pfam; PF01000; RNA_pola_bac; 1.
 CC Pfam; PF03118; RNA_pola_A_CTD; 1.
 CC ProDom; PD001179; RNA_pola_bac_org; 1.
 CC SMART; SM00682; RPOD; 1.
 CC Transference; Transcription; DNA-directed RNA polymerase;
 CC Complete proteome.
 KW DOMAIN 1 246 ALPHA N-TERMINAL DOMAIN (ALPHA-NTD)
 FT (BY SIMILARITY).
 FT DOMAIN 262 333 ALPHA C-TERMINAL DOMAIN (ALPHA-CTD)
 FT (BY SIMILARITY).
 FT SEQUENCE 333 AA; 37907 MW; 7C23D7D86409604A CRC64;
 Query Match 6.8%; Score 84; DB 1; Length 333;
 Best Local Similarity 23.5%; Pred. No. 7.6;
 Matches 38; Conservative 24; Mismatches 38; Indels 62; Gaps 9;
 QY 25 NLKQIY-VYNEKATENK-----ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
 DB 92 NVKNIHLYDENIFEDNKIRGVETKNEKITSSDLKPPEN-----EI 125
 QY 70 DLGSKD---ATNKYGGKVDLYGAYY---GYQCAGGTENKACMGVGLHDNRLEET 122
 DB 126 EIVNKLLEIATN--NGQKPFVWEYVPHVGRY-----ISFDNKKLIEE 167
 QY 123 KKVPIINWID-GKQTTV-----PIDKVTSKKEVTVQELDLQ 158
 DB 168 KVALLNSTIKRGKFLAIDSDSPVEKVKVQVQEIINSSSLNIE 209
 RESULT 28
 ID AMY2_DICTH STANDARD; PRT; 562 AA.
 AC P14898;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-amyase 2 (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMYB.

OS Dictyoglomus thermophilum.
 OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
 OX NCBI_TaxID=14;
 RN [1]
 RC SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
 RP STRAIN=H-6-12; PubMed=2458257;
 RA MEDLINE=88329076; PubMed=2458257;
 RA Horinouchi S., Fukusumi S., Ohshima T., Beppu T.;
 RT "Cloning and expression in Escherichia coli of two additional amylase
 RT genes of a strictly anaerobic thermophile, Dictyoglomus thermophilum,
 RT and their nucleotide sequences with extremely low
 RT guanine-plus-cytosine contents.";
 RL Eur. J. Biochem. 176:243-253(1988).
 CC !- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC !- COFACTOR: Binds 1 calcium ion per subunit (Potential).
 CC !- PATHWAY: Polysaccharide degradation.
 CC !- SUBUNIT: Monomer (By similarity).
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.
 CC !- MISCELLANEOUS: WHEN COMPARED TO AMYA, AMYB PRODUCED LARGER AMOUNTS
 CC OF REDUCING SUGAR.
 CC !- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X13199; CAA31586.1; -
 CC PIR; S01312; S01312.
 CC InterPro; IPR006589; Alp_amy1_cat_sub.
 CC InterPro; IPR006047; Alpha_amy1_cat.
 CC Pfam; PF00128; alpha-amyase; 1.
 CC SMART; SM00642; Amy; 1.
 CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Multigene family.
 FT ACT SITE 309 309 BY SIMILARITY.
 FT ACT SITE 338 338 BY SIMILARITY.
 FT ACT SITE 404 404 BY SIMILARITY.
 FT METAL 236 236 CALCIUM (POTENTIAL).
 FT SEQUENCE 562 AA; 66999 MW; 9583342CFB7A369F CRC64;
 Query Match 6.8%; Score 84; DB 1; Length 562;
 Best Local Similarity 23.0%; Pred. No. 14;
 Matches 60; Conservative 31; Mismatches 94; Indels 76; Gaps 15;
 QY 25 NLKQIYVYNEKA-----ITENKESDDQFL---ENTL---LFK---GFTGHPWN 65
 DB 317 NFWSIFYNKRSEFPETFYGEIVETPKTKYGVKFGDGLDFYLFKIRDFIGRWST 376
 QY 66 D---LLVDLGSKDATNKY-----KGGKVDLYGAYYGYQCAGGTENK 104
 DB 377 KEFVKMIDLEERFYGNKPKRISFLENHSDNRFNLWAKDKLLRLASIFQFSI----NAI 431
 QY 105 ACMYGGV-----TLHDNNRLTEKKVPINLWIDGKQTTVPID----KVTSSKEVT 151
 DB 432 PIINYQEMGSCQYRDILEGNRTLHEARLPIP-WSDDKQDKXELDFYRQLVKIRKSHA 490
 QY 152 VOELDLQARHYLHKGKFLYNSD--SFGGKQV--RGILVFHSSSGSVSYVDLPDAQOYDPT 208
 DB 491 LYK-----GTFIPFSDMISFIKETQESILVLIINIEDKE---EIFNLNGTYRDL 537
 QY 209 LL-RIYRDNKNTINSNLHIAL 228
 DB 538 FSGNIYTNLSKLGPMASALLL 558
 RESULT 29
 ID RFAL_HUMAN STANDARD; PRT; 616 AA.
 RFAL_HUMAN

AC P27694;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Replication protein A 70 kDa DNA-binding subunit (RP-A) (RP-A)
DE (Replication factor-A protein 1) (single-stranded DNA-binding
DE protein)
GN RPA1 OR RPA70 OR RPA1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91268092; PubMed=2050703;
RA Erdlie L.F., Heyer W.-D., Kolodner R., Kelly T.J.;
RT "Characterization of a cDNA encoding the 70-kDa single-stranded DNA-
RT binding subunit of human replication protein A and the role of the
RT protein in DNA replication.";
RL J. Biol. Chem. 266:12090-12098(1991).
RN [2]
RP REVISION TO 217.
RX MEDLINE=9313193; PubMed=8420996;
RA Erdlie L.F., Heyer W.-D., Kolodner R., Kelly T.J.;
RT "Type I human complement C2 deficiency. A 28-base pair gene deletion
RT causes skipping of exon 6 during RNA splicing.";
RL J. Biol. Chem. 268:2268-2268(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 183-420.
RX MEDLINE=97144356; PubMed=8990123;
RA Bochkarev A., Pfuetzner R.A., Edwards A.M., Freppier L.;
RT "Structure of the single-stranded-DNA-binding domain of replication
RT protein A bound to DNA.";
RL Nature 385:176-181(1997).
CC -!- FUNCTION: Absolutely required for simian virus 40 DNA replication
CC in vitro. It participates in a very early step in initiation. RP-A
CC is a single-stranded DNA-binding protein.
CC -!- SUBUNIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-
CC binding activity may reside exclusively on the 70 kDa subunit.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: TO OTHER SPECIES RPA2/RPA2.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; M63488; AAA36584.1; -;
DR EMBL; BC018126; AAH18126.1; -;
DR PIR; A40457; A40457.
DR PDB; 1JMC; 15-OCT-97.
DR PDB; 1EWI; 10-MAY-00.
DR PDB; 1FGU; 14-FEB-01.
DR PDB; 1L1O; 05-JUN-02.
DR Genew; HGNC:10289; RPA1.
DR GK; P27694; -;
DR MM; 179835; -;
DR GO; GO:0005662; C:DNA replication factor A complex; TAS.
DR GO; GO:0003897; F:single-stranded DNA replication; TAS.
DR GO; GO:0006261; P:DNA dependent DNA replication; TAS.
DR GO; GO:0006310; P:DNA recombination; TAS.
DR GO; GO:0006281; P:DNA repair; TAS.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR007199; Rep-A_N.
DR InterPro; IPR004591; Rpa1.
DR InterPro; IPR004385; trna_anti.
DR Pfam; PF04057; Rep-A_N; 1.
DR TIGRfam; TIGR00617; rpa1; 1.
DR TIGRfam; TIGR00617; rpa1; 1.
KW DNA replication; DNA-binding; Zinc-finger; Nuclear protein;
FT 3D-structure. 481 503 C4-TYPE (POTENTIAL).
FT ZN_FING 184 184
FT STRAND 187 189
FT HELIX 192 193
FT TURN 198 206
FT STRAND 210 213
FT STRAND 218 227
FT STRAND 232 238
FT STRAND 239 245
FT HELIX 246 248
FT TURN 251 252
FT STRAND 254 258
FT STRAND 261 264
FT STRAND 267 269
FT HELIX 276 279
FT STRAND 282 283
FT TURN 285 288
FT STRAND 302 302
FT STRAND 305 310
FT HELIX 313 314
FT TURN 316 326
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 349
FT TURN 351 352
FT STRAND 355 361
FT HELIX 362 367
FT TURN 371 372
FT STRAND 375 384
FT TURN 386 387
FT STRAND 390 392
FT STRAND 398 400
FT HELIX 406 417
FT TURN 418 419
SQ SEQUENCE 616 AA; 68138 MW; FE038F40F5886CD1 CRC64;
Query Match 6.8%; Score 84; DB 1; Length 616;
Best Local Similarity 26.5%; Pred. No. 16;
Matches 59; Conservative 28; Mismatches 66; Indels 70; Gaps 15;
QY 6 EINE-----KDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 250 EVNKVYFSKGTLIKANKQFTAVNDYEMTFNNTSVMPC--DDHLP-TVQFD--FTG 304
QY 61 HPWYNLLVDLGSKDAFNKYKKVLDLYGAYGYQCAGGTFNKTACMGVGVTLHDNNRLT 120
DB 305 -----ID-----DLENKSKSLVDIIIGICKSYEDA-----TKITVRSNNREV 341


```

DR EMBL; M96301; AAA47040.1; --
DR PIR; S36595; S36595.
DR InterPro; IPR002210; PV_capsid_L1.
DR Pfam; PF00500; late_protein_L1; 1.
DR PRINTS; PR00865; HPV_Capsid_L1.
DR ProDom; PD00544; PV_capsid_L1; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 507 AA; 57491 MW; 98CA3AD3F031A62F CRC64;

Query Match
Best Local Similarity 20.3%; Pred. No. 14;
Matches 49; Conservative 38; Mismatches 69; Indels 85; Gaps 14;

QY 42 ESDDFLENTLLF-----KGFTGWYNDLLVDLGSKD-----ATNKYKGGKYD 86
DQ 23 QSTDEYVETNIFVHAISSDRLLTVGHPY-----DVRSGDQRIEVPKYSNGYRAFRIS 77
QY 87 -----LYGAYYGYQCAGTTP-----NKTACMYG 109
DQ 78 LPDPNRFALADMSVYNPKERLWACRGIEIGRGQPLGVGTSGHPLFNKVRDTESSNYQ 137
QY 110 GVTLDHNNRLTEEEKVPIINLWIDCKQTTVPI-----DKVTSKKEVTVOELDI-----QAR 160
DQ 138 GTTWDRQNTSFDPK-QVQMEIIG---CICLGEHWDKAKVCKEDAN-NQLGLCPPIELR 192
QY 161 HYLHGKFGLYNSDFG---GKVGRLIVFHSSEGSTVSYDLFDAQGYDPTLLR-----IYR 214
DQ 193 NTV-----IEDGMFDIFGFGNNKLSFNKSD---VSLDIVDETCYDPTLTMANDYVG 244
QY 215 D 215
DQ 245 D 245

RESULT 32
SHPI STAHY
ID SHPI STAHY STANDARD; PRT; 438 AA.
AC Q08002;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neutral metalloprotease precursor (EC 3.4.24.-).
GN SHPI.
OS Staphylococcus hyicus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1284;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 100-115.
RX MEDLINE=94166751; PubMed=8121397;
RA Ayora S., Goetz F.;
RT "Genetic and biochemical properties of an extracellular neutral metalloprotease from Staphylococcus hyicus subsp. hyicus.";
RL Mol. Gen. Genet. 242:421-430(1994).
CC -!- CATALYTIC ACTIVITY: Preferential cleavage of bonds with hydrophobic residues in P1'.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M30.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X73315; CAA51745.1; --
DR PIR; S42581; S42581.
DR MEROPS; M30.001; --
DR InterPro; IPR006025; Pept_M_Zn_BS.

```

```

DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Signal.
FT SIGNAL 1 26
FT PROPEP 27 101
FT CHAIN 102 438
FT ACT_SITE 242 242
FT METAL 243 243
FT ACT_SITE 243 243
FT METAL 246 246
FT METAL 269 269
SQ SEQUENCE 438 AA; 49692 MW; 368FAA36C5E84830 CRC64;

Query Match
Best Local Similarity 21.2%; Pred. No. 13;
Matches 51; Conservative 42; Mismatches 97; Indels 50; Gaps 11;

QY 7 INEKDLRKKSELOGTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFTGHPWYND 66
DQ 33 INEDINKNA--QESSIGTLKQ--NNFKQSTIISMPRNLSQFQEDKVKFAPKEKTP----- 85
QY 67 LLYDLGSKDATNKYKGGKVDLYGAYYGYQCAGTTPNKTACMYGGVTLHNNRLTEEEKVP 126
DQ 86 --ITERARKSENALSNDVRSF-----TTV--NVRTNENRTA 122
QY 127 INLWIDCKQTTVPI-DKVTSKKEVTVOELDIQARHYLHGKFGLYNSDSFGKVGQRLI 184
DQ 123 AKLYNGKNTNVAADNYITDKQKNIGEEFNKIDPLVKEKFGSPDVDDHDKV--NIL 180
QY 185 VFHSSG--STVSY-----DLFD-----AQCGYPTLLRIYRDNKTINSENLHIAL 228
DQ 181 VYDIKDDFTTGTGTYGTFPRDLVDVPHSKAEVYMDTYPMSGTGNLNEKKVYSTL 240

RESULT 33
SYR LISMO STANDARD; PRT; 556 AA.
ID SYR LISMO STANDARD; PRT; 556 AA.
AC Q8Y493;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).
GN ARGS OR LMO2561.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T., Charbit A., Chatouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordstrek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP + diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----

```



```

or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL591983; CAD00639.1; -.
DR PIR: A11394; A11394.
DR LiliList: LMO02561; -.
DR HAMAP: MF_00123; -.
DR InterPro: IPR001278; Arg_tRNA-synt_1c.
DR InterPro: IPR005148; N.
DR InterPro: IPR008909; tRNA-synt_1d_C.
DR InterPro: IPR001412; tRNA-synt_1.
DR Pfam: PF03485; N-Arg_1.
DR Pfam: PF00750; tRNA-synt_1d_1.
DR Pfam: PF05746; tRNA-synt_1d_C_1.
DR PRINTS: PR01038; TRNASYNTHARG.
DR TIGRfam: TIGR00456; args; 1.
DR PROSITE: PS00178; AA_tRNA_LIGASE_I.
KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
FT SITE 134 "HIGH" REGION.
SQ SEQUENCE 556 AA; 62836 MW; A9B8C425B3997820 CRC64;

Query Match 6.7%; Score 83; DB 1; Length 556;
Best Local Similarity 20.6%; Pred. No. 17;
Matches 62; Conservative 47; Mismatches 80; Indels 112; Gaps 16;

QY 5 EBINKDKRKSELOCTALGNLKOI-YYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
Db 259 EWFSETSYEENKVL-PALERLENGYIEQDGTWLRITTFEDDKDRVLKSDGS---- 313
QY 64 YNDLLVDLGSKDANKYK--GKKYDLGA-YGYG-----OCAGGTENKTCMYGGV 111
Db 314 YYYFDPDIAYH--LNKLERGFVLIDWGDHGVIPMRRAIEALGVSP----- 361
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSK--KEVT-----VQELDQARHYLH 164
Db 362 -----NQLVEVEIQLVHLFEDGVQ-----VMSKRTGKSVTMRDLIEEVGLDATRYF- 408
QY 165 GKFGLYNSDF-----GKVGORGLIVHSSSGS 192
Db 409 --FAMRSSDTWNFMDSIAKSTNDNPVYQYAHARISSILRSK-EGGLEVTKDADM 465
QY 193 TV-----SYDLFDAQGQYPTLL-----RIYRDNKNTINSENLH 225
Db 466 LIQTEAEYDLLKVLGFEADVVAEAAKRAPHRIVRYLNDLASAPHRFYNKSNKVLDMNDLE 525
QY 226 I 226
Db 526 V 526

RESULT 34
RPOA_LACPL STANDARD; PRT; 314 AA.
AC Q88XW0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (transcriptase alpha chain) (RNA polymerase alpha subunit).
GN RPOA OR LP_1062.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kuipers O.P., Leer R., Turchini R., Peters S.A., Sandbrink H.M., Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B., De Vos W.M., Siezen R.J.;

```

```

RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + (RNA)(N).
CC -!- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1 beta, 1 beta', and 1 omega subunit (By similarity).
CC -!- DOMAIN: The N-terminal domain is essential for RNAP assembly and basal transcription, whereas the C-terminal domain is involved in interaction with transcriptional regulators and with upstream promoter elements (By similarity).
CC -!- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AL935254; CAD63597.1; -.
DR HAMAP: MF_00059; -.
DR InterPro: IPR009025; RBP1-like RNapo.
DR InterPro: IPR001700; RNA_pol_A_bac_1.
DR Pfam: PF01000; RNA_pol_A_bac; 1.
DR Pfam: PF03118; RNA_pol_A_CTD; 1.
DR Transferrase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome.
FT DOMAIN 1 228 ALPHA N-TERMINAL DOMAIN (ALPHA-NTD) (BY SIMILARITY).
FT DOMAIN 245 314 ALPHA C-TERMINAL DOMAIN (ALPHA-CTD) (BY SIMILARITY).
FT SEQUENCE 314 AA; 34842 MW; 573B3160D42DE7DF CRC64;

Query Match 6.7%; Score 82.5; DB 1; Length 314;
Best Local Similarity 38.3%; Pred. No. 9.5;
Matches 18; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

QY 119 LTBKKVPINLWIDGKQTTVPIDKVTSK--EVTVQELDQARHY 162
Db 217 LTDLHSIFVNLTDKNTDVMVEKEETHKEKMLEMIEELDLSVRSY 263

RESULT 35
YB70_HAEIN STANDARD; PRT; 328 AA.
AC Q57527; O05047;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical paba-like protein H1170.
GN H1170.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Ravelance A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

```

RT Rn; Science 269:496-512 (1995).
 CC -1- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINO BENZOATE SYNTHASE
 CC COMPONENT 1.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U32797; AAC22834.1; -
 CC PIR; F64187; F64187.
 CC TIGR; H1170; -
 CC InterPro: IPR005801; Anth synth. chor.
 CC Pfam; PF00425; chorismate_bind; 1.
 CC PRINTS; PD00095; ANTSYNTHASE1.
 CC ProDom; PD00079; Anth synth. chor; 1.
 CC KW Hypothetical protein; Complete proteome.
 CC SQ SEQUENCE 328 AA; 37734 MW; 1C02BCD008957B0 CRC64;
 CC
 CC Query Match 6.7%; Score 82.5; DB 1; Length 328;
 CC Best Local Similarity 27.3%; Pred. No. 10; Indels 13; Gaps 3;
 CC Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;
 CC
 CC 136 TTVPIDVKTSKKEVT---VOELDLQARHYLHGKFLGKLYNSDFGKVGQGLI-----V 185
 CC 237 TLTPAGSISGAPKKTQIIQAQKQKRGYYTGIFGIFDGKTLQSAVAIRFISQVDEKRY 296
 CC
 CC 186 FHSSEGSTVSVDLFDAGQGPDTLLRIY 213
 CC 297 FHSGGGITH---SNAQDEVEELLEKRY 321
 CC
 CC RESULT 36
 CC PBP_STAUA STANDARD; PRT; 670 AA.
 CC AC P07944;
 CC DT 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-AUG-1988 (Rel. 08, Last sequence update)
 CC DT 01-NOV-1990 (Rel. 16, Last annotation update)
 CC DE Beta-lactam-inducible penicillin-binding protein.
 CC PBP.
 CC GN Staphylococcus aureus.
 CC OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CC OX NCBI_TaxID=1280;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE=87304805; PubMed=3305073;
 CC RA Song M.D., Wachi M., Doi M., Ishino F., Matsubashi M.;
 CC RT "Evolution of an inducible penicillin-target protein in methicillin-
 CC resistant Staphylococcus aureus by gene fusion."
 CC RL FEBS Lett. 221:167-171 (1987).
 CC CC -1- INDUCTION: IN THE PRESENCE OF BETA-LACTAM ANTIBIOTICS, MRSA
 CC CELLS PRODUCE THIS UNIQUE PBP IN EXCESSIVELY LARGE AMOUNTS AND
 CC CAN STILL PROLIFERATE, WHILE ALL THE NORMAL PBPS ARE INACTIVATED
 CC (REVERSIBLE SWITCHING ABILITY OF PBP FORMATION).
 CC CC -1- MISCELLANEOUS: PBP HAS EXTREMELY LOW AFFINITY TO PENICILLIN AND
 CC MOST OTHER BETA-LACTAM ANTIBIOTICS.
 CC CC -1- SIMILARITY: TWO DIFFERENT SETS OF CONSERVED SEQUENCES CONTAINING
 CC S-X-X-K FOR PENICILLIN-BINDING WERE FOUND IN MRSA PBP. THE FIRST
 CC BEING LOCATED AROUND SER-25 (HOMOLOGY WITH THE PENICILLIN-BINDING
 CC DOMAIN OF THE PENICILLINASE) AND THE SECOND AROUND SER-405 (HIGH
 CC HOMOLOGY WITH BOTH THE PUTATIVE TRANSGLYCOSYLASE (N-TERMINAL) AND
 CC TRANSPEPTIDASE (C-TERMINAL) PENICILLIN-BINDING DOMAIN OF E.COLI
 CC PBPS 2 AND 3). THE AUTHORS SUGGEST THE SER-405 RESIDUE TO BE THE
 CC PENICILLIN-BINDING SITE AND THE SEQUENCE AROUND SER-25 TO BE A
 CC RELIC OF THE EVOLUTION OF THIS DOMAIN FROM A PENICILLINASE GENE.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y00688; CAA68684.1; -
 CC MEROPS; S12.UNW; -
 CC InterPro: IPR007887; MacA.N.
 CC InterPro: IPR006311; PBP_dimer.
 CC InterPro: IPR001460; Transpeptidase.
 CC Pfam; PF05223; MacA_N; 1.
 CC Pfam; PF03717; PBP_dimer; 1.
 CC DR Pfam; PF00905; Transpeptidase; 1.
 CC KW Peptidoglycan synthesis; Cell division; Antibiotic resistance;
 CC Cell wall.
 CC FT BINDING 25 25 PENICILLIN (PROBABLE).
 CC FT BINDING 405 405 PENICILLIN (PROBABLE).
 CC SQ SEQUENCE 670 AA; 76463 MW; 2DAA414D35DA993A CRC64;
 CC
 CC Query Match 6.7%; Score 82.5; DB 1; Length 670;
 CC Best Local Similarity 20.3%; Pred. No. 24;
 CC Matches 64; Conservative 44; Mismatches 88; Indels 119; Gaps 15;
 CC
 CC 7 INEKDLRKKSELOG-----TALGNLKOIYYNEK-----AITE 39
 CC 259 INSEELKQK-EYKGYKDDAVIGKGLKLYDKK-QHEDGYRVTVIRVDNSNTAHTLIE 317
 CC
 CC 40 NKESDDQPLENTLFGKFFTHGHPWYNDLLVDLGSKDATNKYKGGKVDL-----YGAYGY 94
 CC 318 KKKDKGDIQITDAK---VQKSIYNNKNDYSGSTAIHPQTGELLALVSTPSVDVY--- 371
 CC
 CC 95 QCAGTNPNTACTMGYGVTLHDNNELTEKKVP-INLMIDGKQTVP--IDKVTSKKEVT 151
 CC 372 -----PFMY-GMSNEEYKLTEDKKEPLNKF---QITTPSGTQKILTAMIGLN 417
 CC
 CC 152 VOELDLQARHYLHGKFLGKLYNSDFG----- 177
 CC 418 NKTLDKTSYKIDGK-GWQDKKSGGYNVTRYEVVNGNIDLKQAISSDNIFARVALEL 476
 CC
 CC 178 ---KVQGRGLIVFHSSEGSTVSVDLFDAG-----GQ-----YPTLLRI 212
 CC 477 GSKKFEKGMKGLGVGEDIPSDYPFYNAQISKNLDBILLADSGYGGGTEILNPVQILSI 536
 CC
 CC 213 Y---RDNKTINSENI 224
 CC 537 YSALENNGNINAPHL 551
 CC
 CC RESULT 37
 CC TOP2_CAEEL STANDARD; PRT; 1520 AA.
 CC ID TOP2_CAEEL
 CC AC Q23670; Q27509;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Probable DNA topoisomerase II (EC 5.99.1.3).
 CC GN K12D12.1.
 CC OS Caenorhabditis elegans.
 CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 CC OC Rhabditidae; Pelodierinae; Caenorhabditis.
 CC OX NCBI_TaxID=6239;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-Bristol N2;
 CC RA Swinburne J.;
 CC RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-Bristol N2;
 CC RA Coles L.;
 CC RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC CC -1- FUNCTION: Control of topological states of DNA by transient

CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z70213; CAA94177.1; -.
CC EMBL; Z49069; CAA94177.1; JOINED.
CC EMBL; Z49069; CAA98867.1; -.
CC EMBL; Z70213; CAA98867.1; JOINED.
CC F01; T23620; T23620.
CC HSP; P06786; LBGW.
CC WormPep; K12D12.1; C06184.
CC InterPro; IPR003594; ATPbind ATPase.
CC InterPro; IPR003957; CBFA NFYB topis.
CC InterPro; IPR001241; DNA_TopoisoII.
CC InterPro; IPR002205; DNA_TopoisoIV.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00521; DNA_topoisoB; 1.
CC Pfam; PF02518; HATPase_C; 1.
CC PRINTS; PR00615; CCAATSUBUNTA.
CC PRINTS; PR00418; TPI2FAMILY.
CC ProDom; PD000742; DNA_topoisoIV; 1.
CC SMART; SM00387; HATPase_C; 1.
CC SMART; SM00433; TOP2C; 1.
CC SMART; SM00434; TOP4C; 1.
CC PROSITE; PS00177; TOPOISOMERASE II; 1.
CC Isomerase; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
CC ACET SITE 156 201 ATP (POTENTIAL).
CC ACET SITE 840 840 DNA CLEAVAGE (BY SIMILARITY).
CC SEQUENCE 1520 AA; 172333 MW; 016226697F41C360 CRC64;
Query Match 6.7%; Score 82.5; DB 1; Length 1520;
Best Local Similarity 21.5%; Pred. No. 64;
Matches 50; Conservative 29; Mismatches 61; Indels 93; Gaps 13;
QY 19 QGTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTH-----PWNLLVDLG 72
Db 889 QGIGTGWSTNPYNPRELVKY-----IKELIAGEPQKALAPYKN----- 929
QY 73 SKDATNKYKGVKVDLYGAVYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVLPINLW-- 130
Db 930 -----FRGKLIQI-----DPSRFAC-YGEVAVLDNTI-EITELFIKQWTO 969
QY 131 -----IDG-----KQTFPIDKVKTSKKBVTVOEL-----DLQARHYLHGRFGL 169
Db 969 DYKEKVLGLESDDKSPFVID-YKEYHTDTTVKVVKLRELERQDLHQVF-- 1025
QY 170 YNSDSFGKGVORGLVHFSSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSE 222
Db 1026 -----KQAVI-----NTCMVLFDAAG-----CLRTYTSPEAITQE 1057
RESULT 38
YA42 MYCPN
ID YA42 MYCPN STANDARD; PRT; 672 AA.
AC P75072;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)

DE Hypothetical protein MPN042 (B01_orf672).
GN MPN042 OR MP112.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
ON NCBI_TaxID=2104;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
Hermann R.;
RP SEQUENCE FROM N.A. / M129;
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RL Nucleic Acids Res. 24:4420-4449 (1996).
CC -!- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE000013; AAB95760.1; -.
CC PIR; S73438; S73438.
CC InterPro; IPR004306; MG032/096/288_1.
CC InterPro; IPR004315; MG032/096/288_2.
CC Pfam; PF03072; DUF237; 1.
CC Pfam; PF03086; DUF240; 1.
CC ProDom; PD004834; MG032/096/288_2; 1.
CC Hypothetical protein; Complete proteome.
CC SEQUENCE 672 AA; 77588 MW; 1A7A593003ADB866 CRC64;
Query Match 6.8%; Score 81.5; DB 1; Length 672;
Best Local Similarity 20.2%; Pred. No. 29;
Matches 73; Conservative 45; Mismatches 79; Indels 165; Gaps 19;
QY 2 EKSEINEKDLRKSELOGTALGNLKQIYYNEKAITENKES---DDQFLENTLLFKGRFF 58
Db 338 KESEKHEKLEEQRIQAEKAKNDEQL---OKPQTELKALGGIDSPVE---PF 386
QY 59 TGHVWYNLLVDLGS-----KDATNKY--K 81
Db 387 TN---NDLRLKLGTYKEDNVNTRAGLFRALFVSGNVRATFYITLLGWKDTTFIKK 442
QY 82 GKXVDL-----YGAY-----YGYCAGGTPNKTACMYGGVTLHDNN 117
Db 443 AKQDIRDDEKFRKAFGLSPKATEKDVGVKTNPGYGYQ---GIYIKDS-LRQGIKYS 498
QY 118 RLTEKKVPTNL-----WIDGKQTFPIDKVKTS---KKE 149
Db 499 TVSEPKNVKSLPGLTVGDNEEGKIWIASHNFRQNHENGAG-----EKFKYSAYRFPD 551
QY 150 VTVO-BLDLQAR-----HYLHGRFGL-YNSD-----SFGGK 178
Db 552 VTVDYDEVSASAKWWTWAFRGSIPGYWRGFKVTSYDFGVVPSWKYGHIOVRTPQYSFNKQ 611
QY 179 VQGLIVHFSSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENLH-----IALY 229
Db 612 EQKILFVPHAIQ-----KIAAGSNLDLINFLLKQDLDEFEHYHPLDKPLDLVAVL 664
QY 230 LY 231
Db 665 LY 666
RESULT 39
GLPK_AQAE
ID GLPK_AQAE STANDARD; PRT; 492 AA.
AC O66746;
DT 30-MAY-2000 (Rel. 39; Created)
DT 30-MAY-2000 (Rel. 39; Last sequence update)

```

28-FEB-2003 (Rel. 41, Last annotation update)
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
(Glycerokinase) (GK)
GN GLPK OR AQ 434
OS Aquifex aeolicus.
CC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SIMILARITY: Belongs to the fucokinase / gluconokinase /
CC glycerokinase / xylulokinase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB000690; AAC0670.1; -
CC DR PIR; F70339; F70339.
CC DR HSP; P08859; IGLC.
CC DR HAMAP; MF 00186; -.
CC DR InterPro; IPR000577; FGGY_kin.
CC DR InterPro; IPR005999; Glycerol_kin.
CC DR Pfam; PF00370; FGGY; 1.
CC DR Pfam; PF02782; FGGY_C; 1.
CC DR TIGRFAMs; TIGR01311; glycerol_kin; 1.
CC DR PROSITE; PS00445; FGGY_KINASES; 2; 1.
CC DR PROSITE; PS00933; FGGY_KINASES; 1; 1.
CC DR GlycoER; G00000; Glycerol_kinase; 1.
CC DR GlycoER; G00000; Glycerol_kinase; 1.
CC DR Complete proteome.
CC NP BIND 148
CC FT NP BIND 148
CC SQ SEQUENCE 492 AA; 53297 MW; CE9F0E8FF593B37 CRC64;

Query Match 6.5%; Score 81; DB 1; Length 492;
Best Local Similarity 26.3%; Pred. No. 22;
Matches 57; Conservative 27; Mismatches 61; Indels 72; Gaps 15;

Qy 26 LKQIYYNEKAIENKESDDQFLENTLLFKGFTGHPWYNDLL-VDLGSKDANKYKGGK 84
Db 67 LKEI---NSTGINTQRE-----TVLLWDKTEGPRVYNAIQLQDURIEDIC-----RK 110
Qy 85 VDLGAYGYQCAGGTGPNKTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTPIDKVK 144
Db 111 LSEYSEYIKENT-----GLLHPYFSASK-----VN-WI-----IENVN 143
Qy 145 TSKEVTVQELDLQARHYLHGK--FGLYNS-----DSFGKGVQRLIVFHSSEGSTVSYD- 197
Db 144 GKVKDIE-----RKVFIFGVTDVTLWNLUTGKGV-----HKTEPSNASRTL 184
Qy 198 LFDAAQ-QYDPTLLRIVRDKNKTINSE-NLHIALYLYT 232
Db 185 LFNKRLKYDELLKIFRIPKNIIPVYNSSSLEFGYT 221

RESULT 40
SYN SYR LISIN STANDARD; PRT; 556 AA.
AC Q927T2;

```

QY 165 GKFGLYNSDSF-----GKVGORGLIVFHSSEGS 192
 Db 409 --FAMRSSDTHNVPMSLAKSTSDNPNVYQYAHARSSILRSKQ-EQGLEVSKDANMS 465
 QY 193 TV-----SYDLFDAQQYDPDTLL-----RYRDNKTINSNLH 225
 Db 466 LLETEABYDLKLVLGEFADVAEAAVKSPHRIYRVLYNLDTAFHFRFYNSKNVLDMDNLE 525
 QY 226 I 226
 Db 526 V 526

RESULT 41
 PFPA SOLTU
 ID PFPA SOLTU STANDARD; PRT; 616 AA.
 AC P21342;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit
 DE (EC 2.7.1.90) (PPP) (6-phosphofructokinase, pyrophosphate-dependent)
 DE (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (Pp1-PFK).
 OS Solanum tuberosum (Potato)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 277-295.
 RC STRAIN=cv. Kennebec;
 RX MEDLINE=91009330; PubMed=2170409;
 RA Carlisle S.M., Blakeley S.D., Hemmingsen S.M., Trevanion S.J.,
 RA Hiroyoshi T., Kruger N.J., Dennis D.T.;
 RT "Pyrophosphate-dependent phosphofructokinase. Conservation of protein
 RT sequence between the alpha- and beta-subunits and with the ATP-
 RT dependent phosphofructokinase";
 RL J. Biol. Chem. 265:18366-18371(1990).
 CC -!- FUNCTION: The alpha subunit may be involved in the regulation of
 CC FPP by Fru-2,6-P.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
 CC phosphate + D-fructose 1,6-bisphosphate.
 CC -!- ENZYME REGULATION: Fru-2,6-P is an activator of the plant enzyme.
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains.
 CC -!- MISCELLANEOUS: The active site might be on the beta subunit.
 CC -!- SIMILARITY: TO OTHER PLANT ALPHA SUBUNITS AND ALSO, STRONG, TO THE
 CC BETA SUBUNITS.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M55190; AAA63451.1; -
 DR PIR; A36094; A36094.
 DR InterPro; IPR000023; Ppfuckinase.
 DR Pfam; PF00365; PFK; 1.
 DR ProDom; PD000707; Ppfuckinase; 1.
 DR Transferrase; Kinase; Allosteric enzyme.
 SQ SEQUENCE 616 AA; 67157 MW; 2D33EP2ADF3AA0AF CRC64;
 Query Match 6.5%; Score 81; DB 1; Length 616;
 Best Local Similarity 30.2%; Pred. No. 29;
 Matches 26; Conservative 8; Mismatches 36; Indels 16; Gaps 3;
 QY 74 KDATNKYKGVLDLYGAYGYQCAGGTPNKTACMGYGVY-----LHNNRUTE 122
 Db 412 KEGT--YKGFNAICHFFGQAGSPLSPKFDYAVLVGVCHVLAAGLNGYMATITN 469

QY 123 KKVPINLWIDGKQTTVPIDKVKTSKK 148
 Db 470 LKNPANKWHCGAS---PISAMTVKR 492

RESULT 42
 MPGP PYRHO
 ID MPGP PYRHO STANDARD; PRT; 243 AA.
 AC OS8690;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mannosyl-3-phosphoglycerate phosphatase (EC 3.1.3.70) (MPGP).
 GN MNGB OR PH0926.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Karabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamanoto S., Sekine Y., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuwa H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-76(1998).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=21570230; PubMed=11562374;
 RA Empadinhas N., Marug J.D., Borges N., Santos H., da Costa M.S.;
 RT "Pathway for the synthesis of mannosylglycerate in the
 RT hyperthermophilic archaeon Pyrococcus horikoshii. Biochemical and
 RT genetic characterization of key enzymes";
 RL J. Biol. Chem. 276:43580-43588(2001).
 CC -!- FUNCTION: Hydrolyzes mannosyl-3-phosphoglycerate (MPG) to form the
 CC osmolyte mannosylglycerate (MG). The enzyme is absolutely specific
 CC for MPG.
 CC -!- CATALYTIC ACTIVITY: 2(alpha-D-mannosyl)-3-phosphoglycerate + H(2)O
 CC = 2(alpha-D-mannosyl)-D-glycerate + phosphate.
 CC -!- COFACTOR: Magnesium.
 CC -!- PATHWAY: Biosynthesis of alpha-mannosylglycerate from GDP-mannose;
 CC second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the HAD superfamily. MPGP family.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF000004; BAA30022.1; -
 DR PIR; H71082; H71082.
 DR HAMAP; MF_00617; -; 1.
 DR InterPro; IPR006379; HAD_SF_IIB.
 DR InterPro; IPR006381; HAD_SF_Yedp.
 DR TIGRFAMs; TIGR01486; HAD-SF-IIB-Yedp; 1.
 DR TIGRFAMs; TIGR01484; HAD-SF-IIB; 1.
 DR Hydrolase; Magnesium; Complete proteome.
 SQ SEQUENCE 243 AA; 27959 MW; FE5EE94DCAAD3636 CRC64;
 Query Match 6.5%; Score 80.5; DB 1; Length 243;
 Best Local Similarity 22.2%; Pred. No. 10;
 Matches 43; Conservative 37; Mismatches 71; Indels 43; Gaps 9;
 QY 27 KQIYYNE-----KAITENKESDDQFLENTLLFKGFF-----TGHWPYNDLLVLSKDAT 77

OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=69013;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 493-517.
 RX MEDLINE=94094330; PubMed=8269515;
 RA XU M.-Q., Southworth M.W., Merisha F.B., Hornstra L.J., Perler F.B.;
 RT "In vitro protein splicing of purified precursor and the
 RT identification of a branched intermediate.";
 RL Cell 75:1371-1377(1993).
 CC -!- FUNCTION: In addition to polymerase activity, this DNA polymerase
 CC exhibits 3' to 5' exonuclease activity.
 CC -!- FUNCTION: INTRIN ENCODED ENDONUCLEASES ARE THOUGHT TO MEDIATE
 CC INTRON MOBILITY BY SITE-SPECIFIC RECOMBINATION INITIATED BY
 CC ENDONUCLEASE CLEAVAGE AT THE "HOMING SITE" IN GENE THAT LACK THE
 CC INTRON.
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -!- PTM: This protein undergoes a protein self splicing that involves
 CC a post-translational excision of the intervening region (intron)
 CC followed by peptide ligation.
 CC -!- BIOTECHNOLOGY: Used in the PCR method because of its high
 CC thermostability and low error rate. Sold by New England Biolabs.
 CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
 CC -!- SIMILARITY: In the intron section, belongs to the homing
 CC endonuclease family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00707; AAA67130.1; -;
 DR EMBL; U00707; AAA67131.1; -;
 DR EMBL; U00707; AAA67132.1; -;
 DR PIR; S68593; S68593.
 DR HSP; P56689; 1TGO.
 DR REBASE; 2819; PI-Pspt.
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006134; DNA_pol_B_dom.
 DR InterPro; IPR006133; DNA_pol_B_exo.
 DR InterPro; IPR003587; Hedgehog_hint_N.
 DR InterPro; IPR003586; Hedgehog_hintC.
 DR InterPro; IPR006142; INTEIN.
 DR InterPro; IPR004842; INTEIN_endonuc.
 DR InterPro; IPR006141; Intron_S.
 DR InterPro; IPR004578; Pol2.
 DR Pfam; PF00136; DNA_pol_B; 2.
 DR PRINTS; PR00106; DNAPOL2.
 DR PRINTS; PR00379; INTEIN.
 DR SMART; SM00305; HintC; 1.
 DR SMART; SM00306; HintN; 1.
 DR SMART; SM00486; POLBc; 1.
 DR TIGRFAMs; TIGR01443; Intron_Cterm; 1.
 DR TIGRFAMs; TIGR01445; Intron_Nterm; 1.
 DR TIGRFAMs; TIGR00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR PROSITE; PS00818; INTEIN_C_TER; 1.
 DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 1.
 DR PROSITE; PS00817; INTEIN_N_TER; 1.
 KW Transferase; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
 KW Protein splicing; Intron homing
 FT CHAIN 1 492 DNA POLYMERASE, 1ST PART.
 FT CHAIN 493 1029 ENDONUCLEASE PI-PSPI.
 FT CHAIN 1030 1312 DNA POLYMERASE, 2ND PART.
 SQ SEQUENCE 1312 AA; 152852 MW; B62518805641D26A CRC64;

Query Match

6.5%; Score 80.5; DB 1; Length 1312;

Best Local Similarity 23.9%; Pred. No. 78;
 Matches 62; Conservative 33; Mismatches 85; Indels 79; Gaps 16;
 QY 4 SEINEXDLRKK-----SELQGTALGNL--KQIYYNEKAITENKESD-----44
 Db 923 NEELKFTFYRKKNVHSHVVKDILKETGKVFQKNISYKKFRELVENGLDREKAKRI 982
 QY 45 -----DQFLENTLLFK-GFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYG 89
 Db 983 EWLINGDIVLDRVVVEIKREYDGVV--DLSVDEBENFLAGFGLYAHNSYVG-----1033
 QY 90 AYGYG-----QCAGGTNKTACMYGGVTLHDNRLTEEK--KVPINLWI--DKQT 136
 Db 1034 -YGYAKARWYKCECA-----ESVTANGREYIFVRKELEKEKFGKV--LYIDTDGLYA 1084
 QY 137 TVPIDKVKTSKKEVTQOELDQARHYLHGKF-GLYNSDSFGGKVQGLIVFHSSEGSTVS 195
 Db 1085 TIFGAPKEEIKKKA-----LEFVDVINAKLPGLLELE-YEGFYVRGFFV-----TKKK 1131
 QY 196 YDLFDAQGGYPTDLLRIYR 214
 Db 1132 YALIDEEGKIITRGLEIVR 1150
 RESULT 45
 PGK_GLOMO STANDARD; PRT; 416 AA.
 ID PGK_GLOMO
 AC 074233;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoglycerate kinase (EC 2.7.2.3).
 GN PGK.
 OS Glomus mosseae.
 OC Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
 OC Glomeraceae; Glomus.
 OX NCBI_TaxID=27381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEG 12;
 RA Harrier L.A., Hooker J.E.;
 RT "Isolation of the 3-phosphoglycerate kinase gene of the arbuscular
 RT mycorrhizal fungus Glomus mosseae Gerdemann & Trappe.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
 CC phospho-D-glyceroyl phosphate.
 CC -!- PATHWAY: Second phase of glycolysis; second step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF072893; AAD09406.1; -;
 DR EMBL; AF074394; AAC26131.1; -;
 DR HSP; P00560; 1QPG.
 DR InterPro; IPR001576; PGK.
 DR Pfam; PF00162; PGK; 1.
 DR PRINTS; PR00477; PHGLYCKINASE.
 DR PROSITE; PS00111; PGLYCERATE_KINASE; 1.
 KW Transferase; Kinase; Glycolysis.
 SQ SEQUENCE 416 AA; 44764 MW; 53179DF32BEFEC48 CRC64;

Query Match

6.5%; Score 80; DB 1; Length 416;

Best Local Similarity 22.5%; Pred. No. 22;
 Matches 53; Conservative 24; Mismatches 59; Indels 100; Gaps 12;

QY 4 SBEINEKDLRKXSE-----LOGTALGNLKOI-----YYNEKAITENKESD 44
 Db 4 SNKLSIRDLNVKDKRVLIRVDFNVPDLGTTINNOBIVAALEFKAKTV-----58
 QY 45 DQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGGVDLYG-----89
 Db 59 -----VLMSHLGRPD-----GKKVDKYSILAPVAKEVERLLGKK 91
 QY 90 AYYGYOCAG-GTPN--KTACMYGGVTLHDNNRLTEK-----KVPINLWIDGKQTTVPIDK 142
 Db 92 VTFLDCVGEVENVYKNAC-DGEVILLLENLAFHAEERSSGKP-----DGKKVADIEK 145
 QY 143 VKTSKEVTVQELDLQARHYLHGKFLGYNDSFGGKVGRLIVPHSSEGSTVSVDL 198
 Db 146 VKFEFRSLTALG-----DVIINDAFG-----TAHRAHSMYGVVEL 180

RESULT 46
 LEC_PARP
 ID_LEC_PARP STANDARD; PRT; 447 AA.
 AC P83304;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mannose/glucose-specific lectin.
 OS Parkia platycephala.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Mimosoideae; Parkieae; Parkia.
 OC NCBI_TaxID=185447;
 RN [1]
 RP SEQUENCE, SUBUNIT, MASS SPECTROMETRY, AND VARIANTS VAL-70; ARG-227 AND
 RP ASN-296.
 RC MEDLINE=21393945; PubMed=11502201;
 RX Mann K., Farias C.M.S.A., Del Sol F.G., Santos C.F., Grangeiro T.B.,
 RA Ngano C.S., Cavada B.S., Calveire J.J.,
 RA "The amino-acid sequence of the glucose/mannose-specific lectin
 RT isolated from Parkia platycephala seeds reveals three tandemly
 RT arranged jacalin-related domains.";
 RL Eur. J. Biochem. 268:4414-4422(2001).
 RN [2]
 RP FUNCTION.

RA Ramos M.V., Cavada B.S., Bomfim L.R., Debray H., Mazard A.-M.,
 RA Calveire J.J., Grangeiro T.B., Rouge P.,
 RA "Interaction of the seed lectin from Parkia platycephala (Mimosoideae)
 RT with carbohydrates and complex glycans.";
 RL Protein Pept. Lett. 6:215-222(1999).
 CC -!- FUNCTION: Mannose/glucose specific lectin. Shows agglutinating
 CC activity against rabbit erythrocytes.
 CC -!- SUBUNIT: Homodimer.
 CC -!- MASS SPECTROMETRY: MW=47946; MW_ERR=6; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=47951; MW_ERR=9; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the jacalin lectin family.
 DR GO; GO:0005536; F:glucose binding; IDA.
 DR GO; GO:0005537; F:mannose binding; IDA.
 DR GO; GO:0000771; P:agglutination; IDA.
 DR InterPro; IPR001229; Jacalin_Lectin.
 DR Pfam; PF01419; Jacalin; 3.
 DR Lectin; Mannose-binding; Repeat.
 FT MOD_RES 1 1
 FT LECTIN 1 447 3 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 1 149 1.
 FT REPEAT 150 295 2.
 FT REPEAT 296 447 3.
 FT REPEAT 70 227 I -> V.
 FT VARIANT 227 K -> R.
 FT VARIANT 296 D -> N.
 SQ SEQUENCE 447 AA; 47521 MW; 8F14ED460874BBB2 CRC64;

Query Match 6.5%; Score 80; DB 1; Length 447;
 Best Local Similarity 23.6%; Pred. No. 24;
 Matches 38; Conservative 20; Mismatches 65; Indels 38; Gaps 8;

QY 60 GHPW-----VNDLLVDLGSKDATNKYKGGVDLYGAYGYOCAGGTPNKTACMYGGVT 112
 Db 311 GDFWSTYANEGINQIIYAGSNIKSVAFK-----DTSGLDSATFGGVN 353
 QY 113 LHDNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKEV--TVQELDLQARHYLHGKFLY 170
 Db 354 PKDTG--EKTVTSIN-WPSEYLTISGTVQYKFKDVFTTITSLSTFTTNLATYGFPGA 409
 QY 171 NSDSFGGKVGRLIV-PHSSEGSTVSVDLFDPAQGY--PDT 208
 Db 410 SATSFSPIHNNMVGVGHGAG-----DYLDAGIGFVKPDT 445

RESULT 47
 YF08_MYCPN
 ID_YF08_MYCPN STANDARD; PRT; 509 AA.
 AC P75278;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN508 (P02_orf509).
 GN MPN508 OR MP334.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RC MEDLINE=97105885; PubMed=8948633;
 RX Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Hermann R.;
 RA "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 RL -!- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).
 CC EMBL; AF000031; AAB95982.1; --
 DR PIR; S73660; S73660.
 DR InterPro; IPR004306; MG032/096/288_1.
 DR InterPro; IPR004319; MG032/096/288_2.
 DR Pfam; PF03072; DUF237; 1.
 DR Pfam; PF03086; DUF240; 1.
 DR ProDom; PD004834; MG032/096/288_2; 1.
 DR Hypothetical protein: Complete proteome.
 KW SEQUENCE 509 AA; 57825 MW; 8DC95BB941A6987 CRC64;
 SQ

Query Match 6.5%; Score 80; DB 1; Length 509;
 Best Local Similarity 22.0%; Pred. No. 28;
 Matches 56; Conservative 39; Mismatches 106; Indels 54; Gaps 13;

QY 3 KSEINEKDLRKXSELQ--TALGNLKQIYYNEKAITENKE-----SDDOFLENTL 52
 Db 234 KAEVVKLEAREAFNKSLSLTAASEFKQYWSKKKQVTDKQLAELAKISLEADNRFTSF 293
 QY 53 LFKGFTGHPWYNLLVDLGSKDATNKYKGGV-----KVDLYGAYGYOCAGGTPNKTAC 106
 Db 294 LIAGFRTALDWTYNAKKE--NNDAKQKAFGSGQIQFKDGLNGIYMPDWLRLGELTSK-- 349
 QY 107 MYGGVTLHDNNRLTEKKV-----PINLWIDGKQTTVPIDKVKTSKEVTVQELDLQAR 160
 Db 350 -----NINLTKELVKYQNKIESPTINWIDG---VGIKQKAMPFNVRFEV-DIKYTG 398
 QY 161 HYLHGKF--GLYNS--DSFGKVGQRLIVPHSSEGSTVSVDLFDPAQGYEDTLLRYRD 215

Query Match 6.5%; Score 80; DB 1; Length 447;
 Best Local Similarity 23.6%; Pred. No. 24;
 Matches 38; Conservative 20; Mismatches 65; Indels 38; Gaps 8;


```

Db      399 YQLYGFYFAALFTKPPSSNSGEMNLKFTV-----DGSIPVYTV--AKKDYPGSLQFQFN-- 450
QY      216 NKTINSNHLIALYL 230
Db      451 -----DKDELLFTLYV 461

RESULT 48
YB64_PASMU
ID YB64_PASMU STANDARD; PRT; 324 AA.
AC Q9CKIY6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical paba-like protein PM1464.
GN PM1464.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:PM70;
RA MEDLINE=21145866; PubMed=11248100;
RX May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
CC -!- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE
CC COMPONENT 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AE006183; AAK03548.1;
DR InterPro; IPR005801; Anth synth chor.
DR Pfam; PF00425; chorismate_bind; 1.
DR PRINTS; PR00095; ANTSYNTHASE1.
DR ProDom; PD000779; Anth synth chor; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 324 AA; 37309 MW; E9336FF3890A32AE CRC64;

Query Match 6.4%; Score 79.5; DB 1; Length 324;
Best Local Similarity 27.3%; Pred. No. 18;
Matches 24; Conservative 17; Mismatches 34; Indels 13; Gaps 3;

QY 136 TVVPIDKVKTSKKEVTVOEL---DLQARHYLHGKFLYNSDSFGKVGQVGH---V 185
Db      236 TLLPAGSISGAPKKTQVQIIHAAEQRPGRYTGIFGLFDGESLQSAVAIRFIEQVDEKLI 295
QY 186 FHSSSGTSVSDYLFPAQCYQPTLLRIY 213
Db      236 FRSGGGITILSELED---EYEOELQKVY 320

RESULT 49
DP3A_HELPY
ID DP3A_HELPY STANDARD; PRT; 1211 AA.
AC P56157;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAE OR HPI460.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RX Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547 (1997).
CC -!- FUNCTION: DNA polymerase III is a complex, multichain enzyme
CC responsible for most of the replicative synthesis in bacteria.
CC This DNA polymerase also exhibits 3' to 5' exonuclease activity.
CC The alpha chain is the DNA polymerase (By similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N)
CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII' complex. PolIII' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-C family. DnaE
CC subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AE000646; AAD08502.1;
DR PIR; D64702; D64702.
DR TIGR; HPI460;
DR InterPro; IPR004013; PHP_C.
DR InterPro; IPR003141; PHP_N.
DR InterPro; IPR004805; PolC_alpha.
DR Pfam; PF02811; PHP_C; 1.
DR Pfam; PF02231; PHP_N; 1.
DR SMART; SM00481; POLIICAC; 1.
DR TIGRFAWS; TIGR00594; polc; 1.
DR Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
SQ SEQUENCE 1211 AA; 138052 MW; FB248DD47E4CBB0C CRC64;

Query Match 6.4%; Score 79.5; DB 1; Length 1211;
Best Local Similarity 25.7%; Pred. No. 87;
Matches 28; Conservative 19; Mismatches 45; Indels 17; Gaps 4;

QY 66 DLLVDLIG-SKDATNKYKGGKVDLYGAYGYQCAGGTPNTACWYGVTLHDNNRLTEEEK 124
Db      936 DLICDAGRAKDKANEMWQGNLSFGA-----MEGTTKEQVLDLMDLGEHDAKTLLECEY 990
QY 125 VPINLWIDGKQTVPIDKVKTS-----KKEVTVOELDLQARHYLHGK 166
Db      991 ETLGIHVSGN-----PLDFEKEIKGFNLVKSIDIEELSIGSQAYLLGK 1035

RESULT 50
PHYB_SOYBN
ID PHYB_SOYBN STANDARD; PRT; 1156 AA.
AC P42499;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

DB GN PHYTOCHROME B.
 OS PHYB.
 OC Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OC NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Palad; TISSUE=Etioolated leaf;
 RA Hahn T.R., Woo T.W., Seo H.S., Choi Y.D.;
 RL Submitted (XX-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Regulatory photoreceptor which exists in two forms that
 CC are reversibly interconvertible by light: the Pr form that absorbs
 CC maximally in the red region of the spectrum and the Pfr form that
 CC absorbs maximally in the far-red region. Photoconversion of Pr in
 CC Pfr induces an array of morphogenic responses, whereas
 CC reversion of Pfr to Pr cancels the induction of those
 CC responses. Pfr controls the expression of a number of nuclear
 CC genes including those encoding the small subunit of ribulose
 CC biphosphate carboxylase, chlorophyll A/B binding protein,
 CC protochlorophyllide reductase, rRNA, etc. It also controls the
 CC expression of its own gene(s) in a negative feedback fashion.
 CC -!- SUBUNIT: Homodimer.
 CC -!- PFM: Contains one covalently linked tetrapyrrole chromophore.
 CC -!- SIMILARITY: Belongs to the phytochrome family.
 CC -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
 CC -!- SIMILARITY: Contains 1 histidine kinase domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L34843; AAA34000.1; --
 CC PIR; T07756; T07756
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003018; GAF.
 DR InterPro; IPR003661; His_kinA_N.
 DR InterPro; IPR005467; His_kinase.
 DR InterPro; IPR000014; PAS domain.
 DR InterPro; IPR001294; Phytochrome.
 DR Pfam; PF01590; GAF; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR Pfam; PF00512; HisKA; 1.
 DR Pfam; PF00989; PAS; 2.
 DR Pfam; PF00360; phytochrome; 1.
 DR PRINTS; PR01033; PHYTOCHROME.
 DR SMART; SMO0065; GAF; 1.
 DR SMART; SMO0387; HATPase_c; 1.
 DR SMART; SMO0388; HisKA; 1.
 DR SMART; SMO0091; PAS; 1.
 DR TIGRFAMs; TIGR00229; sensory_box; 1.
 DR PROSITE; PS50109; HIS_KIN; 1.
 DR PROSITE; PS50112; PAS; 1.
 DR PROSITE; PS00245; PHYTOCHROME_1; 1.
 DR PROSITE; PS50046; PHYTOCHROME_2; 1.
 KW Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
 KW Multigene family.
 FT DOMAIN 646 717 PAS.
 FT DOMAIN 930 1150 HISTIDINE KINASE.
 FT BINDING 358 358 CHROMOPHORE (BY SIMILARITY).
 SQ SEQUENCE 1156 AA; 129085 MW; 76333AABDC42D297 CRC64;
 Query Match 5.4%; Score 79; DB 1; Length 1156;
 Best Local Similarity 23.0%; Pred. No. 90;
 Matches 58; Conservative 34; Mismatches 98; Indels 62; Gaps 14;
 14 KXSELOG-----TALG-NLKQIYYNKAITENK---ESDDQFLENTLLFKGFTGFHFWYN 65

DB 676 KVSLETGLPVEAMGKSLVHDLVFKSEETVKNLLSREEDKNVETKM--RTFCHEQNK 733
 QY 66 DLLV--DLGSKDATNKYK-----KKVDLYGAYYGQACAGTPTNKTCM 107
 DB 734 AFLVNNACSSKHETNNVGVFCVGVQNTVGOKIVMHKFINIQG--DYKAIIVHSPNP--L 787
 QY 108 YGGVTLHNNRLTEEEKVPIINLWIDGQTTPVIDKVKTSKKEVTQVELDQARHYLHGKF 167
 DB 788 IPIFASDDNTCCLE-----W-----NTAEKLDPSNENVTGGVDVIGKMLVGEVF 834
 QY 168 G-----LYNSDSFGGKVQVORGLIVPHSSEG-----STVSVDLFDAGQYPTDLLRIYRNKTI 219
 DB 835 GSCCOLKGSDS---ITKFMIVLHNLALGGDTDKFPESFLDRHGKYYQVOTELTA---NKR 887
 QY 220 NSENLHIALYLY 231
 DB 888 NMEQGIIGAFCF 899
 RESULT 51
 ID P2P_LACLC STANDARD; PRT; 1902 AA.
 AC P15293;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P11-type proteinase precursor (EC 3.4.21.96) (Lactococpin) (Cell wall-
 DE associated serine proteinase) (LP151).
 DE
 GN PRT.
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Plasmid pLP763.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 ON NCBI_TaxID=1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCDO 763;
 RX MEDLINE=89313288; PubMed=2501630;
 RA Kiwaki M., Ikemura H., Shimizu-Kadota M., Hirashima A.;
 RA "Molecular characterization of a cell wall-associated proteinase gene
 RT from Streptococcus lactis NCDO763.";
 RL Mol. Microbiol. 3:359-369 (1989).
 CC -!- FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE
 CC GROWTH OF THE BACTERIA ON MILK.
 CC -!- CATALYTIC ACTIVITY: Endopeptidase activity with very broad
 CC specificity, although some substrate preference have been noted.
 CC e.g. large hydrophobic residues in the P1 and P4 positions, and
 CC pro in the P2 position. Best known for its action on caseins,
 CC although it has been shown to hydrolyze hemoglobin and oxidized
 CC insulin B-chain.
 CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 CC an amide bond (Potential).
 CC -!- SIMILARITY: Belongs to peptidase family S8.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X14130; CAA32350.1; --
 DR PIR; S06997; S06997.
 DR HSSP; P00782; 2SPT.
 DR MEROPS; S08.019; --
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR003137; PA.
 DR InterPro; IPR000209; Peptidase S8.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF02225; PA; 1.
 DR Pfam; PF00082; Peptidase S8; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.

DR PROSITE; PS00847; GRAM_POS ANCHORING; 1.
 DR PROSITE; PS00136; SUBTILASE ASP; 1.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE SER; 1.
 KW Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchored; Zymogen;
 FT SIGNAL; Plasmid.
 FT SIGNAL 1 33
 FT PROPEP 34 187
 FT CHAIN 188 1870
 FT PROPEP 1871 1902
 FT ACT_SITE 217 217
 FT ACT_SITE 281 281
 FT ACT_SITE 620 620
 FT SITE 1867 1871
 FT MOD_RES 1870 1870
 SEQUENCE 1902 AA; 200139 MW; 4B8D8B84D98CDF7 CRC64;
 Query Match 6.4%; Score 79; DB 1; Length 1902;
 Best Local Similarity 24.8%; Pred. No. 1.6e+02;
 Matches 51; Conservative 9; Mismatches 64; Indels 82; Gaps 9;
 QY 46 OFLENTLLFK-----GFTGHPWYNDLLVDLGSDATNKYKGVLDYGYG 93
 DB 805 QFVEGLNFKSGDGLNLPYMGFGD---WND-----GKIVDSLNG-IT 845
 QY 94 YOCAG-----TPNKTACMYGGVTLHDNRLTEKKVPINLWIDKQTTVIDKVK 145
 DB 846 YSPAGGNFTVPLTNKNTQYGGWTD-----ADGNQ----- 881
 QY 146 SKKEVTVCLELDQARHLYHGKFLNYSDFGKVGQVGLVHVSSEGSFVSYDLFDAQQY 205
 DB 882 -----VDDQAFSSDKNALYNDISMKYLLRNI-----SNVQVILDGQGNK 924
 QY 206 PPTLLRVRDNKNTNSNHLIALYLY 231
 DB 925 VTTLSSTNRKTY--YNAHSQQYTY 948
 RESULT 52
 YJEA_BACSU STANDARD; PRT; 467 AA.
 AC Q34798;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein yJea precursor.
 GN YJEA OR BSU12100.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]_TaxID=1423;
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=982404033; PubMed=9579062;
 RA Rivolta C., Soldo B., Lazarevic V., Joris B., Maue C., Karamata D.;
 RT "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
 containing a putative 12.3 kb operon involved in hexuronate catabolism
 and a perfectly symmetrical hypothetical catabolite-responsive
 element.";
 RL Microbiology 144:877-884 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Betero M.G., Bessieres P., Solotini A., Borchert S.,
 RA Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruchet C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Duxterhof A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Ewington J., Fabret C., Ferari E., Foulger D.,
 RA Fritz C., Fujita N., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scallan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yamane K., Yasumoto K., Yata K.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256 (1997).
 CC -1- SIMILARITY: Belongs to the polysaccharide deacetylase family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF015825; AAC46306.1; --
 DR EMBL; Z99110; CAB13067.1; --
 DR PIR; G69849; G69849.
 DR Subtilist; BG13184; yJea.
 DR InterPro; IPR002509; Polysacc deacet.
 DR Pfam; PF01522; Polysacc deacet; 1.
 DR Hypothetical protein; Hydrolase; Signal; Complete proteome.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 467 HYPOTHETICAL PROTEIN YJEA.
 SQ SEQUENCE 467 AA; 53838 MW; 95D2B1245968F804 CRC64;
 Query Match 6.3%; Score 78.5; DB 1; Length 467;
 Best Local Similarity 25.2%; Pred. No. 33;
 Matches 36; Conservative 20; Mismatches 54; Indels 33; Gaps 8;
 QY 11 DLKKSELOGT--ALGNLKIYYNKAITENKESDDQFLENTLLFKGFTGHPWYNDLL 68
 DB 298 DSLKKYKGHATFFVLGS--RVQYYPETLIRMLKEGNE-----VGNHSWHPLL 343
 QY 69 VDLGSKDATNKYKGVLDYGYGVCAGGTGNTACTACMYGGVTLHDNRLTEKKVPIN 128
 DB 344 TRLSVKEALKQINDTQ-DITEKISGYR-----PTLVPPYGGI-----NDELRQMKMDVA 393
 QY 129 LW-IDGKQTTVPIDKVKTSKEV 150
 DB 394 LWDVD-----PDMKDKRKKTI 410
 RESULT 53
 CLSI_BACAA STANDARD; PRT; 509 AA.
 ID CLSI_BACAA
 AC Q81V75;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cardiolipin synthetase 1 (EC 2.7.8.-) (Cardiolipin synthase 1) (CL
 synthase 1).
 GN CLSI OR CLS-1 OR BAO625.
 OS Bacillus anthracis (strain Ames).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=198094;

```

RN RP SEQUENCE FROM N.A.
EX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oksan O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.B., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
PL Nature 423:81-86(2003).
CC -!- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
CC from one phosphatidylglycerol molecule to another to form
CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
CC diphosphatidylglycerol + glycerol.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -!- SIMILARITY: Belongs to the phospholipase D family. Cardiolipin
CC synthase subfamily.
CC -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB017026; AAP24642.1; -
CC TIGR; BA0625; -
CC DR HAMAP; MF_00190; -; 1.
CC DR InterPro; IPR001736; PLD.
CC DR Pfam; PF00614; PLD; 2.
CC DR SMART; SM00155; PLD; 2.
CC DR PROSITE; PS50035; PLD; 2.
CC KW Transferase; Phospholipid biosynthesis; Transmembrane; Repeat;
CC KW Complete proteome.
CC FT TRANSMEM 5 22 Potential.
CC FT TRANSMEM 27 49 Potential.
CC FT TRANSMEM 58 80 Potential.
CC FT DOMAIN 238 265 PLD phosphodiesterase 1.
CC FT DOMAIN 422 449 PLD phosphodiesterase 2.
CC FT ACT_SITE 243 243 POTENTIAL.
CC FT ACT_SITE 427 427 POTENTIAL.
CC SQ SEQUENCE 509 AA; 58107 MW; 54AFD680C2A095FA CRC64;
Query Match 6.3%; Score 78.5; DB 1; Length 509;
Best Local Similarity 25.6%; Pred. No. 37;
Matches 30; Conservative 26; Mismatches 30; Indels 31; Gaps 7;
QY 115 DNNRLTEKKVPINLWIDGKQTTVPIDKY-----KTSKKEVT-----VQE 154
Db 105 EGRRLSLKVLPS-----ERSVLTVEVQKFGGPAADRTTKLLINGDQTFSEILQA 158
QY 155 LDQARHYLHGKFGLYNSDFGKVGQGLVIFHSSEGSTVSVDLPDAQGYDPTLLR 211
Db 159 IE-QAKHHIHIQYIYKSDIEIGTKV-RDALIKKAKGVIVRF-LYDGLGS--NTLLR 210
RESULT 54
ETFL_YABAM
ID ETFL_YABAM STANDARD; PRT; 635 AA.
AC O90B97;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

```



```
Db 590 -VDSEAGHGGY 600
::||| |::
1590 -VDSEAGHGGY 600

RESULT 57
COBQ_METMA STANDARD; PRT; 485 AA.
ID COBQ_METMA STANDARD; PRT; 485 AA.
AC Q800P3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable cobyrinic acid synthase.
GN COBQ OR MM0093.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobria; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppe-Meyer U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: Catalyzes amidations at positions B, D, E, and G on
adenosylcobyrinic A,C-diamide. NH(2) groups are provided by
glutamine, and one molecule of ATP is hydrolyzed for each
amidation (By similarity).
CC -!- PATHWAY: Cobalamin biosynthesis.
CC -!- SIMILARITY: Belongs to the cobB/cobQ family. CobQ subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; AB013230; AAM29789.1; ALT_INIT.
CC HAMAP; MF_00028; -; 1.
CC InterPro; IPR002586; CblA_P.
CC InterPro; IPR004459; CobQ_synth.
CC Pfam; PF01656; CblA; 1.
CC TIGRFAMs; TIGR00313; cobQ; 1.
CC Cobalamin biosynthesis; Complete proteome.
SQ SEQUENCE 485 AA; 53324 MW; 329A8E85515528D0 CRC64;

Query Match 6.3%; Score 78; DB 1; Length 485;
Best Local Similarity 23.7%; Pred. No. 38;
Matches 62; Conservative 40; Mismatches 102; Indels 58; Gaps 18;

QY 1 SEKSEETNEK-DLRKKSELOGTA-----LGNLKIYYNKAITENKESDD 45
DB 233 SEDSVSLGDEDSKAEKIEVAVIRLPRISNFTDFELEGIVKRVYD---INEELGNDP 289
QY 46 QFL-----ENTILFKGFTGHPWNLDLVGSKDATNK---YRKGVLDLYGAYGQCAG 98
DB 290 AIMPGFKNTV-----NDLL-DLRASGMDKKIQAQXG-KVPFICGGYQMLG 335
QY 99 -----GTPNKTAQNYGGVILHD--NNRLTEKK--VPINLWIDGKQTTV-PIDKVTSKK 148
DB 336 RTIFDPSGVENGVEAEFEGGLGLDITGTFGRYKRTVQVTKKXNGYGPILPIDGEEIKGY 395
QY 149 ETVTQELDLQARHYLHGKFGKLYNSDSFG-GKVQRGLIVFHSSEGSTVSYDLFDAQG-QY- 205
DB 396 EIHGVYD--SNRTVFGDDGAIDEGVIGTYLHGLFDNRNINLAVRY-LYEKKGLYE 452
```

```
QY 206 PDLTLR---IYRNKNTINSNL 224
DB 453 PDEAISENDAYEEELANVVEQNI 474

RESULT 58
CSDI_ECOLI STANDARD; PRT; 819 AA.
ID CSDI_ECOLI STANDARD; PRT; 819 AA.
AC P53512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane usher protein cssd precursor (CS6 fimbria usher
protein).
GN CSSD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=0167:HS / E10703;
RA Wolf M.K., de Haan L., Casseis F.C., Willshaw G.A., van Gestel E.,
RA Gastra W., Warren R., Boedeker E.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF C6 FIMBRIAL
SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
(BY similarity).
CC -!- SIMILARITY: Belongs to the fimbrial export usher family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; U04844; AAC45096.1; -.
CC FIR; I83350; I83350.
CC InterPro; IPR000015; Fimb_usher.
CC Pfam; PF00577; Usher; 1.
CC PROSITE; PS01151; FIMBRIAL USHER; FALSE NEG.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 819 OUTER MEMBRANE USHER PROTEIN CSSD.
SQ SEQUENCE 819 AA; 92378 MW; 6E8718FE28C8AA89 CRC64;

Query Match 6.3%; Score 78; DB 1; Length 819;
Best Local Similarity 20.6%; Pred. No. 72;
Matches 53; Conservative 37; Mismatches 97; Indels 70; Gaps 11;

QY 6 EINEKDLRKKSELOGTALGNLKIYYNKAITENKESDDQFLENTLLEKGFTHGPWYN 65
DB 206 EFNQNDKKTWK-----RNYTLKSFYDKK-----INLVGESYTSNYYNN 248
QY 66 DLLVDLGSKDATNKYKGVLDLYGAYGQCAGGTPNKTAQNYGGVILHDNRNLTTEKKV 125
DB 249 YSFTGISVSTDTDMYTPSEIDYTPTEIHG-----VADSDSQIIVRQNTIINESV 298
QY 126 P-----INLWDGKQTTVPIDKVTSKKEVTV-----QELDLQARHYLHGK--- 166
DB 299 PAGPFPFPTNLMTYGGQINVEITDIYGNKQYIVSNSSLPVWRKAGLMVTFISGKLTK 358
QY 167 -----FGL-YNSDSFGKVGKQVGLIVFHSSEGSTVSYDLFDAQGQYPTLL 210
DB 359 KNSCEDGDFFAQGDINYGTHYNSTLFGG-YQPSKYNFNLSTG--IGTDL----GFGAWLL 411
QY 211 RIYRN-KTINSNLHI 226
DB 412 NVRSRNFKDKNGYNINL 428
```

```

RESULT 59
PIP_LACLC STANDARD; PRT; 1902 AA.
ID PIP_LACLC
AC 16271;
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE PI-TYPE proteinase precursor (EC 3.4.21.-) (Wall-associated serine
DE proteinase).
DE PRTP.
GN Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WG2;
RX MEDLINE=88149035; PubMed=3278687;
RA Kok J., Leenhouts K.J., Haandrikman A.J., Ledebor A.M., Venema G.;
RT "Nucleotide sequence of the cell wall proteinase gene of
RT Streptococcus cremoris Wg2.";
RL Appl. Environ. Microbiol. 54:231-238 (1988).
CC -!- FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE
CC GROWTH OF THE BACTERIA ON MILK.
CC -!- CATALYTIC ACTIVITY: Endopeptidase activity with very broad
CC specificity, although some substrate preference have been noted,
CC e.g. large hydrophobic residues in the P1 and P4 positions, and
CC Pro in the P2 position. Best known for its action on caseins,
CC although it has been shown to hydrolyze hemoglobin and oxidized
CC insulin B-chain.
CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -!- SIMILARITY: Belongs to peptidase family S8.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24767; AAA17677.1; -.
CC HSP; F00782; I501.
CC MEROPS; S08.019; -.
CC InterPro; IPR001899; Gram_pos_anchor.
CC InterPro; IPR003137; PA.
CC InterPro; IPR002029; Peptidase_S8.
CC Pfam; PF00746; Gram_pos_anchor; 1.
CC Pfam; PF02225; PA; 1.
CC Pfam; PF00082; Peptidase_S8; 1.
CC PRINTS; PR00723; SUBTILISIN.
CC TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
CC PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
CC PROSITE; PS00136; SUBTILASE_ASP; 1.
CC PROSITE; PS00137; SUBTILASE_HIS; 1.
CC PROSITE; PS00138; SUBTILASE_SER; 1.
CC Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen;
KW Signal; Plasmid.
FT SIGNAL 1 33
FT PROPEP 34 187
FT CHAIN 188 1870
FT PROPEP 1871 1902
FT ACT_SITE 217 217
FT ACT_SITE 281 281
FT ACT_SITE 620 620
FT SITE 1867 1871
FT MOD_RES 1870 1870
FT SEQUENCE 1902 AA; 199910 MW; 2901C7F19B2E5DOB CRC64;
Query Match 6.3%; Score 78; DB 1; Length 1902;
Best Local Similarity 24.8%; Pred. No. 2e+02;

Matches 51; Conservative 9; Mismatches 64; Indels 82; Gaps 9;
QY 46 QFLENTLLFK-----GFFTHPWYNDLLVLLGSKDATNKYKGGKVDLYGAYYG 93
DB 805 QFVEGLNEFKGSGRLNLPYMGFGD---WND-----GKIVDSLNG-IT 845
QY 94 YQCAGS-----TPNKTACMYGGVTLHDNNRLTEKKVPINLMDGKQTTVPIDKVKY 145
DB 846 YSPAGGNFQVFLTNKNTGTQYGGWTD-----ADGNQT----- 881
QY 146 SKKEVTQELDQARHYLHGKFLYNSDSFGGKVGQRLTVFHSSEGSTVSYSLDFDAQGY 205
DB 882 -----VDDQATAFSDKKNALYNDISKYLLRNI-----SNVQVDILDGQGNK 924
QY 206 PPTLFIYRDNKTIENSENLHIALYLY 231
DB 925 VITLSS--STNLTKIYNAHSQQYIY 948

RESULT 60
Y650_METJA STANDARD; PRT; 692 AA.
ID Y650_METJA
AC Q57852;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0650 precursor.
GN MJ0650.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U67512; AAB98647.1; -.
CC PIR; B64381; B64381.
CC TIGR; MJ0650; -.
CC Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 24
FT CHAIN 25 692
FT SEQUENCE 692 AA; 80607 MW; 25D0A91A08177188 CRC64;
Query Match 6.3%; Score 77.5; DB 1; Length 692;
Best Local Similarity 19.5%; Pred. No. 65;
Matches 52; Conservative 44; Mismatches 95; Indels 75; Gaps 11;
QY 8 NEKDLRKSKLQGTALGNLQKIYYINEKAITENKESDDQFLENTLLFKGFTGHPWY--- 64
DB 404 NITDLTKRANISDDL--ISSIAYGKDCWMLGLDEVLNHLHYPSKSLI---KFDGKKFYDLT 458
QY 65 -----NDLLVDLGSKDATNKYKGGKVDL-----YGAYYGVQCAGGTENK 103

```


Db 459 NISNITICKILSKNEKIVILGTRKVLKNGSFTIINTVYKGLCYFEAMDYNPK 518
 QY 104 TACMYGGVTLHDNNRLTEEEKVPIINLWIDGKQTVPIDKVTSKKEVTQVELDLQARHYL 163
 Db 519 RYMLVGGVCLY--NHPYSSDAILKYVDNGSYESLPIN-----DNLHKEI 560
 QY 164 HGKFG-----LYNSDSFGGKVGORGL-----IVFHSSEGSTV--SYDL 198
 Db 561 YGDFGPAVLSLIKYPKNSFLIKVWGLNDHMLIKNNLTFTFVTKRPGSFIIDNYTL 620
 QY 199 FDAQGQYPTLLRIYRDKNKTINSEN 224
 Db 621 YIF--NYINT-IBIYDNKKLLSTVEL 643

RESULT 61

RNRL_LACLA
 ID RNRL_LACLA STANDARD; PRT; 817 AA.
 AC Q9CH00;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease R 1 (EC 3.1.-.-) (RNase R 1) (VacB protein homolog 1).
 GN RNRL OR VACB1 OR L10942.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallou O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 CC -/- FUNCTION: 3'-5' exoribonuclease that participates in an essential
 CC cell function. Acts nonspecifically on poly(A), poly(U) and
 CC ribosomal RNAs (By similarity).
 CC -/- SIMILARITY: Belongs to the ribonuclease II (RNB) family.
 CC -/- SIMILARITY: Contains 1 S1 motif domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AR006326; AAK05040.1; -
 CC FR: F86742; F86742.
 CC PR: P05055; ISRO.
 CC InterPro: IPR004476; 3_prime_RNase.
 CC InterPro: IPR008994; Nucleic acid OB.
 CC InterPro: IPR001900; Ribonuclease_II.
 CC InterPro: IPR003029; S1.
 CC Pfam: PF00773; RNB; 1.
 CC Pfam: PF00575; S1; 1.
 CC SMART: SM00316; S1; 1.
 CC TIGRFAMs: TIGR00358; 3_prime_RNase; 1.
 CC PROSITE: PS01175; RIBONUCLEASE_II; 1.
 CC PROSITE: PS0126; S1; 1.
 CC Hydrolase; Exonuclease; Nuclease; RNA-binding; Complete proteome.
 FT DOMAIN 633 717
 SQ SEQUENCE 817 AA; 92250 MW; 44079115E6F624D73 CRC64;

Query Match

Best Local Similarity 27.8%; Pred. No. 79;

Matches 27; Conservative 12; Mismatches 37; Indels 21; Gaps 3;

QY 131 IDGKQTVPIDK----VKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVGORGLIVF 186

Db 106 LDGDEVFIEDKNALKGSAGHVVEIRHVDHQVVGTFVALNDDE---KEQTGLIGF 162
 QY 187 HSSGSESTVSYDLFDAQGQYPTLLRIYRDKNKTINSEN 223
 Db 163 VKSRNKKIPY-----RVYLENEGLIPEN 185

RESULT 62

UB32_HUMAN
 ID UB32_HUMAN STANDARD; PRT; 1604 AA.
 AC Q8NFA0; Q9BX85; Q9Y591;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ubiquitin carboxyl-terminal hydrolase 32 (EC 3.1.2.15) (Ubiquitin
 DE thiolesterase 32) (Ubiquitin-specific processing protease 32)
 DE (Deubiquitinating enzyme 32) (NY-REN-60 antigen).
 GN USP32 OR USP10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22506395; PubMed=12604796;
 RA Paulding C.A., Ruvelo M., Haber D.A.;
 RT "The Tre2 (USP6) oncogene is a hominoid-specific gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:2507-2511(2003).
 RN [2]
 RP SEQUENCE OF 331-1604 FROM N.A.
 RC TISSUE=Testis;
 RA Sha J.H.;
 RT "Identification of a novel ubiquitin specific protease gene related to
 RT testes development from human testes cDNA library.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 536-1363 FROM N.A.
 RX MEDLINE=99438124; PubMed=10508479;
 RA Scanlan M.J., Gordan J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jorgeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with renal-
 RT cell carcinoma.";
 RL Int. J. Cancer 83:456-464(1999).
 CC -/- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
 CC ubiquitin + a thiol.
 CC -/- SIMILARITY: Belongs to peptidase family C19.
 CC -/- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF533230; AA097922.1; -
 CC EMBL: AF350251; AA030207.1; -
 CC EMBL: AF155116; AA042882.1; -
 CC MEROPS: C19.044; -
 CC Genew: HGNC:19143; USP32.
 CC InterPro: IPR006615; DUSP.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001394; Peptidase_C19.
 CC InterPro: IPR001125; Recoverin.
 CC Pfam: PF00036; ehand; 2.
 CC Pfam: PF00443; UCH; 1.
 CC PRINTS: PR00450; RECOVERIN.
 CC SMART: SM00695; DUSP; 1.
 CC SMART: SM00054; EPH; 2.

DR PROSITE; PS00018; EF_HAND; 2.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS0235; UCH_2_3; 1.
 KW Ubi conjugation pathway; Hydrolase; Thiol protease; Multigene family;
 KW Calcium-binding; Repeat.
 FT CA_BIND 241 252 EF_HAND 1 (POTENTIAL).
 FT CA_BIND 277 288 EF_HAND 2 (POTENTIAL).
 FT ACT_SITE 743 743 BY SIMILARITY.
 FT ACT_SITE 1518 1518 BY SIMILARITY.
 FT ACT_SITE 1526 1526 BY SIMILARITY.
 FT CONFLICT 884 884 H -> R (IN REF. 2).
 FT CONFLICT 1167 1167 C -> S (IN REF. 2).
 FT CONFLICT 1167 1167 C -> S (IN REF. 2).
 SQ SEQUENCE 1604 AA; 181654 MW; A621F764B7632E3 CRC64;
 Query Match 6.3%; Score 77.5; DB 1; Length 1604;
 Best Local Similarity 24.3%; Pred. No. 1.8e+02;
 Matches 41; Conservative 18; Mismatches 53; Indels 57; Gaps 9;
 QY 74 KDATNKYGGKVDLYGAYGYQC-----AGGTENKTA-----CMYGGVT--LHDNNRLTE 121
 DB |||||
 DB 29 KDAFKRTCG-----LSYYMGQHCFTREVLDGVPKVAEVIYCSFGGTSGKGLHFNLI-- 81
 QY 122 EKKVPIINWIDKQTTVIDIKVTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGKQVQR 181
 DB |||||
 DB 82 ---VGLVLLTRGK-----DEERAKVI---FSLFSSES-GNYVIR 113
 QY 182 GLIVPHSSEGSVSYDLFDAGQCYPTTLRIYVRDNTKINSENLHIALYL 230
 DB |||||
 DB 114 -----HEMERMLHVVDGKVPDTLRKCFSEGEKYNKFRNWLF 152
 RESULT 63
 ID POLG PSBMV STANDARD; PRT; 3206 AA.
 AC P29152;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [Contains: N-terminal protein (P1); Helper
 DE component proteinase (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
 DE protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 DE (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
 DE (NIA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
 DE (EC 2.7.7.48); Coat protein (CP)].
 DE Pea seed-borne mosaic virus (strain DpD1).
 OS Pea seed-borne mosaic virus, no DNA stage; Potyviridae;
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 CC Potyvirus.
 CC NCBI_TaxID=31736;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92044431; PubMed=1940858;
 RA Johansen E., Rasmussen O.F., Heide M., Borkhardt B.;
 RT "The complete nucleotide sequence of pea seed-borne mosaic virus
 RT RNA.";
 RL J. Gen. Virol. 72:2625-2632(1991).
 CC -!- FUNCTION: Helper component-proteinase is required for aphid
 CC transmission and also has proteolytic activity.
 CC -!- FUNCTION: Cytoplasmic inclusion protein has helicase activity. It
 CC may be involved in replication.
 CC -!- FUNCTION: Nuclear inclusion protein A has proteolytic activity,
 CC further restricted by preferences for the amino acids in P6 - P1,
 CC that vary with the species of potyvirus, e.g. Glu-Xaa-Tyr-Xaa-
 CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA] (N).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the

CC processing of the potyviral polypeptide.
 CC -!- PTM: VPG is covalently linked to the genomic RNA.
 CC -!- PTM: The viral RNA of potyviruses is expressed as a single
 CC polypeptide which undergoes posttranslational proteolytic
 CC processing resulting in the production of at least eight
 CC individual proteins.
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -!- SIMILARITY: Belongs to the potyviruses polypeptide family.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D10930; BAA01726.1; --
 DR PIR; J01331; GNVSPV.
 DR MEROPS; C04.010; --
 DR MEROPS; C06.002; --
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR001730; Peptidase_C4.
 DR InterPro; IPR001456; Peptidase_C6.
 DR InterPro; IPR001592; Poty_coat.
 DR InterPro; IPR002540; Poty_P1.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00271; helicase_C_1.
 DR Pfam; PF00863; Peptidase_C4; 1.
 DR Pfam; PF00851; Peptidase_C6; 1.
 DR Pfam; PF00757; Poty_coat; 1.
 DR Pfam; PF01577; Poty_P1; 1.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR PRINTS; PR00966; NIAPOTYPTAGE.
 DR SMART; SMC0487; DEXDC; 1.
 DR SMART; SMC0490; HELIC; 1.
 KW Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 ?
 FT CHAIN 857 ? 856
 FT CHAIN ? 1266
 FT CHAIN 1267 1902 1902
 FT CHAIN 1903 1955 1955
 FT CHAIN 1956 ?
 FT CHAIN ? 2395
 FT CHAIN 2396 2915 2915
 FT CHAIN 2916 3206 3206
 FT CHAIN 1266 1267
 FT SITE 1902 1903
 FT SITE 1955 1956
 FT SITE 2395 2396
 FT SITE 2915 2916
 FT BINDING 2016 2016
 FT NP_BIND 1351 1358
 FT SEQUENCE 3206 AA; 364271 MW; 42A3D921BE9A0CBF CRC64;
 Query Match 6.3%; Score 77.5; DB 1; Length 3206;
 Best Local Similarity 25.4%; Pred. No. 4.1e+02;
 Matches 47; Conservative 22; Mismatches 55; Indels 61; Gaps 9;
 QY 38 TENKESDDDFLE-----NTLLFKGFTGHPWYNDLLVLDGSKDANKYKG 82
 DB |||||
 DB 1489 TEUSLFDQFVQAQSGGANGCDILKKGHNILVYSSVNEVDRLSKULLVDGFX--VTKVDG 1546
 QY 83 KKVLDYGAYGYQCAGGTENKTAACMYGGVTTLHDNNRLTEKK---VPINLWIDGKQTTVP 139
 DB |||||

Db 1547 RTMKL-----GGVEI--NTSGTAEKPHFIVATNIENG--VTLD 1581

Qy 140 IDKVKTSKEVTVQELDLQARHYLHGKFLYNSDGGKQVQ-----GLIVFHS 188

Db 1582 IDVVDFGVKV-VAEILDADARTWYNKQAI-----SYGERIQRLGRVGRKQGHALRIGHT 1636

Qy 189 SEGST 193

Db 1637 EKGIT 1641

RESULT 64

V212_FOWPV STANDARD; PRT; 303 AA.

AC Q9523;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable serine/threonine protein kinase PPV212 (EC 2.7.1.-).

GN PPV212.

OS Fowlpox virus (FPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Avipoxvirus.

OX NCBI_TaxID=10261;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20193820; PubMed=10729156;

RA Afonso C.L., Tulman E.R., Lu Z., Zeak L., Kutish G.F., Rock D.L.;

RT "The genome of fowlpox virus."

RL J. Virol. 74:3815-3831(2000).

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC POXVIRUSES SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL; AF198100; AAF44556.1; -

DR HSP; Q06486; ICK1.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser Thr_pkin_AS.

DR Pfam; PF00069; pkinase; 2.

DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.

DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 25 303 PROTEIN KINASE.

FT NB_BIND 31 39 ATP (BY SIMILARITY).

FT BINDING 54 54 ATP (BY SIMILARITY).

FT ACT_SITE 160 160 BY SIMILARITY.

Qy SEQUENCE 303 AA; 34775 MW; 4818FD17C5220716 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 303;

Best Local Similarity 19.9%; Pred. No. 27;

Matches 51; Conservative 42; Mismatches 69; Indels 94; Gaps 13;

Qy 10 KDRLKSELOQTALGN--LKOIYYNEK-----AITENKESDDOFLNTLLFGFFTG 60

Db 18 EDITKNWILKQLGSGGFLGVQVSCSKSEIDCVAKIELKESG-----GLFCE 66

Qy 61 HPWVNDLLVLDGSKDAIKYKGGKVDLYG--AYGYQCAGGTENKTACMYGGVTLHDN-- 116

Db 67 INFYRWKNTSLDTW--MKQKIDVIGPSFHGF-----GITIYKVE 109

Qy 117 -----NRTEKKVPINLWDGKQTTPVDPIDKVKTSKEVTVQELDLQARHY 162

Db 110 YRFALIQRLGRDLENILSEKEFNI-----TVIKKLAIKILDI--LKF 150

Qy 163 LHOKFLGYNSDSFGKQVQRLIVFHSSEGST--VSYDL---PDAQGYPTLLIRYDNK 217

Db 151 IHSG-----EFSGHDIKAGNILFGKDDKVKYLVLDYGLATKYSSNGKHKE-----Y 195

Qy 218 TINSNLHIALYLYTT 233

Db 196 TINKPHNGTMAFTS 211

RESULT 65

TYPH_MYCPI STANDARD; PRT; 419 AA.

AC P4717;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Thymidine phosphorylase (EC 2.4.2.4) (TdrPase).

GN DEOA.

OS Mycoplasma plium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2122;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=BER;

RX MEDLINE=93352438; PubMed=8349569;

RA Tham T.N., Ferris S., Kovacic R., Montagnier L., Blanchard A.;

RT "Identification of Mycoplasma plium genes involved in the salvage pathways for nucleosides".

RL J. Bacteriol. 175:5281-5285(1993).

CC -!- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES, OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-ribose 1-phosphate.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SIMILARITY: Belongs to the thymidine/pyrimidine-nucleoside phosphorylase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).

CC EMBL; L13289; AAA25432.1; -

DR FIR; C53312; C53312.

DR HSP; P77836; IERW.

DR InterPro; IPR000312; Glyco_trans_3.

DR InterPro; IPR000053; Thymid_phosphils.

DR Pfam; PF02885; Glycos_trans_3N; 1.

DR Pfam; PF00591; Glycos_transf_3; 1.

DR PIRSF; PIRSF00478; Thymid_phosphils; 1.

DR ProDom; PD001864; Glyco_trans_3; 1.

DR ProDom; PD001864; Glyco_trans_3; 1.

DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.

KW Transferase; Glycosyltransferase.

Qy SEQUENCE 419 AA; 47278 MW; C1620F2EF33929E3 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 419;

Best Local Similarity 27.8%; Pred. No. 39;

Matches 44; Conservative 22; Mismatches 58; Indels 34; Gaps 10;

Qy 36 AITENKESDDO--FLENTLLFKG--FTGHPWVNDLLVLDGSKDAIKYKGGKVD----- 86

Db 44 AIFWFLDNDNELYFLTKAMIDSGIKYKFPPEYKILID--KHSTGGI-GDKVSIALLRPI 99

Qy 87 -----LYGAYGYQCAGGTENKTACMYGGVTLHDNRLTEKKV--PINLWDGK 134

Db 100 LVSFGLGVAKLSRGLGF--TGGTIDKLE-----SINVNTDIDLKNSKILNIAMFVQG 153


```

Db 213 KUKGKPKFNTKSKYISFGTCNNNDYYINYEKSKAILFHNKIVDTSNILL-----N 267
QY 60 GHPWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRL 119
Db 268 GHNYENILTSLAISQMFQDKVSINVLLKFL-----GLPHRFQ-----TVHNNNI 315
QY 120 TEKKVPEINLWI-DGKQTTVPIDKVKTSKEVTVQ 153
Db 316 S-----WINDSKSTNV--DSTKAALKNLKIK 339

RESULT 68
Y314_MYCGE
ID Y314_MYCGE STANDARD; PRT; 443 AA.
AC Q49415; Q49279;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG314.
GN MG314.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
ON NCBI_TaxID=2097;
[1]
SEQUENCE FROM N.A. / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Karp P., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.F., Dougherty B.A., Bost K.F., Hu P.C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
[2]
RN SEQUENCE OF 70-171 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.C., Bost K.F., Hutchison C.A. III;
RA "A survey of the Mycoplasma genitalium genome by using random
RT sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; U39712; AAC71536.1; -.
DR EMBL; U02151; AAD12432.1; -.
DR PIR; G64234; G64234.
DR TIGR; MG314; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 443 AA; 51132 MW; 3EPB03F9168015D7 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 443;
Best Local Similarity 21.5%; Pred. No. 42;
Matches 41; Conservative 26; Mismatches 82; Indels 42; Gaps 7;

QY 8 NEXDLRKK-----SELOGTALGNLKQIYYNKAITENKESDDQPLENTLLFKGFFTHGPW 63
Db 19 NNETLTRIKTSDPAKTLAQKLILYFLEEKQKVKTKKPHFLFGS----- 66
QY 64 YNDLLVLDGSKDATNK-YKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNR 118
Db 67 FHDKFIQLGQNLSEKELKAAPFDLTDALNLYNVAVKLNFNK-----ELNSETK 118
QY 119 LTEKKVPEINLWIDGKQTTVPIDKVKTSKEVTVQ-----SKKEVTVQELDLQARHYLHGKFG 168

```

```

Db 119 LAETQVKPSELOENNKTKVDNPSFOTINNQQSLNGLNNILQOTLQVRAR---DRAFG 175
QY 169 LYNDSDFGGKV 179
Db 176 RFTSEKLVGKI 186

RESULT 69
ID BMP_FWVD
ID BMP_FWVD STANDARD; PRT; 512 AA.
AC P09524;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inclusion body matrix protein (Viroplasm).
GN VI.
OS Figwort mosaic virus (strain Dxs) (FMV).
OC Viruses; Retroviruses; Caulimoviridae; Caulimovirus.
ON NCBI_TaxID=10650;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88040466; PubMed=3671088;
RA Richins R.D., Scholthof H.B., Shepherd R.J.;
RA "Sequence of figwort mosaic virus DNA (caulimovirus group).";
RL Nucleic Acids Res. 15:8451-8466(1987).
CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC POLYICISTRONIC MRNA'S DERIVED FROM FIGWORT MOSAIC VIRUS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC -1- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X06166; CAA29528.1; -.
DR PIR; S01284; WMCVFM.
DR InterPro; IPR002609; Caulimo.VI.
DR Pfam; PF01693; Caulimo VI; 1.
KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 512 AA; 58207 MW; AE34455BF2FB0391 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 512;
Best Local Similarity 23.6%; Pred. No. 50;
Matches 56; Conservative 34; Mismatches 91; Indels 56; Gaps 11;

QY 5 BEINEKDLRKKSELOGTALGNLK-QIYYNKAITENKESDDQPLENTLL----FKGF 57
Db 2 EEL--KALRLKEKILELNSVKNQIHAYEESLKATTVNSVQSGEILQTESIECEPAQK 59
QY 58 FTGHPWYND-LLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDN 116
Db 60 ETPNPKADSLKLTILGNERNQNPLEGKSKL-----VNLTPK 96
QY 117 NLTTEKKVPEINLWIDGKQTTVPIDKVKTSKEVTV--OELD-----LQARHYLHG 165
Db 97 SDKDKVSSPVANG-SGKDSINPLNPLFVALGSKSKITLGQKQADEEKKPDLRAANGQS 155
QY 166 KFGLY--NSDSFGG-----KVQRGLIVFHSSEGSTVSYDLFPAQGYPTLLR 211
Db 156 WFAFYKGPNEKFFTEWEIVADICKRQKSRFRSKEQAEVSIISLYNKDIQDPVFLR 212

RESULT 70
YNN6_YEAST
ID YNN6_YEAST STANDARD; PRT; 425 AA.
AC P53911;

```

```

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 49.4 kDa protein in NAM9-FPR1 intergenic region.
GN YNL136W OR N1212 OR NU843.
OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C;
RC MEDLINE=96109932; PubMed=8619318;
RA Wallat L., Bussereau P., Jacquet M.;
RT "A 43.5 kD segment of yeast chromosome XIV, which contains MFA2,
RT MPF2, CAP/SRV2, NAM9, FKBP1/FPR1/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames." ;
RY Yeast 11:1195-1209(1995).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z45843; CAA86889.1; --
DR EMBL; Z71412; CAA96018.1; --
DR PIR; S55147; S55147.
DR GerMOnline; 143142; -.
DR SGD; S0005080; YNL136W.
KW Hypothetical protein.
SQ SEQUENCE 425 AA; 49391 MW; 4C99805F529B4CF1 CRC64;
Query Match 6.2%; Score 76.5; DB 1; Length 425;
Best Local Similarity 22.9%; Pred.No.44;
Matches 43; Conservative 21; Mismatches 49; Indels 75; Gaps 9;

QY 11 DLRKKELOCTALGNLKQIYYNEKATENKES-----DDQPLENTLL-----FKG 56
DB 74 NLBKEDMENT-----YSLEATTESRNGNGNGDAEITHEETLELNRIVRVKQ 123
QY 57 FFTGHFW--YNDDLIV-----DLGSKDATNKYKKVDLYGAYGYOCA 97
DB 124 DFT-LPWEEXGELILENARKSPNSNEEYPVEDMNKDXSTIPKESPSTD----- 172
QY 98 GGTFPNKTACMYGGVTLHDNNLTTEKKVPINL----WIDGKOITVPDKVTSKEVTVQ 153
DB 173 -----KNDNNK--QEKNAIKVKELPEYTEENDSPDIQVEPIKEVQSD 215
QY 154 ELDLQARH 161
DB 216 EKELQREH 223

RESULT 71
YWAD_BACSU
ID YWAD_BACSU STANDARD; PRT; 455 AA.
AC P25152;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical peptidase ywad precursor (EC 3.4.11.-).
GN YWAD OR IPA-8R OR BSU38470.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,

```



```
Db 229 LNIKQDVCLIEBVTGLSEFPVILGKIPQKFLPEEIVSMRTHQKYKFCLEKNGSFA 288
Qy 195 SYDLFDAGQVPTDLRLRYDRNKTNSVHIALYLY 231
Db 289 PYFLFVINGRFVNTL-ITQNEKVLRLADALYFY 324

RESULT 74
SYA_RALSO STANDARD; PRT; 884 AA.
ID TAGA_VIBCH
AC Q8V193;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine-tRNA ligase) (AlaRS).
GN ALAS OR RSC0757 OR RS05040.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Wesselsenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RL Nature 415:497-502 (2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA (Ala) = AMP +
CC di-phosphate + L-alanyl-tRNA (Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AL646061; CAP14499.1; -
CC HAMAP; MF_00036; -; 1.
CC InterPro; IPR003156; DHAL.
CC InterPro; IPR002318; tRNA-synt_2c.
CC InterPro; IPR006193; tRNA_synt_Ala.
CC Pfam; PF02272; DHAL; 1.
CC Pfam; PF01411; tRNA-synt_2c; 1.
CC PRINTS; PR00980; TRNASYNTHALA.
CC TIGRFAMS; TIGR00344; alas; 1.
CC PROSITE; PS08060; AA tRNA LIGASE II Ala; 1.
CC Aminoacyl-tRNA synthetase, Protein Biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SEQUENCE 884 AA; 96738 MW; GDF71962D1305880 CRC64;
Query Match 6.2%; Score 76.5; DB 1; Length 884;
Best Local Similarity 25.4%; Pred. No. 1.1e+02;
Matches 51; Conservative 30; Mismatches 73; Indels 47; Gaps 12;
Qy 16 SELOGTALGNLKQIYYNEKATENKESDDQFLENTLLFKGFT-GHPV-----YND 66
Db 377 SLIDG-ALGSEK-----AAGDKQKRLDGLAFKLDHTYGFPLDLTDQVCREND 425
Qy 67 LLDVLSKDATNKYKGGKVDLYGAYGYQCAGGTNNKTACMGVTLHDNNRUTEKKVP 126
Db 426 VIVDEAAFDAMNRQREARAGK---FKVAAGTLDTY3---DKTFHGVDDQLLSSTSRV 479
Qy 127 INLWIDGKQTVTIDKVKTSKEVTVOELDQARHYLHGKFLGYNLSDSPGKVGQRLIVF 186
```

```
Db 480 TALFVVG--ASVP--EMRPGQTGVV--LD-----HTPF--YAESGQVGDQGL-- 521
Qy 187 HSSEGSTVSVDLFDAGQVDPD 207
Db 522 ---KAATVWFVDVADTKVLPE 539

RESULT 75
TAGA_VIBCH STANDARD; PRT; 1002 AA.
ID TAGA_VIBCH
AC P24019; O68335; Q56595; Q9KTR9;
DT 01-MAR-1992 (Rel. 21, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ToxR-activated gene A lipoprotein precursor.
GN TAGA OR VC0820.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=98169509; PubMed=9501228;
RA Karolis D.K.R., Johnson J.A., Bailey C.C., Boedeker E.C., Kaper J.B.,
RA Reeves P.R.;
RT "A Vibrio cholerae pathogenicity island associated with epidemic and
RT pandemic strains."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3134-3139 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eise J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483 (2000).
RN [3]
RP SEQUENCE OF 1-576 FROM N.A.
RC STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1;
RX MEDLINE=95189108; PubMed=7883190;
RA Harkey C.W., Everiss K.B., Peterson K.M.;
RT "Isolation and characterization of a Vibrio cholerae gene (tagA) that
RT encodes a ToxR-regulated lipoprotein."
RL Gene 153:81-84 (1995).
RN [4]
RP SEQUENCE OF 1-68 FROM N.A.
RC STRAIN=KP8.56;
RX MEDLINE=91210174; PubMed=1902210;
RA Farset C.R., Mekalanos J.J.;
RT "Expression of the Vibrio cholerae gene encoding aldehyde
RT dehydrogenase is under control of ToxR, the cholera toxin
RT transcriptional activator."
RT J. Bacteriol. 173:2842-2851 (1991).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- CAUTION: Ref.3 sequence differs from that shown in the C-terminus
CC due to a frameshift.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC
```

Thu Aug 12 13:48:08 2004

```

or send an email to license@isb-sib.ch).
-----
CC  EMBL; AF034434; AAC12274.1; --
DR  EMBL; AE004167; AAF93983.1; ALT INIT.
DR  EMBL; U12285; AAG6830.1; ALT FRAME.
DR  EMBL; M60658; AAG3050.1; --
DR  PIR; T09438; T09438.
DR  TIGR; VC0820; --
DR  InterPro; IPR008957; FN III-like.
DR  InterPro; IPR003961; FN III.
DR  InterPro; IPR000437; Prot_lipoprot_S.
DR  Pfam; PF00041; fn3; 1.
DR  SMART; SM00060; FN3; 1.
DR  PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW  Lipoprotein; Signal; Complete proteome; Palmitate.
FT  SIGNAL 1 21
FT  CHAIN 22 1002 TOXR-ACTIVATED GENE A LIPOPROTEIN.
FT  DOMAIN 42 135 FIBRONECTIN TYPE-III.
FT  LIPID 22 22 N-palmitoyl cysteine (Potential).
FT  LIPID 22 22 S-diacylglycerol cysteine (Potential).
FT  CONFLICT 67 67 W -> S (IN REF. 4).
FT  CONFLICT 341 341 T -> S (IN REF. 3).
SQ  SEQUENCE 1002 AA; 114629 MW; 5497258E19D552E9 CRC64;

Query Match 6.2%; Score 76.5; DB 1; Length 1002;
Best Local Similarity 28.8%; Pred. No. 1.2e+02;
Matches 23; Conservative 18; Mismatches 20; Indels 19; Gaps 5;

QY 65 NDLLVLDGSKDATNKYKGV---DLYGAYGYQCAGGTPNKTACM-----YGGVTLHD 115
DB 921 NEINIELSKE--NDFEWSLVRDKNLVGSKIEFD-----NNKTLGVLDNRSFYGAGYLDE 973

QY 116 NNRLETEKKVPINLWIDGKQ 135
DB 974 NNRCTQDRQIH---WSNGKQ 990

```

Search completed: August 12, 2004, 13:30:35
Job time : 9.11863 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 20.2698 Seconds
(without alignments)
3626.866 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEENEDLRKSELOG.....RDNKTINSENLHLYVTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037	83.8	260	16 Q931M4	Q931M4 staphylococ
2	992	80.1	260	16 Q99SU3	Q99SU3 staphylococ
3	821	66.3	268	2 Q85217	Q85217 staphylococ
4	481.5	38.9	229	16 Q8NW97	Q8NW97 staphylococ
5	453.5	36.6	258	16 Q9EZM4	Q9EZM4 staphylococ
6	389	31.4	179	2 Q52075	Q52075 staphylococ
7	380.5	30.7	260	16 Q99T46	Q99T46 staphylococ
8	380.5	30.7	261	2 Q9EZM8	Q9EZM8 staphylococ
9	360	29.1	217	2 Q8RR76	Q8RR76 staphylococ
10	360	29.1	241	16 Q53585	Q53585 staphylococ
11	339.5	27.4	242	16 Q8S383	Q8S383 staphylococ
12	333	26.9	240	16 Q9F0L7	Q9F0L7 staphylococ
13	332	26.8	240	16 Q8NXJ5	Q8NXJ5 staphylococ
14	331.5	26.8	218	2 Q8RR75	Q8RR75 staphylococ
15	330.5	26.7	225	2 Q8VWV1	Q8VWV1 staphylococ
16	324.5	26.2	225	2 Q9L921	Q9L921 streptococ

17	323.5	26.1	225	16 Q99Z21	Q99Z21 streptococ
18	310	25.0	239	16 Q99T47	Q99T47 staphylococ
19	309.5	25.0	242	16 Q8NVM3	Q8NVM3 staphylococ
20	308.5	24.9	256	2 Q8VLW7	Q8VLW7 staphylococ
21	306.5	24.8	242	2 Q93CC6	Q93CC6 staphylococ
22	306	24.7	239	2 Q9EZM7	Q9EZM7 staphylococ
23	302.5	24.4	239	2 Q06531	Q06531 staphylococ
24	301.5	24.4	239	2 Q06535	Q06535 staphylococ
25	300.5	24.3	239	2 Q05157	Q05157 staphylococ
26	300.5	24.3	266	16 Q8NXJ6	Q8NXJ6 staphylococ
27	299.5	24.2	239	2 Q06533	Q06533 staphylococ
28	299	24.2	242	16 Q8NVM2	Q8NVM2 staphylococ
29	298.5	24.1	207	2 Q7X0E8	Q7X0E8 staphylococ
30	298	24.1	242	2 Q93CC5	Q93CC5 staphylococ
31	298	24.1	242	2 Q54476	Q54476 staphylococ
32	295.5	23.9	239	2 Q06532	Q06532 staphylococ
33	294.5	23.8	218	2 Q7X0E7	Q7X0E7 staphylococ
34	294.5	23.8	234	2 Q9RSX4	Q9RSX4 staphylococ
35	293.5	23.7	218	2 Q7X0E9	Q7X0E9 staphylococ
36	287.5	23.2	207	2 Q7X0E6	Q7X0E6 staphylococ
37	283.5	22.9	271	2 Q9F0L6	Q9F0L6 staphylococ
38	282.5	22.8	239	2 Q53678	Q53678 staphylococ
39	282.5	22.8	251	16 Q8K6K5	Q8K6K5 streptococ
40	276.5	22.3	239	2 Q06534	Q06534 staphylococ
41	275	22.2	260	2 Q54971	Q54971 streptococ
42	273	22.1	260	2 Q54738	Q54738 streptococ
43	273	22.1	260	16 Q54739	Q54739 streptococ
44	270.5	21.8	236	2 Q54696	Q54696 streptococ
45	269.5	21.8	236	2 P97163	P97163 streptococ
46	268.5	21.7	222	2 Q9S524	Q9S524 streptococ
47	268.5	21.7	222	2 Q938P4	Q938P4 streptococ
48	268.5	21.7	236	2 Q54779	Q54779 streptococ
49	267.5	21.6	222	2 Q9R931	Q9R931 streptococ
50	264	21.3	258	2 Q9ZNF2	Q9ZNF2 streptococ
51	263.5	21.3	236	2 Q57453	Q57453 streptococ
52	256	20.7	233	2 Q8RR77	Q8RR77 staphylococ
53	256	20.7	258	2 Q9EZM3	Q9EZM3 staphylococ
54	244.5	19.7	209	2 Q93Q05	Q93Q05 streptococ
55	241.5	19.5	209	2 Q9LAE0	Q9LAE0 streptococ
56	241.5	19.5	209	2 Q9LAD8	Q9LAD8 streptococ
57	239.5	19.3	209	2 Q9LAC6	Q9LAC6 streptococ
58	239	19.3	209	2 Q9LAD1	Q9LAD1 streptococ
59	237.5	19.2	209	2 Q9LAE1	Q9LAE1 streptococ
60	237.5	19.2	209	2 Q9LAC4	Q9LAC4 streptococ
61	235.5	19.0	209	2 Q9LAC5	Q9LAC5 streptococ
62	232.5	18.8	209	2 Q9LAD6	Q9LAD6 streptococ
63	232	18.7	209	2 Q9LAD2	Q9LAD2 streptococ
64	231.5	18.7	207	2 Q7WY99	Q7WY99 streptococ
65	231.5	18.7	209	2 Q9LAC7	Q9LAC7 streptococ
66	230.5	18.6	209	2 Q9LAD9	Q9LAD9 streptococ
67	230	18.6	233	16 Q8NZ89	Q8NZ89 streptococ
68	229.5	18.5	209	2 Q9LAC9	Q9LAC9 streptococ
69	228.5	18.5	209	2 Q9LAD4	Q9LAD4 streptococ
70	228.5	18.5	259	2 Q936G4	Q936G4 staphylococ
71	227.5	18.4	209	2 Q9LAC8	Q9LAC8 streptococ
72	227.5	18.4	209	2 Q9LAC3	Q9LAC3 streptococ
73	226.5	18.3	256	2 Q9S1H8	Q9S1H8 streptococ
74	225.5	18.2	209	2 Q9LAD5	Q9LAD5 streptococ
75	222.5	18.0	209	2 Q9LAD7	Q9LAD7 streptococ
76	221.5	17.9	209	2 Q9LAD3	Q9LAD3 streptococ
77	220.5	17.8	233	16 Q99XW1	Q99XW1 streptococ
78	216.5	17.5	209	2 Q9LAD0	Q9LAD0 streptococ
79	212	17.1	234	16 Q8K8Q7	Q8K8Q7 streptococ
80	209	16.9	240	16 Q8P2R5	Q8P2R5 streptococ
81	208	16.8	210	2 Q9K2G9	Q9K2G9 streptococ
82	200	16.2	157	16 Q99TP7	Q99TP7 staphylococ
83	194	15.7	136	16 Q99T49	Q99T49 staphylococ
84	193	15.6	236	2 Q9L920	Q9L920 streptococ
85	189	15.3	234	2 Q93RR9	Q93RR9 streptococ
86	189	15.3	234	2 Q8G9K7	Q8G9K7 streptococ
87	179	14.5	232	16 Q99QW1	Q99QW1 streptococ
88	176.5	14.3	235	16 Q8KX2	Q8KX2 streptococ
89	175.5	14.2	256	2 Q9X9R8	Q9X9R8 streptococ

90 175.5 14.2 256 2 Q9S1H9 streptococc
91 163 13.2 206 2 Q54512 streptococc
92 157.5 12.7 108 2 Q9EZM5 streptococc
93 149.5 12.1 167 2 Q7X0E4 streptococc
94 141.5 11.4 167 2 Q7X0E5 streptococc
95 136.5 11.0 167 2 Q7WS59 streptococc
96 136 11.0 62 16 Q99TP8 streptococc
97 125 10.1 132 2 Q9EZM6 streptococc
98 125 10.1 133 16 Q99TP8 streptococc
99 123.5 10.0 227 2 Q849U3 streptococc
100 123.5 10.0 262 16 Q9P0S0 streptococc

ALIGNMENTS

```
RESULT 1
Q931M4 PRELIMINARY; PRT; 260 AA.
AC Q931M4;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SAV1948.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizukani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sakimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58110.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:coxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bactl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00277; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 83.8%; Score 1037; DB 16; Length 260;
Best Local Similarity 83.3%; Pred. No. 4.1e-73;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTD 87

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 147

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 148 EEKVPINLWIDGKQNTVPLGTVKTNKKNVTVQELDQARRYLQEKRYINLYNSDVFQKQV 207

Query Match 80.1%; Score 992; DB 16; Length 260;
Best Local Similarity 78.5%; Pred. No. 1.3e-69;
Matches 183; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 87

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 147

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 148 EEKVPINLWIDGKQNTVPLGTVKTNKKNVTVQELDQARRYLQEKRYINLYNSDVFQKQV 207

RESULT 3
Q85217
```

```
181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
208 RGLIVFHTSTEPSVNYDLFCAQOQYNTLLRIYRDNKTINSENHMDIYLYTS 260

RESULT 2
Q99SU3 PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SA1761.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J., Ito T., Kanamori M.,
Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003335; BAB43036.1; -.
DR PIR; C89984; C89984.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00277; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 80.1%; Score 992; DB 16; Length 260;
Best Local Similarity 78.5%; Pred. No. 1.3e-69;
Matches 183; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLKSKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 87

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 147

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 148 EEKVPINLWIDGKQNTVPLGTVKTNKKNVTVQELDQARRYLQEKRYINLYNSDVFQKQV 207

181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
208 RGLIEFHPSSGDSYGYDLFCAQOQYPTQLRIYRDNKTIIKKNHDIYLYTT 260

RESULT 3
Q85217
```


RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Hosoyama A.,
RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF285760; BAG3856.1; -;
DR EMBL; AF003363; BAB57987.1; -;
DR EMBL; AF003135; BAB42911.1; -;
DR PIR; H89968; H89968.
DR HSSP; P13163; 15XT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin; 1.
DR PRINTS; P00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F31EF82D2 CRC64;

Query Match 36.8%; Score 453.5; DB 16; Length 258;
Best Local Similarity 40.8%; Pred. No. 1.4e-27;
Matches 95; Conservative 45; Mismatches 78; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOQTALGNLKIYYNEKAITENKSDDOFLENTLLFKGFFTG 60
DB 32 EVDKDLKKKSDLSKLFNLTS--YITD--ITWQDSENKISTQLLNNTLLKNIDIS 87

QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGAIVYQYQAGGTPNKTCMYGVTLLHNNRLT 120
DB 88 VLKTSLSKVEFNSSDLANQFKGNIDYGLYFGNCKVGLTEKTSCLYGGVTHDGNQLD 147

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKVTYQELDLQARHVLHGKFGYNSDFGKVQ 180
DB 148 EEKVGIVNFKVGQVQEGFV--IKTKAKVTYQELDTKRVFKLENLYKIYNKDT--GNIQ 203

QY 181 RGLIVFHS--SEGTSVSYDLFDAGQGYPTLLRIYRDNKNTINSENLHIALYLY 231
DB 204 KGCIFTHSHNHQDSFYDLYNKGVSVAEGFFQFYSDNRTVSSNHYIDVFLY 256

RESULT 6
Q52075 PRELIMINARY; PRT; 179 AA.
AC Q52075; (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DE Enterotoxin D.
GN VIRC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D".
RL J. Bacteriol. 171:4799-4806(1989).
DR EMBL; M94872; AAA98133.1; -;
DR HSSP; P13163; 15XT.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20563 MW; 579FEE81BC08747 CRC64;

Query Match 31.4%; Score 389; DB 2; Length 179;
Best Local Similarity 50.0%; Pred. No. 9.8e-23;
Matches 75; Conservative 22; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKSDDOFLENTLLFKGFFTG 60
DB 26 NENIDSVKEKELKSELSSTALNNKHSYADKNPIIGENKSTGDOFLENTLLKFFTD 85

QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGAIVYQYQAGGTPNKTCMYGVTLLHNNRLT 120
DB 86 LINFEDLLINFNSKEMAQHFKNVDVPIRYINCYGGEIDTACTYGGVTPHEGNK 145

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEV 150
DB 146 EEKKIPINLWINGVQEVSLDKVQTDKNL 175

RESULT 7
Q99T46 PRELIMINARY; PRT; 260 AA.
ID Q99T46
AC Q99T46; (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin SeO.
GN SEO OR SAVI830 OR SA1548.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
[1]
SEQUENCE FROM N.A.
RP SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RC MEDLINE=21311952; PubMed=11418146;
RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003363; BAB57992.1; -;
DR EMBL; AP003135; BAB42916.1; -;
DR PIR; E89969; E89969.
DR HSSP; P13163; 15XT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin; 1.
DR PRINTS; P00279; BACTRLTOXIN.

```

Query Match      30.7%; Score 380.5; DB 2; Length 261;
Best Local Similarity 39.5%; Pred. No. 7.2e-27;
Matches 96; Conservative 31; Mismatches 87; Indels 29; Gaps 8;
QY      8 NKD-----LRKSELOQTALGNLQIYYNNE-----KAITENKESDDPLENTILFKGFF 58

```

Db 170 TPRDYSFDYDLKGENDYDEIKYEDNKTLSDDSHIDVNLVT 213

RESULT 10

Q53585 PRELIMINARY; PRT; 241 AA.

AC Q53585; (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Enterotoxin H.

GN SEH OR MW0051.

OS Staphylococcus aureus, and

OS Staphylococcus aureus (strain MW2)

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280, 196620;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=D4508;

RC MEDLINE=95053699; PubMed=7964453;

RX Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,

RA Fischetti V.A., Zabriskie J.B.;

RT "Characterization and biological properties of a new staphylococcal

RT exotoxin.";

RL J. Exp. Med. 180:1675-1683(1994).

[2]

RN SEQUENCE FROM N.A.

RP STRAIN=MW2;

RC MEDLINE=22040717; PubMed=12044378;

RX Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,

RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,

RA Yamamoto K., Hiramatsu K.;

RT "Genome and virulence determinants of high virulence community-

RT acquired MRSA.";

RL Lancet 359:1819-1827(2002).

DR EMBL; U11702; AAA19777.1; -.

DR EMBL; AF004822; BAB93916.1; -.

DR PDB; 1ENF; 10-JAN-01.

DR PDB; 1EWC; 10-JAN-01.

DR PDB; 1F47; 10-JAN-01.

DR PDB; 1HXY; 27-JUN-01.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0015070; P:toxin activity; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bctrl_tox.

DR InterPro; IPR006123; Staph/Strep toxin.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

DR SIGNAL; Complete proteome.

FT SIGNAL 1 24

FT CHAIN 25 241

FT ENTEROTOXIN H.

FT SEQUENCE 241 AA; 27858 MW; 70F7798587616CE CRC64;

Query Match 29.1%; Score 360; DB 16; Length 241;

Best Local Similarity 37.5%; Pred. No. 2.6e-20;

Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;

QY 10 KDLRKSSEGTALGNLKOIYYNEKAITENKESDDQFLENTLLKGFTHPTWYNDLLV 69

Db 25 EDLHDKSELTDLALAN--AVQYNHPFIFENIKSDEISEKDLIFRN--QGSUG-NDLRV 79

QY 70 DLGSKATNKYKGVKVDLYGAYGYOCAGTGNPKTACMTGGVTLHDNNRLTBEKKVPINL 129

Db 80 KEATADLAQKFNKNVDIYGASFYKCEKISENSEISCLYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIGKQQTVPIDKVKTSKEVTVQELDLOARHYLHGKFLGYNLSDSGGKQVQGLIVFHSS 189

Db 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSDKYIYKDS---BISKGLIEFDWK 193

QY 190 EGSTVSVDLFDAGQYPTLLRIYRDNKTINSENL-HIALYLYT 232

Db 194 TPRDYSFDYDLKGENDYDEIKYEDNKTLSDDSHIDVNLVT 237

RESULT 11

O85383 PRELIMINARY; PRT; 242 AA.

ID O85383

AC O85383; (TREMELrel. 08, Created)

DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Extracellular enterotoxin type I precursor (SEI).

GN SEI OR SAV1828 OR SA1646.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N315), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158878, 158879, 1280;

[1]

RN SEQUENCE FROM N.A.

RP SPECIES=S.aureus; STRAIN=FR1445;

RC MEDLINE=98298056; PubMed=9632603;

RX Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;

RA "Identification and characterization of staphylococcal enterotoxin

RT types G and I from Staphylococcus aureus.";

RL Infect. Immun. 66:3337-3348(1998).

[2]

RN SEQUENCE FROM N.A.

RP SPECIES=S.aureus; STRAIN=A900322;

RC MEDLINE=20571956; PubMed=11123352;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani U.Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Shiba T.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hiramatsu K.;

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus.";

RL Lancet 357:1225-1240(2001).

DR EMBL; AF064774; AAC26661.1; -.

DR EMBL; AF285760; AAC36953.1; -.

DR EMBL; AP003363; BAB57990.1; -.

DR EMBL; AP003135; BAB42914.1; -.

DR PIR; C89969; C89969.

DR HSSP; P13163; ISXT.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0015070; P:toxin activity; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bctrl_tox.

DR InterPro; IPR006123; Staph/Strep toxin.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF01123; Staph_Strep_toxin; 1.

DR Pfam; PF02876; Staph_Strep_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

DR SIGNAL; Complete proteome.

FT SIGNAL 1 24

FT CHAIN 25 242

FT ENTEROTOXIN TYPE I.

FT SEQUENCE 242 AA; 27863 MW; C5C8B4ACEE5414A8 CRC64;

Query Match 27.4%; Score 339.5; DB 16; Length 242; -

```

Best Local Similarity 35.6%; Pred. No. 1e-18;
Matches 84; Conservative 37; Mismatches 78; Indels 37; Gaps 9;

QY 8 NEXDLRKKSELQG-TALGNLKQIV-----YNEKAITENKESDDOFLNTLLFKGFFTHGP 62
Db 17 NIKDL---TAAQDIGNLNRNFTKDYIDLKGVTDNPIANQLB-----FSTG-- 64
QY 63 WYNLLVLDGSKDATNKKYKKVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122
Db 65 -TNDLISENNWDEISKFKGKKLDFIGIDYNGPC-----KSKMYGGATL-SQYLNSA 116
QY 123 KKVFINLWDGKQTVTIDKVKTSKVTVOELDLQARHYLHGKFGYNSDSG-GK-- 178
Db 117 RKIPINLWVGKHTISTDKTIATNKLVTAGEIDVKLRRLVQEEYNIYGHNTTKGKEYG 176
QY 179 -----VQRGGLIVFHSSEGTSVSYDLFDAQGGYPTDLLRIYRDNKTIINSENLI 226
Db 177 YKSFYSGFNGKVLFLHNLNKSYSYDLFTYGDGLVPSFLKIYEDNKIESEKPHL 232

RESULT 12
ID Q9FOL7 PRELIMINARY; PRT; 240 AA.
AC Q9FOL7;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Sel (Extracellular enterotoxin L).
GN SEL OR SAV2008 OR SA1816.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158679, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus;
RX MEDLINE=20566668; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens.";
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF217235; BAG29598.1; -
DR EMBL; AF003364; BAB58170.1; -
DR EMBL; AF003135; BAB43096.1; -
DR PIR; G89991; G89991.
DR HSSP; P13163; 1ESP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.

```

```

DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27496 MW; 85CD62DA73197881 CRC64;

Query Match 26.9%; Score 333; DB 16; Length 240;
Best Local Similarity 35.0%; Pred. No. 3.3e-18;
Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 24 GNLKQIV-----YNEKAITENKESDDOFLNTLLFKGFFTHGPWYND-LLVLDGSKDATN 78
Db 31 GNLRNFTKYEVVNLKNVKNKNSPESHRL-----YSYKNDTLVAEFDNEYITS 79
QY 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWDGKQTV 138
Db 80 DLKGNVDVFGISYKY-----GNSRT--IYGGVTAKENKLDSPRIIPINLWNGKHQTV 133
QY 139 PIDKVKTSKKEVTVOELDLQARHYLHGKFGY-----NSDSFGGKVGQGLIYF 186
Db 134 TTKSVSTDKKMTAQEIDVKLRKYLODEENIYGHNDTGKKEYGTSKSFYSGFDKGSVVF 193
QY 187 HSSEGTSVSYDLFDAQGGYPTDLLRIYRDNKTIINSENLI 226
Db 194 HMNDGSNFSYDLFTYGTGYGLPESFLKIYKDNKTVDSTQFHL 233

RESULT 13
Q8NKJ5
ID Q8NKJ5 PRELIMINARY; PRT; 240 AA.
AC Q8NKJ5;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Extracellular enterotoxin L.
GN SEL2 OR MW0760.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AF004824; BAE94625.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.
DR KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 26.8%; Score 332; DB 16; Length 240;
Best Local Similarity 35.0%; Pred. No. 4e-18;
Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 24 GNLKQIV-----YNEKAITENKESDDOFLNTLLFKGFFTHGPWYND-LLVLDGSKDATN 78
Db 31 GNLRNFTKYEVVNLKNVKNKNSPESHRL-----YSYKNDTLVAEFDNEYITS 79
QY 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWDGKQTV 138

```

Db 80 DLKGNVDFGYSYK---GNSRT--YGVTVKAENKLDSPRIIPINLIINGKHQTV 133
 QY 139 PIDKVTSKKEVTVOELDLQARHVLHGKFGLY-----NDSFGGKVQVGLIVF 186
 Db 134 TTKSVSTDKKMTVAQEIADVLRKYLQDEFNIYGHNDTGKGYCTSKFYSGFDKGSVVF 193
 QY 187 HSEGSVSYDLFDAQQYPTDLRIYRDNKTINSENLIH 226
 Db 194 HINDGSNFSYDLFTVGYGLPESFLKIYKDKNTVDSQFHL 233

RESULT 14

Q8RR75 ID Q8RR75 PRELIMINARY; PRT; 218 AA.
 AC Q8RR75;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Enterotoxin I (Fragment).
 GN SEI.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21871379; PubMed=11880405;
 RA Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
 RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
 RT Isolates and Determination of the Enterotoxin Productivities of S.
 RT aureus Isolates Harboring seg, seh or sei Genes.";
 RL J. Clin. Microbiol. 40:857-862(2002).
 DR EMBL; AB060537; BAB5991.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_toxin; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 SQ SEQUENCE 218 AA; 24909 MW; 1017728F71BF662 CRC64;

Query Match 26.8%; Score 331.5; DB 2; Length 218;
 Best Local Similarity 35.0%; Pred. No. 3.9e-18;
 Matches 77; Conservative 37; Mismatches 73; Indels 33; Gaps 7;

QY 23 LGNLKQIY----YNEKATENKESDDQFLENTLLFKGFTGHPWYNDLLVLGSKDATN 78
 Db 6 VGNLRFNYKHGVIDLKGVTDKNLPANQLE-----PSTG---TNDLISESNWDBIS 55
 QY 79 KYGKKVLYGAYYQVQAGGTPNKTACMYGVTLHNNRLTEKKVPINLWIDGKQTV 138
 Db 56 KFKGKKLIDFGIDYNGPC-----KSKYMGFGATL--SGQYLSARKIPINLWNGKHXTI 108
 QY 139 PIDKVTSKKEVTVOELDLQARHVLHGKFGLYNSDFG-GK-----VQVGLIVF 186
 Db 109 STDXTAINKLVTQAIDVLRKYLQDEFNIYGHNTGKGYCTSKFYSGFDKGSVVF 168
 QY 187 HSEGSVSYDLFDAQQYPTDLRIYRDNKTINSENLIH 226
 Db 169 HLNNEKFSYDLFTVGYGLPESFLKIYEDNKKIIESEKPHL 208

RESULT 15

Q8VWV1 ID Q8VWV1 PRELIMINARY; PRT; 225 AA.
 AC Q8VWV1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Exotoxin I.
 GN SPEI.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M1;
 RX MEDLINE=21259899; PubMed=11359827;
 RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
 RT "Immunological and biochemical characterization of Streptococcal
 RT pyrogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus
 RT pyogenes.";
 RL J. Immunol. 166:6711-6719(2001).
 DR EMBL; AF438524; AAL31571.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; BctxI_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 225 AA; 25654 MW; DB193667890ACDAF CRC64;

Query Match 26.7%; Score 330.5; DB 2; Length 225;
 Best Local Similarity 33.9%; Pred. No. 4.8e-18;
 Matches 75; Conservative 43; Mismatches 80; Indels 23; Gaps 6;

QY 25 NLKQIYYNEKATENKESDDQFLENTLLFKGFTGHPWYNDLLVLGSKDATNKYK 81
 Db 8 NLRNLVSTYDPTFVTKINEGPPFSGSLFYKNI----PYGNSIELKVELNSVEKANFFS 63
 QY 82 GKVDLYGAYYQVQAGGTPNKTACMYGVTLHNNRLTEKKVPINLWIDG---KQTV 138
 Db 64 GKRVDFTELYSPPCSNIKNS---YGGITLSDGNRI-DKNIPVNFIDGVQVQXSYT 119
 QY 139 PIDKVTSKKEVTVOELDLQARHVLHGKFGLY-----NDSFGGKVQVGLIVFHS 189
 Db 120 DISTVSTDKKEVTIQEELDVSRKRYLQKHFNIYGVGVDFGRSFRSQSGFEENIIFHLN 179
 QY 190 EGSTVSYDLFDAQQYPTDLRIYRDNKTINSENLIHLYL 230
 Db 180 SGERISYNLDTGHDRESMLKKYSNDKTAYSQQLHIDIYL 220

RESULT 16

Q9L921 ID Q9L921 PRELIMINARY; PRT; 225 AA.
 AC Q9L921;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 25.7 kDa protein.
 OS Streptococcus equi.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CF32;
 RA Artushin S.C., Timoney J.F., Sheoran A.S.;
 RT "Identification and molecular characterization of mitogens from
 RT Streptococcus equi.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF186180; AAF72808.1; -
 DR HSP; P13163; 1SXT.

DR GO:GO:0005576; C:extracellular; IEA.
DR GO:GO:0015070; F:toxin activity; IEA.
DR GO:GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25684 MW; EB43D47B26FB9F89 CRC64;

Query Match 26.2%; Score 324.5; DB 2; Length 225;
Best Local Similarity 33.5%; Pred. No. 1.4e-17;
Matches 74; Conservative 43; Mismatches 81; Indels 23; Gaps 6;

QY 25 NLKQIYYNEKAITENKESDDQLENTLLFGFTGHFWYN---DLLVDLGSKDATNKYK 81
DB 8 NLRNLYSYDPTVEVKGKINEGPPFSGSLFYKNI---PYGNSSIELKVELNSVEKAKFFS 63
QY 82 GKVDLYGAYGYQACAGTGNKTACMYGGVTLHNNRLTEKKVPINLWIDG---KQTTV 138
DB 64 GKRVDFITLSEYPPCNSNIKKNS---YGGITLSDGNRI-DKXNIPVNIFFIDGVQQKYSY 119
QY 139 PIDKVKTSKKEVTQVQLDQARHYLHGKFLY-----NSDSFGGKVGQGLIVPHSS 189
DB 120 DISTVSTDKKEVTIQELDVKSRVYLQKHFNIGYGVKDFGRSSRFQSGFEENIIIFHLN 179
QY 190 EGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYL 230
DB 180 SGERISYNLFDTHGDRSMLKKYSNDKNTAYSDQLHIDIYL 220

RESULT 17
Q99Z21 ID Q99Z21 PRELIMINARY; PRT; 225 AA.
AC Q99Z21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Streptococcus exotoxin 1.
GN SPEI OR SPI007.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., Xuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006546; AAK33906.1; -.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CC11CC04 CRC64;

Query Match 26.1%; Score 323.5; DB 16; Length 225;
Best Local Similarity 33.5%; Pred. No. 1.7e-17;
Matches 74; Conservative 43; Mismatches 81; Indels 23; Gaps 6;

QY 25 NLKQIYYNEKAITENKESDDQLENTLLFGFTGHFWYN---DLLVDLGSKDATNKYK 81
DB 8 NLRNLYSYDPTVEVKGKINEGPPFSGSLFYKNI---PYGNSSIELKVELNSVEKAKFFS 63
QY 82 GKVDLYGAYGYQACAGTGNKTACMYGGVTLHNNRLTEKKVPINLWIDG---KQTTV 138
DB 64 GKRVDFITLSEYPPCNSNIKKNS---YGGITLSDGNRI-DKXNIPVNIFFIDGVQQKYSY 119
QY 139 PIDKVKTSKKEVTQVQLDQARHYLHGKFLY-----NSDSFGGKVGQGLIVPHSS 189
DB 120 DISTVSTDKKEVTIQELDVKSRVYLQKHFNIGYGVKDFGRSSRFQSGFEENIIIFHLN 179
QY 190 EGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYL 230
DB 180 SGERISYNLFDTHGDRSMLKKYSNDKNTAYSDQLHIDIYL 220

RESULT 18
Q99T47 ID Q99T47 PRELIMINARY; PRT; 239 AA.
AC Q99T47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin SEM.
GN SEM OR SAVI1829 OR SA1647.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OC NCBI_TaxID=158878; 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Murayama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003363; BAB57991.1; -.
DR EMBL; AF003135; BAB42915.1; -.
DR PIR; D89969; D89969.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match 25.0%; Score 310; DB 16; Length 239;
Best Local Similarity 32.1%; Pred. No. 2.1e-16;
Matches 70; Conservative 40; Mismatches 82; Indels 26; Gaps 5;


```

RESULT 21
Q93CC6 PRELIMINARY; PRT; 242 AA.
AC Q93CC6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Seq.
GN SEQ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RC STRAIN=COL;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RT Schlievert P.M.;
RL "Staphylococcus aureus pathogenicity island 3 (SapI3).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410775; AAL04146.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR008375; Staph exotoxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PRINTS; PR01800; STAPHSTREPTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH STREP_TOXIN 2; 1.
DR PROSITE; PS00278; STAPH STREP_TOXIN 2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F5EEFD4AF8C30D85 CRC64;

Query Match 24.8%; Score 306.5; DB 2; Length 242;
Best Local Similarity 32.4%; Pred. No. 3.9e-16;
Matches 73; Conservative 32; Mismatches 69; Indels 51; Gaps 7;

QY 17 ELQGTALGNLK--QIYYNEKATENKESDDQLENTLLPKGFTGHPWYNDLLVDLGS 73
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
44 KLGVSNGNSTSQLEVIDGK-----YTLYSQF---HNEYE----- 77

QY 74 KDATNKYKKVDLYGAYGYQCAGTGNKTAACMYGVTLDHNNRLTEKKVPINLWIDG 133
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 ---AKRLKHKVDIFGISYSLC-----NFKYWGGITLANQN-LDKPNIPINLWVG 127

QY 134 KQTVIPDKYKTSKEVTVOELDLOARHYLHGKGLYN-----SDSFGKGKQVR 181
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
128 KQNTISTDKYSTQKEVTAQIDIKRLKYLQNEYNIYGFNKKTKGQBYGYCQKFN 187

QY 182 GLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKNTINSENLHI 226
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 GKITFHLNNEPSFYDLYFYGTGQAESFLKIYDNDKNTIDTENFHL 232

RESULT 22
Q9EZM7 PRELIMINARY; PRT; 239 AA.
AC Q9EZM7;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SEM.
GN SEM.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=A900322;
RC MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lira G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RT J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAG36952.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match 24.7%; Score 306; DB 2; Length 239;
Best Local Similarity 31.7%; Pred. No. 4.2e-16;
Matches 69; Conservative 41; Mismatches 82; Indels 26; Gaps 5;

QY 23 LGLNKGIIYYNEKATENK--ESDDQLENTLLKGFTHGHPWYNDLLVDLGSKDATNKY 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 VGVNLNRYNGSYPIEDHOSINPENNLHSHQVFS-----MDNSTVTAETKXNDVDF 77

QY 81 KKKVDLYGAYGYQCAGTGNKTAACMYGVTLDHNNRLTEKKVPINLWIDGKQTVPI 140
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 KXHAVDVYGLSYSGYCL-----KNKYIYGGVTL-AGDYLEKRRRIPINLWVNGEHT 131

QY 141 DKVKTSSKEVTVOELDLOARHYLHGKGLY-----NSDSFGKGKQVGLIVFHS 188
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 DKVSTNKKLVTAQIDIKRLKYLQNEYNIYGFNNDNKNKNGYGNKSKFSSGFNAGKILFHL 191

QY 189 SEGSTVSYDLFDAQGOVPTLLRIYRDNKNTINSENLHI 226
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:
192 NDSGSSFYDLFGTGTGQAESFLKIYDNDKNTVETKFEHL 229

RESULT 23
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OC Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_TaxID=1280;
RC STRAIN=4446;
RC MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins;
RT biological and evolutionary implications.";
RL Infect Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26618.1; -.
DR HSSP; P34071; LSE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
```



```

[1]
RN      SEQUENCE FROM N.A.
RC      STRAIN=MNCopeland;
RX      MEDLINE=94011313; PubMed=8406814;
RA      Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT      "Characterization of novel type C staphylococcal enterotoxins:
RT      biological and evolutionary implications.";
RL      Infect Immun. 61:4254-4262 (1993).
DR      EMBL; L13378; AAA26622.1; -.
DR      HSP; P34071; ISTE.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0015070; F:toxin activity; IEA.
DR      GO; GO:0009405; P:pathogenesis; IEA.
DR      InterPro; IPR008992; Bact_endotox.
DR      InterPro; IPR006177; Bct_X_tox.
DR      InterPro; IPR006123; Staph/Strep_toxin.
DR      InterPro; IPR006173; Staph_tox_OB.
DR      Pfam; PF01123; Staph_strip_toxin; 1.
DR      Pfam; PF02876; Staph_strip_tox_C; 1.
DR      PRINTS; PR00279; BACTELTOXIN.
DR      PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR      PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT      NON_TER
FT      FT
SQ      SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 24.2%; Score 299.5; DB 2; Length 239;
Best Local Similarity 32.9%; Pred. No. 1.4e-15;
Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEENEKDLRKKSBLQGTALGNLKHQIYYNEKAITENK-ESDQDFLENTLLFKGFFTG 60
DB 1 ESQDPDTPDELHKSSEFTGT-MGNMK--LYLDHYVSATKVKSVDFLAHDLIYNISDKK 57
QY 61 HPWYNDLLVDSKDATNKYKGVLDYGAHYGYQC-----AGTFPNKTACWYGVTLL 113
DB 58 LKNYDKVKVELLNEDLAKYKDEVDVGYSGNYVNCYFSSKDNVKGVTGKTCWYGITK 117
QY 114 HDNNRLTEE--KKVPINLWIDGQTTPVDIKVTSKEVTVQVELDQARHYLHGKFGLYN 171
DB 118 HEGNHFDNGNLQNLVLRVY-ENKNTISPE-VQTDKKSVTQAELDIKARNFLINKXGLYE 175
QY 172 SDSFGKQVQGLIVFHSSSGSTVSYDLFPAQGYPD--TLIRYRDNKTIINSENHLIAY 229
DB 176 FNS--SPYETGYIKFIENNNGNTFWYDMPAPGPKFDQSKYLMYNDNKTVDSKVKLEIVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 28
Q8NVW2 ID Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC Q8NVW2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin sek.
GN SEK2 OR MW1938.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
SQ      SEQUENCE FROM N.A.
RX      MEDLINE=22040717; PubMed=12044378;
RA      Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA      Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA      Yamanoto K., Hiramatsu K.;
RT      "genome and virulence determinants of high virulence community-
RT      acquired MRSA.";
RL      Lancet 359:1819-1827 (2002).
DR      EMBL; AP004828; BAB95803.1; -.

```

```

179 -----VQRGLIVFHSSEGSTVSVDLF 199
      : : : : :
      : : : : :
Db    177 YKSRFYSGFNKGKVLFLHNDKSFSDLF 205

RESULT 30
Q93CC5
ID Q93CC5 PRELIMINARY; PRT; 242 AA.
AC Q93CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

```

GN SEK. OS Staphylococcus aureus. QC Bacteria; Firmicutes; Bacillales; Staphylococcus.

[1]_	
SEQUENCE FROM N.A.	
RC STRAIN=COI;	
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,	
RA Schlievert P.M.;	
RT "Staphylococcus aureus pathogenicity island 3 (sapI3).";	
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF410775; AAL04147.1; .	
DR GC; GO:0005576; C:extracellular; IEA.	
DR GC; GO:0015070; F:toxin activity; IEA.	
DR GC; GO:0009405; P:pathogenesis; IEA.	
DR InterPro; IPRO0892; Bact_endotox.	
DR InterPro; IPRO06177; Bctrl_tox.	
DR InterPro; IPRO06123; Staph/Strep_toxin.	
DR InterPro; IPRO06173; Staph_tox_OB.	
DR Pfam; PF01123; Stap_strep_toxin; I.	
DR Pfam; PF02876; Stap_strp_tox_C; I.	
DR PRINTS; PR00279; BACTRLTOXIN.	
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
DR SEQUENCE 242 AA: 27727 MW: 207938B999DC9A9A CRC64;	

Query Match	24.1%	Score 298	DB 2	Length 242
Best Local Similarity	32.3%	Pred. No. 1.8e-15		
Matches	70	Conservative 40	Mismatches 81	Indels 26
Gaps	7			
QY	23	LGNLKQIYYNEKAITENKSSDQFLENTLFXGFTTGHWPYNDLLVLDLGSKDATNKYKG	82	
DB	29	IDNLNFYTKDQVLDLKDVKDNTPIANQLQF-----SNESY-DLISESKDFNKSNFKG	82	
QY	83	KKVLDLYGAYGYQCAGGTGPKNTACMGVTLHDNNRLTEBKVPINLWIDGKQTTVPIDK	142	
DB	83	KKLDVFGISYNGQC-----NTRYIYGVTATN-EYLDKSRNIPINIMINGNHKTIKTNK	135	
QY	143	VKTSKKEVTVQELDQARHVLHGKFGIY-----NSDSFGK-----VQRGILIVFHSSE	190	
DB	136	VSTNKKFVTAQEDIDVKURKLOEYNIYGHNGTKGEEYGHKSKFYSGNGIKVTFHLNN	195	
QY	191	GSTVSYDLF-DAQQYPTDLLRIYRDNKTIENSENLHI	226	
DB	196	NDTFSYDLFTVGGDGLPKSLKYVEDNKTVESKPHL	232	

	RESULT	31	
	O54476		
ID	O54476	PRELIMINARY;	PRT; 242 AA.
AC	O54476;		
DT	01-JUN-1998	(TrEMBLrel. 06, Created)	
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Enterotoxin.		
GN	ENT.		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcuss.		
OX	NCBI_taxid=1280;		
RN	[1]		

DR	Pfam: PF02876; Staph_strep_tox_C; 1.
DR	PRINTS; P00279; BACTRLTOXIN.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER 1
SQ	SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;
Query Match	
Best Local Similarity 23.3%; Score 295.5; DB 2; Length 239;	
Matches 78; Conservative 47; Mismatches 90; Indels 19; Gaps 9;	
QY	11 DLRKSELOQTALGNLKLQYYNYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDDLIV 69
Dd	10 DLHKSSEFTGT-MDNWK--YLVDHDVVSATKYSDVKFLAHLDIYNISDKLKKNYDKVKT 66
QY	70 DLGSKDATNKYGKKGVLDLYGAYGYQC-----AGTPTNKTACMYGGVTLLHNNELTEE 122
Dd	67 ELLNEDLAKKYDEVVDVVGYSYNYNCYESSKDNVKGVTGGTKMCGGTTKEGHNFNG 126
QY	123 --KKVPINLWIDGKOTTIPIDIKVTSKKEVTVOELDQARHYLHGFGLYNSDSFGKVQ 180
Dd	127 NLQNVLVRVY-EKRNKITSFE-VQTDKKSVTQAQLDKARNFLINKNIYEFNSS--SPYE 182
QY	181 RGLIVFHSSEGSTVSYDLFDAAQQYPD--TLRIYRDNKNTINSNLIAILYLT 232
Dd	183 TGYIKFIENGNTFWYDMMPAFGDKRFDQSXYLMYNDNKTVDKSKVIEHLJT 236
RESULT 33	
Q7XOE7	PRELIMINARY; PRT; 218 AA.
ID	Q7XOE7
AC	Q7XOE7;
DT	01-OCT-2003 (TrEMBLrel. 25, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Enterotoxin type I (fragment).
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX	NCBI TaxID=1280;
RN	[1]
RP	SEQUENCE FROM N.A..
RC	STRAIN=AS14;
RA	Blaiotta G., Pennacchia C., Casaburi A., Ercoleini D., Fusco V., Villani F.;
RT	"Detection of staphylococcal enterotoxin type G precursors on Staphylococcus spp. strains isolated from meat and dairy products."; Submitted (MAY-2003) to the ENMBL/GenBank/DBJ databases.
RRL	EMBL; AY291445; AAP78526.1; --
DR	NON_TER 218
SQ	SEQUENCE 218 AA; 24993 MW; 698B8BCE49754350 CRC64;
Query Match	
Best Local Similarity 23.8%; Score 294.5; DB 2; Length 218;	
Matches 76; Conservative 36; Mismatches 73; Indels 37; Gaps 9;	
QY	8 NEKDRLKSELQG-TALGNLKOIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHP 62
Dd	17 NIKDL---TYAQGDIGVGNLNRFNFKTHDYIDLKGVTDKNLPANQLE-----FSTG-- 64
QY	63 WYNDLLVDLGSKDATNKKYGGKVDPLYGAYGYCQAGGTPTNKTACMYGGVTLLHNNELTEE 122
Dd	65 -TNDLISESNWDIEISKFPGKKLDIFGIDYNGPC-----KSKYMYGGATL-SGOYLNSA 116
QY	123 KKVPINLWIDGKOTTIPIDIKVTSKKEVTVOELDQARHYLHGFGLYNSDSFG-GK--- 178
Dd	117 RKIPINLWNGKKHTISTDKIATNKKLVATAQEIDVKLRRLYQEEYNIYGHNNYTGKKEYG 176
QY	179 -----VQRGLIVFHSSEGSTVSYDLFDAAQQGPDTLLRI 212
Dd	177 YKSFYGFNGNKKVLFHLNNEKSFSLFYTFGTGNGLPVSFLKI 218
RESULT 34	

Thu Aug 12 13:48:08 2004

```

DR EMBL; AY291443; AAP78522.1; -.
FT NON TER 218
SQ SEQUENCE 218 AA; 24994 MW; 698329CE49754350 CRC64;

Query Match 23.7%; Score 293.5; DB 2; Length 218;
Best Local Similarity 34.2%; Pred. No. 3.6e-15;
Matches 76; Conservative 36; Mismatches 73; Indels 37; Gaps 9;

QY 8 NEKDLRKKSELOG-TALGNLKOIY----YNEKAITENKESDDQFLENTLLFKGFPTGHP 62
DB 17 NIKDL---TYAQDQIGVGNLRFYTKHDYIDLKGVTDKNLPIANOLE-----FSTG-- 64
QY 63 WYNDLLVDLGSKDATNKYKGVLDLYGAYYVQCGAGTPTNKACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISESNWDEISFKFGKLDIFGIDYNGPC-----KSKMYGGATL-SGQYLNSA 116
QY 123 KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK--- 178
DB 117 RKIPINLWNGKHKTISTDKIATNKLVTAQIDVLRLOEYNIYCHNNTGKKEYG 176
QY 179 -----VQRLIVFHSSEGSTVSVDLFDAGQGYPTDLRI 212
DB 177 YKSKFYSGFNNGKVLPHLNNEKSFSDYDFTGDLGVPSPFKI 218

RESULT 36
Q7X0E6 PRELIMINARY; PRT; 207 AA.
ID AC Q7X0E6;
AD Q7X0E6;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS49;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RA Villani F.;
RT "Detection of staphylococcal enterotoxin type G precursors on
RT Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291446; AAP78528.1; -.
FT NON TER 207
SQ SEQUENCE 207 AA; 23867 MW; C815DEC021FAA681 CRC64;

Query Match 23.2%; Score 287.5; DB 2; Length 207;
Best Local Similarity 34.9%; Pred. No. 9.8e-15;
Matches 73; Conservative 34; Mismatches 65; Indels 37; Gaps 9;

QY 8 NEKDLRKKSELOG-TALGNLKOIY----YNEKAITENKESDDQFLENTLLFKGFPTGHP 62
DB 17 NIKDL---TYAQDQIGVGNLRFYTKHDYIDLKGVTDKNLPIANOLE-----FSTG-- 64
QY 63 WYNDLLVDLGSKDATNKYKGVLDLYGAYYVQCGAGTPTNKACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISESNWDEISFKFGKLDIFGIDYNGPC-----KSKMYGGATL-SGQYLNSA 116
QY 123 KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK--- 178
DB 117 RKIPINLWNGKHKTISTDKIATNKLVTAQIDVLRLOEYNIYCHNNTGKKEYG 176
QY 179 -----VQRLIVFHSSEGSTVSVDLFD 199
DB 177 YKSKFYSGFNNGKVLPHLNNEKSFSDYD 205

RESULT 37
Q9F0L6 PRELIMINARY; PRT; 271 AA.
ID AC Q9F0L6;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

```


DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Staphylococcal enterotoxin C-bovine.
GN	SEC-BOV.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1].
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20566668; PubMed=11114901;
RY	Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
SA	Meaney W.J., Smyth C.J.,
RT	"Characterization of a putative pathogenicity island from bovine
RT	Staphylococcus aureus encoding multiple superantigens.";
EL	J. Bacteriol. 183:63-70(2001).
DR	EMBL; AF217235; AAG29599.1; -.
DR	HSSP; P34071; LSE2.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	Interpro; IPR008992; Bact_endotox.
DR	Interpro; IPR006177; Bctr_tox.
DR	Interpro; IPR006123; Stap/Strep_toxin.
DR	Interpro; IPR006126; Staph/strept tox.
DR	Pfam; PF011123; Stap_Strp_toxin; 1.
DR	Pfam; PF02876; Stap_Strp_tox_C; 1.
DR	PRINTS; PR00279; BACTRLTOXIN_
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ	SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;
Query Match 22.9%; Score 283.5; DB 2; Length 271;	
Best Local Similarity 31.6%; Pred. No. 2.8e-14;	
Matches 77; Conservative 51; Mismatches 97; Indels 19; Gaps 9;	
QY	1 SEKSEEINEKDRLRKSELQGTALGNLKQIYYYNFKAITENK-ESDQPLENTLLFGGFT 59
Db	32 AESQDPDTPDELHKASKFTG-LMENMKVL--YDDRYVSATKVKGVDKFLAHDLIYNSDK 88
QY	60 GHPWNDLLVDLGSKDATNKYGKKVDLYGAYGVQC-----AGGTPNKTCWGGVT 112
Db	89 KLNKYVKVTELLNEDLAKKYDEVVDYGSNYTVNCYVFSSKDNWGKVTGGKTCWGGIT 148
QY	113 LHDNNRLTEEK-KVPINLMIDGKQTTPIDKVTSTKEVTVQELDQAHYHLGKFGLY 170
Db	149 KHEGNHFDNGKLQNVLIRVY-ENKRNTISFE-VQTDKKSVAQELDIKARNFLKNKLY 206
QY	171 NSDSFGKVGQGLIVFHSSSEGSTSVSYDLFDQGQYPD--TLRIYRDNKTINSNLHAL 228
Db	207 EFNs--SPYETGYIKFIENNNGTFWDMMPAPGDQFSQKYLMMYNDNKTVDKSVKIEV 264
QY	229 YLYT 232
Db	265 HLTT 268
RESULT 38	
ID	Q53678 PRELIMINARY; PRT; 239 AA.
AC	Q53678;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Enterotoxin (Fragment).
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1].
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9401133; PubMed=8406814;
RY	Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Schach G.A.;

STRAIN-SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.,
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SF370 and MGAS8232,"
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014161; AAC79908.1; -
DR EMBL; AP005142; BAC63655.1; -
DR PIR; A60108; A60108.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin 1; 1.
DR PROSITE; PS00278; Staph/Strep toxin 2; 1.
DR Complete proteome.
KW SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;
SQ
Query Match 22.8%; Score 282.5; DB 16; Length 251;
Best Local Similarity 33.3%; Pred. No. 3.1e-14;
Matches 79; Conservative 45; Mismatches 94; Indels 19; Gaps 10;
QY 4 SSEEINKEKLRKSELOGTAL-GNLKQIYV-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
DB 25 SQEVFAQQDDPSQLRHSRLVRLNQLNIFLYEGDPVTHENVKSVQLLHDLIYN---VS 81
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHNNRL 119
DB 82 GPNYDKLTKELNQEMATLFDKNDIYGVVYHLCYLCENAEASACIYGGVTHNEGNHL 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFLYNSDFGKGV 179
DB 142 EIPKIVKVKVSDIGQ-SLSFD-IETNKQWTAQELDYKVRKYLTDNKLQYNGP--SKY 197
QY 180 QRLGVFHSSEGSTVSDYLD-AGQYPTLLRIYRDNKTINSENHLIALYLYT 232
DB 198 ETGYIKFIPKNKESFWDFEPPEFTQSKY----LMYKDNETLDSNTSQIEWLTT 250
RESULT 40
Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Iupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications,"
RL Infect Immun. 61:4254-4262 (1993).
DR EMBL; L13379; AAA26623.1; -
DR HSP; P34071; ISE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
SQ

DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin 1; 1.
DR PROSITE; PS00278; Staph/Strep toxin 2; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;
Query Match 22.3%; Score 276.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 8.5e-14;
Matches 76; Conservative 50; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLKSKSELOGTALGNLQIYVYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQFDPTDPDELHKASKFTG-LMENMKVL--YDRYVSATKSVKVKFLAHDLIYINISDKK 57
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGVTL 113
DB 58 LKNYDKVKTLELLNEDLAKKYKDEVDVYGSNYVNCFFSKDNVGVKVTGGKTCMYGGITK 117
QY 114 HDNNRLTEB--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFLY 171
DB 118 HEGNHFNDGNLQNLVIRVY-ENKRNITISFE-VOTDKKSVTAQELDIKARSLINKNLVE 175
QY 172 SD3FGGKVGORGLIVFHSSEGSTVSDYLDFAQGYPD--TLRIYRDNKTINSENHLIALY 229
DB 176 FNS--SPYFGYIKFIENNGNTFWYDMFAPGDKFQSKYLMYNDNKTVDKSVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236
RESULT 41
Q54971 PRELIMINARY; PRT; 260 AA.
ID Q54971
AC Q54971;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Superantigen.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Weller;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes,"
RL Infect Immun. 62:1867-1874 (1994).
DR EMBL; L29565; AAA65928.1; -
DR PDB; 1BXT; 22-DEC-99.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00277; Staph/Strep toxin 1; 1.
DR PROSITE; PS00278; Staph/Strep toxin 2; 1.
DR SEQUENCE 260 AA; 29797 MW; 2DD96017DE9D4F49 CRC64;
SQ

Query Match 22.2%; Score 275; DB 2; Length 260;
Best Local Similarity 33.8%; Pred. No. 1.2e-13;
Matches 78; Conservative 37; Mismatches 98; Indels 18; Gaps 9;

QY 10 KDLRKSELOGTALGNLKQIYYNKAITENKESDDQFLENTLLFKGFTGHFWNDLIV 69
DB :
DQ 35 EQLNKSQFTG-VNGNRCL-YDNHFVEGTVRSTGQLQHDLIFPIKDCLKNYDSVKT 92
DY :
QY 70 DLGSKDATNKYGKKVDLYGAYIGYCAGTNP-----KTACWGGVTLDHNNRLTEBKK 124
DB :
DQ 93 EFNKSLATKYKNKVDIFGSNNYYCYSEGNSCKNAKTCMYGVTEHRNQI--EGK 150
DY :
QY 125 VPINLMI---DGQTTVPIDKVTSKEVTVOELDQARHYLHGFGLYNSDFSGKVQR 181
DB :
DQ 151 FP-NITVKVEDNENILSPD-ITTNNKQVTVQELDKTRKILVRKNLYEFNN--SPYET 206
DY :
QY 182 GLIVFHSSGSESVSYDLFDAQGQYPD--TLIRYDRNKTINSNLHIALYL 230
DB :
DQ 207 GYIKFISSGDSFWYDMWPAPGAIFDQSKYLMYNDKTVSSSAIAIEVHL 257
DY :

RESULT 42

ID Q54738 PRELIMINARY; PRT; 260 AA.

AC Q54738; Q54737;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE SUPERANTIGEN SSA (Streptococcus superantigen SSA-phage associated)

DE SSA precursor.

GN SSA OR SPYM3 0920 OR SPS1119.

OS Streptococcus pyogenes, and

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=M GAS 1842;

RX MEDLINE=94222556; PubMed=8168951;

RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M., Rich R.R.;

RT "Molecular characterization and phylogenetic distribution of the streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";

RL Infect. Immun. 62:1867-1874(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=M GAS 1842;

RX MEDLINE=96178602; PubMed=8606073;

RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;

RT "Phylogenetic distribution of streptococcal superantigen SSA allelic variants provides evidence for horizontal transfer of ssa within Streptococcus pyogenes.";

RL Infect. Immun. 64:1161-1165 (1996).

RN [3]

RP SEQUENCE FROM N.A.

RC SPECIES=S.pyogenes; STRAIN=M GAS315 / Serotype M3;

RX MEDLINE=22133808; PubMed=1212206;

RA Beres S.B., Sylva G.L., Barban K.D., Lei B., Hoff J.S., Mammarilla N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D., Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M., Schlievert P.M., Musser J.M.;

RT "Genome-encoded toxins of a serotype M3 strain of group A Streptococcus: phage-associated toxins, the high-virulence phenotype, and clone emergence";

RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083 (2002).

RN [4]

RP SEQUENCE FROM N.A.

RC SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;

RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A., Yanagaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M., Hayashi H., Hamada S.;

RT "The genome of invasive Streptococcus pyogenes: a comparative analysis of S. pyogenes SSI-1, SF370 and MGAS8232.";

RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: U48794; AAB02150.1 -

[illegible]

RESULT 45	
P97163	PRELIMINARY; PRT; 236 AA.
ID	P97163
AC	P97163; P97164;
DT	01-MAY-1997 (TReMBLrel. 03, Created)
DT	01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE	Type A exotoxin precursor (Fragment).
DE	SPEA.
OS	Streptococcus pyogenes.
OS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OC	Streptococcus.
OX	NCBI_TaxID=1314;
OX	[1] _
RN	SEQUENCE FROM N.A.
RP	STRAIN-MGAS156, and MGAS500;
RP	STRAIN-MGAS156, and MGAS500;
RC	MEDLINE=920434323; PubMed=194804;
RC	MEDLINE=920434323; PubMed=194804;
RA	Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RA	"Characterization and clonal distribution of four alleles of the speA
RT	gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT	Streptococcus pyogenes."
RT	Streptococcus pyogenes."
RL	J. Exp. Med. 174:1271-1274 (1991).
RL	J. Exp. Med. 174:1271-1274 (1991).
DR	EMBL; X61556; CAA43754.1; -
DR	EMBL; X61557; CAA43755.1; -
DR	EMBL; X61558; CAA43756.1; -
DR	EMBL; X61559; CAA43757.1; -
DR	EMBL; X61556; CAA43754.1; -
DR	EMBL; X61557; CAA43755.1; -
DR	EMBL; X61558; CAA43756.1; -
DR	EMBL; X61559; CAA43757.1; -
DR	EMBL; X61554; CAA43752.1; -
DR	PIR; A60108; A60108.
DR	HSP; P08095; 1B1Z.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005070; P:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPRO08992; Bact_endotox.
DR	InterPro; IPRO06177; Bact_tox.
DR	InterPro; IPRO06123; Strp/Strep toxin.
DR	InterPro; IPRO06126; Staph/Strep tox.
DR	InterPro; IPRO06173; Staph tox OB.

```

DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON TER 1 1
FT SIGNAL <1 22
FT CHAIN 23 >236
FT NON TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 21.8%; Score 269.5; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.9e-13;
Matches 77; Conservative 43; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEEINEKDLRKKSLOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLNTLLPKGFFTG 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 SQEYFAQQDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLLSHDLIYN--VS 73

QY 61 HPWTNDLLVLGSKDAINKYKKGVLDIYGAYGYQC-AGGTPNKTCACMYGGVTLHDNRL 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 GPNYDKLKTLEKNQEMATFLFKDKNDYIGVEYYHLCVLCENAEBSACIYGVVTHEGNHL 133

QY 120 TEEKKVPINLWIDGKQTTPVIRDKVTKSKKEVTVOELDLQASHYHLHGKFLGYNDSDFGKV 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 EIPKIVVYSGIDGIQ-SLSFD-IETNCKMVTAGELDYKVKYLTNDNKQLYNGP--SKY 189

QY 180 QRGLIVFHSSEGSVSYDLFD-----AQQYPTDLLIRYRDKNTINSENLHI 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 ETGVIKIPKPKKEFWDFDPEPEFTQSKY----LMYIKDNETLDSNTSQI 236

```

```

RESULT 46
Q9SSZ4          PRELIMINARY;      PRT;   222 AA.
ID              Q9SSZ4;
AC              Q9SSZ4;
DT              01-MAY-2000 (TrEMBLrel. 13, Created)
DT              01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT              01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE              Exotoxin type A (Fragment).
GN              SPEA.
OS              Streptococcus pyogenes.
OC              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC              Streptococcus.
OX              NCBI_TaxID=1314;
RN              [1]
RP              SEQUENCE FROM N.A.
RC              STRAIN=D633;
RX              MEDLINE=99137798; PubMed=9952369;
RA              Bessen D.E., Izso M.W., Fiorentino T.R., Caringal R.M.,
RA              Hellingshhead S.K., Beall B.;
RT              "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT              tropism in group A streptococci";
RL              J. infect. Dis. 179:627-636(1999).
DR              EMBL; AF029051; AAD21315.1; -.
DR              HSP; P08095; 1B1Z.
DR              GO; GO:0005576; C:extracellular; IEA.
DR              GO; GO:0015070; F:toxin activity; IEA.
DR              GO; GO:0009405; P:pathogenesis; IEA.
DR              InterPro; IPRO08992; Bact_endotox.
DR              InterPro; IPRO06177; Bact_tox.
DR              InterPro; IPRO06123; Staph/Strep_toxin.
DR              InterPro; IPRO06126; Staph/Strep_tox.
DR              InterPro; IPRO06173; Staph_toxOB.
DR              Pfam; PF01123; Staph_Strep_toxin; 1.
DR              Pfam; PF02876; Staph_Strep_tox_C; 1.
DR              PRINTS; PF00279; BACTRLTOXIN_
DR              PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR              PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT              NON TER      1
FT              NON TER      1
FT              NON TER      222
FT              NON TER      222
SQ              SEQUENCE      222 AA; 25984 MW; 121F8460992818F8 CRC64;

```

Query Match	21.7%; Score 268.5; DB 2; Length 222;	
Best Local Similarity	33.3%; Pred. No. 3.3e-13;	
Matches	74; Conservative 41; Mismatches 96; Indels 11; Gaps 7;	
Qy	4 SEBINEKDLRKKSELOQTAL--GNLKQIY--YYNEKAITENKESDDQFLENTLLFKGFFTG 60	
Db	5 SQEVAQDNPSPQLHRESSLVKLNQNIPLYEGDPVVHENVKSVDDLSDLIYN---VS 61	
Qy	61 HPWYNLLVDLGSKDATNKYGGKVDLYGAYGYQC--AGGTPNKTAQMYGGVTLHDNNRL 119	
Db	62 GLNYDKLKTLEKNREMTLTFKNKNVDIYGVEYYHYCHYLCRNNAKRACIYGGVNTNHEGNHL 121	
Qy	120 TEKKKVPINLWIDGKQTTVPIDKVKTSKEBVTVQELDLQARHYLHGKFGLYNSDSFGKV 179	
Db	122 EIPKNILVKSIDIGIQ-SUSFD--IEFSKQWVTAQELDYKVRKHLTDNNQLYTNGP--SKY 177	
Qy	180 QRGILVHFHSEGSTVSVDYFDAQOGYPDTLLRIYRDNKTINS 221	
Db	178 ETGYIKFISKDKETFWDFPEPEFNQVKYLM-YKONETLDS 219	
RESULT 47		
Q938P4	PRELIMINARY; PRT; 222 AA.	
ID Q938P4		
AC Q938P4;		
DT 01-DEC-2001 (TrEMBLrel. 19, Created)		
DT 01-DEC-2003 (TrEMBLrel. 19, Last sequence update)		
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE Pyrogenic exotoxin A (Fragment).		
GN SPEA.		
OS Streptococcus equisimilis.		
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC Streptococcus.		
OX NCBI_TaxID=119602;		
ON [1]		
RP SEQUENCE FROM N.A.		
RC STRAIN=4951.		
RA Kalia A., Bessen D.E.;		
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human		
RT isolates of group G Streptococci,"		
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR EMBL; AY049745; AAL06068.1; -		
DR GO; GO:0005576; C:extracellular; IEA.		
DR GO; GO:0015070; F:toxin activity; IEA.		
DR GO; GO:0009405; P:pathogenesis; IEA.		
DR InterPro; IPR008992; Bactl_endotox.		
DR InterPro; IPR006177; Bactl_tox.		
DR InterPro; IPR006123; Staph/Strep_toxin.		
DR InterPro; IPR006126; Staph/Strep_tox.		
DR InterPro; IPR006173; Staph_tox_OB.		
DR Pfam; PF01123; Staph_strep_toxin1.		
DR Pfam; PF02876; Staph_strep_tox_C.		
DR PRINTS; PR00279; BACTSTOXIN.		
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
DR NON TER	1	
FT NON TER	1	
SQ SEQUENCE	222 AA; 25884 MW; 121P8460992818F8 CRC64;	
Query Match	21.7%; Score 268.5; DB 2; Length 222;	
Best Local Similarity	33.3%; Pred. No. 3.3e-13;	
Matches	74; Conservative 41; Mismatches 96; Indels 11; Gaps 7;	
Qy	4 SEBINEKDLRKKSELOQTAL--GNLKQIY--YYNEKAITENKESDDQFLENTLLFKGFFTG 60	
Db	5 SQEVAQDNPSPQLHRESSLVKLNQNIPLYEGDPVVHENVKSVDDLSDLIYN---VS 61	
Qy	61 HPWYNLLVDLGSKDATNKYGGKVDLYGAYGYQC--AGGTPNKTAQMYGGVTLHDNNRL 119	
Db	62 GLNYDKLKTLEKNREMTLTFKNKNVDIYGVEYYHYCHYLCRNNAKRACIYGGVNTNHEGNHL 121	
Qy	120 TEKKKVPINLWIDGKQTTVPIDKVKTSKEBVTVQELDLQARHYLHGKFGLYNSDSFGKV 179	

Db	122	ETPKNMLVKVSDIGIQ-SLSFD-IETSKOMVTAQELDYKVRKHLTDNNQLYTNGP--SKY 177
Qy	180	ORGLVIFVHSSGSGTVSYDLFDAQOQYDPTLLIRIVRDNKTINS 221
Db	178	ETGYIKFISKDKETWDFEPEFQNVKYLMIYKONETLDS 219
RESULT 48		
Q54779		
ID	Q54779	PRELIMINARY; PRT: 236 AA.
AC	Q54779; Q54613; Q54736; Q54740; Q54741;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	Type A exotoxin precursor (Fragment).	
OS	Streptococcus pyogenes.	
OS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
NCBI_TaxID	13114;	
RN	[1]	
RC	SEQUENCE FROM N.A.	
RC	STRIN+MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;	
RX	MEDLINE=92044323; PubMed=1940804;	
RT	Nelson K., Schlievert P.M., Salander R.K., Musser J.M.;	
RT	"Characterization and clonal distribution of four alleles of the speA	
RT	gene encoding pyrogenic exotoxin A (scarlet fever toxin) in	
RT	Streptococcus pyogenes."	
RL	J. Exp. Med. 174:1271-1274 (1991).	
DR	EMBL; X61569; CAA43767.1; -	
DR	EMBL; X61572; CAA43770.1; -	
DR	EMBL; X61568; CAA43766.1; -	
DR	EMBL; X61570; CAA43768.1; -	
DR	EMBL; X61571; CAA43769.1; -	
DR	PIR; A60108; A60108.	
DR	HSSP; P08095; 1B1Z.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0015070; F:toxin activity; IEA.	
DR	GO; GO:0003405; P:pathogenesis; IEA.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR006177; Bctr1 tox.	
DR	InterPro; IPR006123; Staph/Strep toxin.	
DR	InterPro; IPR006126; Staph/Strep tox.	
DR	InterPro; IPR006173; Staph tox OB.	
DR	Pfam; PF01123; Staph_Strep_toxin; 1.	
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.	
DR	PRINTS; P000279; BACTRUF0XIN.	
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.	
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
FT	SIGNAL	
FT	NON_TER	
FT	SIGNAL	
FT	CHAIN	
FT	NON_TER	
SQ	SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;	
Query Match		
Best Local Similarity	32.9%;	Score 268.5; DB 2; Length 236;
Matches	76; Conservative	44; Mismatches 92; Indels 19; Gaps 10
Qy	4	SEINEKDLRKSELOQTAL-GNLIKQIYY-YNEKAIT-ENKESDDOFLENTLLFKGFFTG 60
Db	17	SOEVEFAQDPPPSQLHRSSLVNLCNIYFLYEGDPVTHENVKSDQLLSHDLIYN---VS 73
Qy	61	HPWYNDLLVDLGSKDATNKYKGVLDYLGAYGYQC-AGCTPNKTAOMVGGVTLHDNNEL 119
Db	74	GNYPDLKXTELKQSMATLFDKKNIDIGVEYHYLVCYLCEAERSACIYGVGVNHEGNEH 133
Qy	120	TEEEKVPLNWDGKQTTVPIDKVKTSKVEVTQELDQARHYLHGKFLGYSNDSFGVK 179
Db	134	ETPKKIVKVSIDIGIQ-SLSFD-IETSKOMVTAQELDYKVRKYLTDNNQLYTNGP--SKY 189


```
QY 92 -----YGYCCAGGTPNKTACMGVTLHNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNVLKSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSDKYSFDL 174
QY 199 FDAQGYDPDILLRIYRDKNKTINSEN 224
Db 175 FYVGYRDKESIIFKYKDNKSNFNIDKI 200

RESULT 55
Q9LAE0 PRELIMINARY; PRT; 209 AA.
AC Q9LAE0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-4 (Fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9893;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143654; AAF66655.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 209 AA; 24108 MW; 67EC279BEC4A8247 CRC64;

Query Match 19.5%; Score 241.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 3.9e-11;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVDFKTSNHLVTKLDVDRDFFINSEMDYEAANDFKD 62
QY 92 -----YGYCCAGGTPNKTACMGVTLHNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNVLKSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSDKYSFDL 174
QY 199 FDAQGYDPDILLRIYRDKNKTINSEN 224
Db 175 FYVGYRDKESIIFKYKDNKSNFNIDKI 200

RESULT 57
Q9LAC6 PRELIMINARY; PRT; 209 AA.
AC Q9LAC6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-20 (Fragment).
GN SMEZ-20.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
```

```
QY 92 -----YGYCCAGGTPNKTACMGVTLHNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNVLKSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSDKYSFDL 174
QY 199 FDAQGYDPDILLRIYRDKNKTINSEN 224
Db 175 FYVGYRDKESIIFKYKDNKSNFNIDKI 200

RESULT 56
Q9LAD8 PRELIMINARY; PRT; 209 AA.
AC Q9LAD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-7 (Fragment).
GN SMEZ-7.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11574;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143657; AAF66657.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;

Query Match 19.5%; Score 241.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 3.9e-11;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVDFKTSNHLVTKLDVDRDFFINSEMDYEAANDFKA 62
QY 92 -----YGYCCAGGTPNKTACMGVTLHNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNVLKSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSDKYSFDL 174
QY 199 FDAQGYDPDILLRIYRDKNKTINSEN 224
Db 175 FYVGYRDKESIIFKYKDNKSNFNIDKI 200

RESULT 57
Q9LAC6 PRELIMINARY; PRT; 209 AA.
AC Q9LAC6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-20 (Fragment).
GN SMEZ-20.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
```

```

RP SEQUENCE FROM N.A.
RC STRAIN=10989;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143670; AAF66669.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF0123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 53049A11599BBA68 CRC64;

Query Match 19.3%; Score 239.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 5.5e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPW-VNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DB 3 VDNLSLRNIYSTIYVSDTLDFTSHNLVTKLDVDRDFFINSEMDEYAANDFKA 62

QY 92 -----YGYOCAGTGNKTCMYGGVTLHDNNELTEKVPINLWIDGKQTTVP 139
DB 63 GDIAVFSVPFDWNLVSKG---KVTATYGGITPYQKTSI--PKNIPVNLWNGKQIPVP 117

QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
DB 118 YNQISNKTVTVAQEIIDLKVRKELIAHQHLYSS---GSSYKSGRLVFNHNSDKYSFDL 174

QY 199 FDAQGGQVPTLLRIYRDNKTINSNL 224
DB 175 FYGYRDKESIFKVKYDNKSNFNDKI 200

RESULT 58
Q9LADI PRELIMINARY; PRT; 209 AA.
AC Q9LADI
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-14 (Fragment).
GN SMEZ-14.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10989;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143670; AAF66669.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF0123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 53049A11599BBA68 CRC64;

Query Match 19.3%; Score 239; DB 2; Length 209;
Best Local Similarity 29.6%; Pred. No. 6.1e-11;
Matches 60; Conservative 42; Mismatches 65; Indels 36; Gaps 6;

QY 50 NTLFLKGFHTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DB 6 NSLLRNIYSTIYVSDTLDFTSHNLVTKLDVDRDFFINSEMDEYAANDFKA 65

QY 92 -----YGYOCAGTGNKTCMYGGVTLHDNNELTEKVPINLWIDGKQTTVP 142
DB 66 IAVFSVPFDWNLVSEG---KVIATYGGITPYQKTSI--PKNIPVNLWNGKQISVPYNE 120

QY 143 VKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGS-TVSYDL 201
DB 121 ISTNKTVTVAQEIIDLKVRKELIAHQHLYSS---GSSYKSGRLVFNHNSDKYSFDL 177

QY 202 QGQVPTLLRIYRDNKTINSNL 224
DB 178 GYRDKESIFKVKYDNKSNFNDKI 200

RESULT 59
Q9LAEL PRELIMINARY; PRT; 209 AA.
AC Q9LAEL
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1081;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143653; AAF66654.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF0123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24071 MW; FDAFCDLDAAG7271 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

```

```
QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYAAANDFKA 62
QY 92 -----YGYOCAGGTPNKACMYGGVTLHDNNRLTEEEKVPINLWIDGKQTTPV 139
Db 63 GOKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTVTVAQIEDLKVRFKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 60
Q9LAC4
ID Q9LAC4 PRELIMINARY; PRT; 209 AA.
AC Q9LAC4;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR Pfam; PF01123; Stap_strep_toxin; OB.
DR Pfam; PF02876; Stap_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6E8 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYAAANDFKA 62
QY 92 -----YGYOCAGGTPNKACMYGGVTLHDNNRLTEEEKVPINLWIDGKQTTPV 139
Db 63 GOKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTVTVAQIEDLKVRFKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 60
Q9LAC4
ID Q9LAC4 PRELIMINARY; PRT; 209 AA.
AC Q9LAC4;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR Pfam; PF01123; Stap_strep_toxin; OB.
DR Pfam; PF02876; Stap_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6E8 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYAAANDFKA 62
QY 92 -----YGYOCAGGTPNKACMYGGVTLHDNNRLTEEEKVPINLWIDGKQTTPV 139
Db 63 GOKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTVTVAQIEDLKVRFKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200
```

```
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 61
Q9LAC5
ID Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-21 (Fragment).
GN SMEZ-21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11227;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR Pfam; PF01123; Stap_strep_toxin; OB.
DR Pfam; PF02876; Stap_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696F4BC55A CRC64;

Query Match 19.0%; Score 235.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 1.1e-10;
Matches 57; Conservative 47; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYAAANDFKT 62
QY 92 -----YGYOCAGGTPNKACMYGGVTLHDNNRLTEEEKVPINLWIDGKQTTPV 139
Db 63 GOKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTVTVAQIEDLKVRFKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSFDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 62
Q9LAD6
ID Q9LAD6 PRELIMINARY; PRT; 209 AA.
AC Q9LAD6;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-9 (Fragment).
GN SMEZ-9.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
```

```

OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11299;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; AF143659; AAF66659.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctx1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24213 MW; B21587BA343BDD5 CRC64;

Query Match 18.8%; Score 232.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 1.9e-10;
Matches 59; Conservative 45; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPWYNDLLVD-----LGSKDANKYKGGKVDLYGAY--- 91
DB 3 VDNNSLLRNIYSTIVYEYSDTVDFKTSNHLVTKLDVRDARDFINSEMDYANDFKA 62
QY 92 -----XYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 63 GDKIAVFSVPFDWNYLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 117
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS-TVSYDL 198
DB 118 YNQISTNKTITVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGRLVFHTNDSKYSFOL 174
QY 199 FDAQGOYPTDLLRIYRDNKTINSEN 224
DB 175 FYGYRDKESIFKLYKDNKSFNIDKI 200

RESULT 63
Q9LAD2 PRELIMINARY; PRT; 209 AA.
AC Q9LAD2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95/31;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; AF143663; AAF66663.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.

```

```

DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctx1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;

Query Match 18.7%; Score 232; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 2.1e-10;
Matches 59; Conservative 42; Mismatches 66; Indels 36; Gaps 6;

QY 50 NTLFLKGFEGTGHFWYNDLLVD-----LGSKDANKYKGGKVDLYGAY----- 91
DB 6 NSLLRNIYSTIVYEYSDTVDFKTSNHLVTKLDVRDARDFINSEMDYANDFKAGDK 65
QY 92 -----XYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
DB 66 IAVFSVPFDWNYLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 120
QY 143 VKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS-TVSYDLFDA 201
DB 121 ISTNKTITVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSLDLFYV 177
QY 202 QGOYPTDLLRIYRDNKTINSEN 224
DB 178 GYRDKESIFKLYKDNKSFNIDKI 200

RESULT 64
Q7WY99 PRELIMINARY; PRT; 207 AA.
AC Q7WY99
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z (Fragment).
GN SMEZ.
OS Streptococcus canis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1329;
RN [1]
RP SEQUENCE FROM N.A.
RA Igwe E.I., Gertz B.;
RT "Streptococcal superantigen genes in human pathogenesis group G
RT streptococcus.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564198; CAD91900.1; -.
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 24034 MW; C9D5C7B1603BFDCA CRC64;

Query Match 18.7%; Score 231.5; DB 2; Length 207;
Best Local Similarity 27.7%; Pred. No. 2.3e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPWYNDLLVD-----LGSKDANKYKGGKVDLYGAY--- 91
DB 2 VDNNSLLRNIYSTIVYEYSDTVDFKTSNHLVTKLDVRDARDFINSEMDYANDFKA 61
QY 92 -----XYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 62 GDKIAVFSVPFDWNYLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 116
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS-TVSYDL 198
DB 117 YNQISTNKTITVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSLDL 173

```

```
QY 199 FDAQQYPTLLRIYRDNKTINSENL 224
DB 174 FVTGYRDXESIFKVKYDKNSFNIDKI 199

RESULT 65
Q9LAC7 PRELIMINARY; PRT; 209 AA.
AC Q9LAC7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-18 (Fragment).
GN SMEZ-18.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10763;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143668; AAF66668.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match 18.7%; Score 231.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 2.3e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
DB 3 VDNNSLLRNIYSTIVVEYSVTVIDFTKSHNLVTKLDVDRDARDFINSKMDVYAANDFKT 62

QY 92 -----YGYCCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 63 GDKIATVSPVPPNNVLSK3---KVTATYGGITPQKTSI--PRNIPVNLWINKQIIVP 117

QY 140 IDKVTSKKEVTQVELDQARHYLHGKFLGYNDSFGKVGQRLIVFHSSGSGS-TVSYDL 198
DB 118 YNQISTNKTITVTAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLVFHTNDNSDKYSPDL 174

QY 199 FDAQQYPTLLRIYRDNKTINSENL 224
DB 175 FVTGYRDXESIFKVKYDKNSFNIDKI 200

RESULT 66
Q9LAD9 PRELIMINARY; PRT; 209 AA.
AC Q9LAD9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-5 (Fragment).
GN SMEZ-5.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11244;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
  Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
  Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143655; AAF66656.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24079 MW; 24CA3885469CB9B CRC64;

Query Match 18.6%; Score 230.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 2.8e-10;
Matches 57; Conservative 47; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
DB 3 VDNNSLLRNIYSTIVVEYSVTVIDFTKSHNLVTKLDVDRDARDFINSKMDVYAANDFKD 62

QY 92 -----YGYCCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 63 GDKIATVSPVPPNNVLSK3---KVTATYGGITPQKTSI--KNIPVNLWINKQIIVP 117

QY 140 IDKVTSKKEVTQVELDQARHYLHGKFLGYNDSFGKVGQRLIVFHSSGSGS-TVSYDL 198
DB 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLVFHTNDNSGKYL 174

QY 199 FDAQQYPTLLRIYRDNKTINSENL 224
DB 175 FVTGYRDXESIFKVKYDKNSFNIDKI 200

RESULT 67
Q8NZ89 PRELIMINARY; PRT; 233 AA.
AC Q8NZ89;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z.
GN SMEZ OR SPYM18 2064.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
  Sylva G.L., Sturdevant D.B., Ricklefs S.M., Forcella S.F.,
  RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
  RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
```

```

RT group A Streptococcus strains associated with acute rheumatic fever
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE010110; AAL98535.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 233 AA; 26859 MW; 23E07C9C06A866 CRC64;

Query Match 18.6%; Score 230; DB 16; Length 233;
Best Local Similarity 29.1%; Pred. No. 3.5e-10;
Matches 59; Conservative 42; Mismatches 66; Indels 36; Gaps 6;

QY 50 NTLFLKGFTHGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DQ 30 NSLLRNIYSTIMYEYSVDIVDFKTSNHLVTKLDVRDARDFINSEMDYEAANDFKDGDK 89
QY 92 -----XGYQCAGGTPNKTCMYGGVTLHDNNRLTEBKVPIINLWIDKQTTVPIDK 142
DQ 90 IAFSVFDPDNYLSEG---KVIAITYGGMPYQKTSI--PKNIPVNLWINGQISVPYNE 144
QY 143 VKTSKKEVTQVELDLQARHYLHGKFLGYNDSFGKVQVGLIVFHSSEGS--TVSYDLFDA 201
DQ 145 ISINKTITVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTNDSKYSLDLFVY 201
QY 202 QGQYPTDLLRIYRDNKTINSEN 224
DQ 202 GYRDKESIFKVKYKDKNSFNIDKI 224

RESULT 68
Q9LAC9 PRELIMINARY; PRT; 209 AA.
AC Q9LAC9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-16 (Fragment).
GN SMEZ-16
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10649;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776 (2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 4e-10;
Matches 58; Conservative 44; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
DQ 3 VDNSSLNIIYSTIVYEYSVDIVDFKTSNHLVTKLDVRDARDFINSEMDYEAANDFKA 62
QY 92 -----YGYQCAGGTPNKTCMYGGVTLHDNNRLTEBKVPIINLWIDKQTTVP 139
DQ 63 GRIATVSVFDPDNYLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINKQISVP 117
QY 140 IDKVTSKKEVTQVELDLQARHYLHGKFLGYNDSFGKVQVGLIVFHSSEGS--TVSYDL 198
DQ 118 YNEISTNKITVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTNDSKYSLDL 174
QY 139 FDAQGYPTDLLRIYRDNKTINSEN 224
DQ 175 FYTGDRKESIFKVKYKDKNSFNIDKI 200

RESULT 69
Q9LAD4 PRELIMINARY; PRT; 209 AA.
ID Q9LAD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9779;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776 (2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 4e-10;
Matches 58; Conservative 44; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
DQ 3 VDNSSLNIIYSTIVYEYSVDIVDFKTSNHLVTKLDVRDARDFINSEMDYEAANDFKA 62
QY 92 -----YGYQCAGGTPNKTCMYGGVTLHDNNRLTEBKVPIINLWIDKQTTVP 139
DQ 63 GRIATVSVFDPDNYLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINKQISVP 117
QY 140 IDKVTSKKEVTQVELDLQARHYLHGKFLGYNDSFGKVQVGLIVFHSSEGS--TVSYDL 198
DQ 118 YNEISTNKITVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTNDSKYSLDL 174
QY 139 FDAQGYPTDLLRIYRDNKTINSEN 224
DQ 175 FYTGDRKESIFKVKYKDKNSFNIDKI 200

```

```
Db 63 GDRIAVSFVDFMNYLSKG---KVTATYGGVTPYQKTSI--PKNIPVNLWNRKQIPVP 117
Qy 140 IDKVKTSKKEVTQELDLQARHYLHGKFGLYNSDFGKVGQVGLIVFHSSEGS--TVSYDL 198
Db 118 YNQISTNKTVTYTAQEIDLKVRKFLISQHLVSS---GSNYKSGKLVFHTNDNSDKYSLDL 174
Qy 199 FDAQGQYPTDLLRIYRDNKTINSENL 224
Db 175 FYTGDRKESIFKYKONKSFNIDKI 200

RESULT 70
Q936G4 PRELIMINARY; PRT; 259 AA.
ID Q936G4 AC Q936G4
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin-like protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RX MEDLINE=95050273; PubMed=7961465;
RA Lin W.S., Cunnell T., Lee C.Y.;
RT "Sequence analysis and molecular characterization of genes required for the biosynthesis of type 1 capsular polysaccharide in Staphylococcus aureus."
RL J. Bacteriol. 176:7005-7016(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RT "The Type 1 Capsular Polysaccharide of Staphylococcus aureus is carried in a Staphylococcal Cassette Chromosome Genetic Element."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U10927; AAL26674.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR GO: GO:0006810; P:transpos; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR005666; Lipocin_cytFABP.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00213; LIPOCALIN; 1.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 259 AA; 29981 MW; 783E1E4FEF057EDB CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 259;
Best Local Similarity 28.3%; Pred. No. 5.2e-10;
Matches 69; Conservative 41; Mismatches 109; Indels 25; Gaps 9;

Qy 1 SEKEEINEKDLRKSLOQTALGNLQIYY-YNEKAITENK-ESDDQFLENTLLFKGFF 58
Db 24 AETQDNFENISLNKSSQY---TGSWNIWLYNSDPVNAKKIKLSDKFLSHBFIVPINN 79
Qy 59 TGHFWYNDLLVGLSGKDATNKKYKKVLDLYGAYGYOC-----AGGTPNKTACM 107
Db 80 PSH--YDYVKTSLKSTMASSFDGKEVDIFGVNYFDQCYFLENICDSNQGAGSKKTCM 137
Qy 108 YGGVTLHDNNRLTEBEKVPINLWI--DCKQTTPVTDKVKTSKKEVTQELDLQARHYLHGK 166
Db 138 YGGITLNN--TNNRQPIVVKYVENDSVLTSFD--INIDKEVTIQEILDYKVRNKLISK 194
```

```
Qy 167 FGLYNSDSFGKVGQVGLIVFHSSEGSTVSYDLDFAQGQYPTDLLRIYRDNKTINSENLHI 226
Db 195 INLYHLG--GTSVEGYIKFIENGARYWYDMPPDPGFTQSKYLMYRGNEIVESAETEI 252
Qy 227 ALYL 230
Db 253 EVHL 256

RESULT 71
Q9LAC3 PRELIMINARY; PRT; 209 AA.
ID Q9LAC3 AC Q9LAC3
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-17 (Fragment).
GN SMEZ-17.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11686;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weiler K.D., Paterson A., Martin D., Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation, Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143667; AAF66667.1; -
DR HSSP: P13163; LSXT.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox OB.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin; 1.
DR PRINTS: PR00279; BACTRTOXIN.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24181 MW; A333F466398D9DC2 CRC64;

Query Match 18.4%; Score 227.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 4.8e-10;
Matches 57; Conservative 45; Mismatches 67; Indels 37; Gaps 7;

Qy 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKKYKKVLDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYYSSTVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAAANDFKA 62
Qy 92 -----YGYQCAGGTENKTACMYGGVTLHDNNRLTEEEKVPIINLWIDGKQTTPV 139
Db 63 GDRIAVSFVDFMNYLSKG---KVTATYGGVTPYQKTSI--PKNIPVNLWNRKQIPVP 117
Qy 140 IDKVKTSKKEVTQELDLQARHYLHGKFGLYNSDFGKVGQVGLIVFHSSEGS--TVSYDL 198
Db 118 YNQISTNKTVTYTAQEIDLKVRKFLISQHLVSS---GSNYKSGKLVFHTNDNSDKYSLDL 174
Qy 199 FDAQGQYPTDLLRIYRDNKTINSENL 224
Db 175 FYTGDRKESIFKYKONKSFNIDKI 200

RESULT 72
Q9LAC3 PRELIMINARY; PRT; 209 AA.
ID Q9LAC3 AC Q9LAC3
```

```
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-24 (Fragment).
GN SMEZ-24.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR HSSP; AF143674; AAF66672.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER.
FT SIGNAL.
SQ SEQUENCE 209 AA; 24137 MW; 301587A9A995F715 CRC64;

Query Match 18.4%; Score 227.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred.No. 4.8e-10;
Matches 57; Conservative 45; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLFGKFFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
DB 3 VDNNSLRNIYSTIVVEYSDTVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDFKA 62
QY 92 -----YGYOCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTPV 139
DB 63 GKIAVFSVPFDWNLVSKG---KVTATYGGITPY--PKNIPVNLWLNKQIPIVP 117
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSGGKVGQRLIVFHSSEGS-TVSYDL 198
DB 118 YNQISNTKTTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDL 174
QY 199 FDAQGYPTLLRIYDKNKTINSEN 224
DB 175 FYGYRDKESIFKVKYDNKSNFNIDKI 200

RESULT 73
Q9S1H8 PRELIMINARY; PRT; 256 AA.
ID Q9S1H8
AC Q9S1H8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE SpeX protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12714 type 12;
RX MEDLINE=20374978; PubMed=10913699;
RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S.,
```

```
RA Reichardt W.;
RT "Purification and Biochemical Characterization of a Basic Superantigen
RT (SPEX/SMEZ3).";
RL FEMS Microbiol. Lett. 188:153-163(2000).
DR EMBL; AJ245403; CAB51744.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR SIGNAL.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29706 MW; 873D0BAFB6DC332 CRC64;

Query Match 18.3%; Score 226.5; DB 2; Length 256;
Best Local Similarity 28.2%; Pred.No. 7.3e-10;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;

QY 48 LENTLFGKFFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
DB 50 VDNNSLRNIYSTIVVEYSDTVDFKTSNHLVTKKLDVRDARDFINSEMDEYAANDFKT 109
QY 92 -----YGYOCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTPV 139
DB 110 GKIAVFSVPFDWNLVSKG---KVTATYGGITPY--QKQVLYKLSLVNLWLNKQISVP 164
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSGGKVGQRLIVFHSSEGS-TVSYDL 198
DB 165 YNEISTNKTTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGRLVFTNDNSDKYSFDL 221
QY 199 FDAQGYPTLLRIYDKNKTINSEN 224
DB 222 FYGYRDKESIFKVKYDNKSNFNIDKI 247

RESULT 74
Q9LADS PRELIMINARY; PRT; 209 AA.
ID Q9LADS
AC Q9LADS;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-10 (Fragment).
GN SMEZ-10.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11580;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143660; AAF66660.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox_OB.
```



```

DR Pfam; PF01123; Strep_Strp_toxin; 1.
DR Pfam; PF02876; Strep_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24102 MW; 8B4C953751A56D06 CRC64;

Query Match 18.2%; Score 225.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. 6.9e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLIFKGFFFGHPW-NDLLVD-----LQSKDATNKYKGKVDLYGAV--- 91
Db 3 VDNNSLRNIYSTIVVEYSDVIDFKSHNLVTKLVDVDARDFINSEMDVANDPKD 62
QY 92 -----YGCQAGGTPTNTACMWGVTLHDNNLTTEKKVPINLWDGKQTVP 139
Db 63 GDKIAMFSPFDNNYLSKG---KVIAITYGMPICEEPIS--KNIPVNLWNGKQISVP 117
QY 140 IDKVKTSKKEVTVQSLDLQASHLYLHGKFGVYNSDSFGKVGQRGLIVFHSSGGS--TVSYDL 198
Db 118 YNEISTNKTVTVAQELIDLVKVKFLIAHQIYSS---GSSYKSKGLVFHINDNSDKYSLDL 174
QY 199 FPAQCQYPTDLLRIYRDNKTINSENL 224
Db 175 FTVGYRDKESIFKVKYKKNKSNFDKI 200

```

RESULT	75	
Q9LAD7	PRELIMINARY;	PRT; 209 AA.
Q9LAD7		
AC	Q9LAD7;	
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, last annotation update)	
DE	Mitogenic exotoxin Z-8 (Fragment).	
DE	SMEZ-8.	
GN	Streptococcus pyogenes.	
OS	Streptococcus pyogenes.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OC	Streptococcus.	
OX	NCBI_TaxID=1314;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=1/5045;	
RC	MEDLINE=20273982; PubMed=10811859;	
RX		
RA	Prof. T., Moffatt S.L., Weiler K.D., Paterson A., Martin D.,	
RA	Fraser J.D.;	
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,	
RT	Mosaic Structure, and Significant Antigenic Variation.";	
RRT	J. Exp. Med. 191:1765-1775(2000).	
DR	EMBL; AF143658; AAF66658.1; -.	
DR	HSSP; P13163; ISX1.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0015070; F:toxin activity; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR008177; Bctrl_tox.	
DR	InterPro; IPR006123; Staph/Strep_toxin.	
DR	InterPro; IPR006173; Staph_tox_OB.	
DR	Pfam; PF01123; Staph_Strep_toxin; 1.	
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.	
DR	PRINTS; PR00279; BACTRLTOXIN ¹	
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
FT	NON_TER ¹	
SQ	SEQUENCE 209 AA; 24091 MW; 7680E9B35513DF28 CRC64;	

```

Query Match      18.0%; Score 222.5; DB 2; Length 209;
Best local Similarity 27.2%; Pred. No. 1.2e-09;
Matches 56; Conservative 47; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLPGKFTGHPW-YNDLLVD-----IGSKDATNKYKGKVDLYGAY----- 91
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 VDNNSLRNRYIVYEYSVTVDFTKSTHNLVTKKLDVRDARDFINSEMDYAAADFKA 62

```

```

Qy 92 -----YGVQCAAGTGNPKTACWYGVTLHDNNRLTEBKQVPIINLWIDGKQTTVP 139
Db 63 GSKIAVSPVDNMYLSG---KVIAITYGMPYQEEPIIS--KNIPVNLWINGKQISVT 117
Qy 140 IDPKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQKRGRLIVFHSEGS--TVSYDL 198
Db 118 YNEISNTKTTVTAQEBIDLKVRKFLIAHQLYSS---GSSYKSGKLVFHTNDSKYSL 174
Qy 199 FPAQCQYPTDLLRIYRDNKTIENSEL 224
Db 175 FVGYRDKESIFKYVKNKSNFNIDKI 200

```

Search completed: August 12, 2004, 13:32:32
Job time : 22.2698 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 29.2786 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-3
Perfect score: 1238
Sequence: 1 SEKSEINEKDLRKSEKELQ.....RDNKTINSENLHLYLYTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database 1: Genesep23Jan04.*

2: Genesep1980s.*

3: Genesep1990s.*

4: Genesep2000s.*

5: Genesep2001s.*

6: Genesep2002s.*

7: Genesep2003as.*

8: Genesep2003bs.*

9: Genesep2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	6	ABP58457 Engineere
2	1216	98.2	245	2	AAW35375 Staphyloc
3	1210	97.7	233	6	ABP58456 Staphyloc
4	1210	97.7	257	4	AAU14103
5	1210	97.7	257	4	ABP10268 S. aureus
6	1196	96.6	230	4	AAW67339 Staphyloc
7	1194	96.4	245	2	AAW35374 Staphyloc
8	1168	94.3	248	6	ABU79072 S. aureus
9	1151	93.0	230	2	AAW45012 Staphyloc
10	1147	92.6	230	5	ABW76235 Staphyloc
11	1130	91.3	233	6	ABP58455 Engineere
12	1130	91.3	672	6	ABP58454 Engineere
13	1128	91.1	230	2	AAW13204 Staphyloc
14	1109	84.7	233	2	AAW13203 Staphyloc
15	1037	83.8	233	6	ABP58458 Staphyloc
16	1037	83.8	257	4	AAU14104 Peptide s
17	1037	83.8	257	6	ABO10269 S. aureus
18	1037	83.8	257	7	ADD44368 Staphyloc
19	1033	83.4	233	2	AAW06738 Staphyloc
20	1030	83.2	233	4	AAW35373 Staphyloc
21	1030	83.2	233	4	AAW67338 Staphyloc
22	1027	83.0	233	2	AAW45011 Staphyloc
23	1024	82.7	257	6	ABU79068 S. aureus
24	1018	82.2	233	5	ABW76234 Staphyloc
25	1014	81.9	257	5	ABW79501 Staphyloc

26	1014	81.9	257	6	ABU10081
27	1014	81.9	257	7	ABU62324 S. aureus
28	1014	81.9	257	7	AAE37676 Protein #
29	1010	81.6	233	3	AAE37676 Amino aci
30	1010	81.6	233	5	ABW79502 Staphyloc
31	1010	81.6	233	6	ABU10082 Staphyloc
32	1010	81.6	233	7	ABU62325 S. aureus
33	1010	81.6	233	7	AAE37677 Protein #
34	1006	81.3	233	6	ABU10099 Staphyloc
35	1001	80.9	233	6	ABU10098 Staphyloc
36	997	80.5	257	3	AAW70102 Staphyloc
37	992	80.1	233	3	AAW70103 Mutant St
38	663	53.6	258	6	ABU79071 S. aureus
39	657	53.1	228	2	AAW45013 Staphyloc
40	657	53.1	228	4	AAW67340 Staphyloc
41	657	53.1	228	5	ABW76236 Staphyloc
42	649	52.4	228	2	AAW13205 Staphyloc
43	523	42.2	203	6	ABP58459 Staphyloc
44	483.5	39.1	250	6	ABW70958 Staphyloc
45	457	36.9	82	6	ABU10091 Bacterial
46	457	36.9	82	7	ABU62338 S. aureus
47	399	32.2	82	6	ABU10089 Bacterial
48	399	32.2	82	7	ABU62336 S. aureus
49	370	29.9	91	2	AAW24299 Staphyloc
50	360	29.1	217	6	ABP58460 Staphyloc
51	327.5	26.5	259	5	ABP29357 Streptoco
52	310.5	25.1	239	2	AAW06254 Staphyloc
53	310.5	25.1	240	6	ABG71370 Staphyloc
54	305.5	24.7	239	2	AAW06253 Staphyloc
55	305.5	24.7	240	6	ABG71369 Staphyloc
56	304.5	24.6	239	2	AAW06256 Staphyloc
57	304.5	24.6	240	6	ABG71372 Staphyloc
58	304.5	24.6	266	6	ABU79069 S. aureus
59	303.5	24.5	239	4	AAW64647 Synthetic
60	303.5	24.5	239	4	AAW67341 Staphyloc
61	303.5	24.5	255	2	AAW06737 Staphyloc
62	302.5	24.4	239	2	AAW06255 Staphyloc
63	302.5	24.4	240	6	ABG71371 Staphyloc
64	300.5	24.3	239	2	AAW06252 Staphyloc
65	300.5	24.3	240	6	ABG71368 Staphyloc
66	300.5	24.3	266	7	ABU62455 S. aureus
67	298.5	24.1	238	2	AAW45016 Staphyloc
68	298.5	24.1	238	4	AAW67343 Staphyloc
69	296.5	23.9	238	5	ABW76239 Staphyloc
70	296.5	23.9	239	2	AAW13206 Staphyloc
71	296.5	23.9	239	2	AAW45014 Staphyloc
72	296.5	23.9	266	3	AAW92319 Plant-Opt
73	296.5	23.9	266	5	ABW79503 Staphyloc
74	296.5	23.9	266	6	ABU10083 Staphyloc
75	296.5	23.9	266	7	ABU62326 S. aureus
76	296.5	23.9	266	7	AAE37678 Protein #
77	294.5	23.8	239	5	ABW76237 Staphyloc
78	294.5	23.8	266	2	AAW13208 Staphyloc
79	293.5	23.7	266	3	AAW54464 Amino aci
80	293.5	23.7	266	3	AAW54465 Mutant St
81	292.5	23.6	240	3	AAW54465 Mutant St
82	291.5	23.5	239	5	ABW79505 Staphyloc
83	291.5	23.5	239	6	ABU10085 Staphyloc
84	291.5	23.5	239	7	AAE37680 Protein #
85	291.5	23.5	239	7	AAE37680 Protein #
86	290.5	23.5	239	3	AAW70106 Mutant St
87	290.5	23.5	266	7	ABU62454 S. aureus
88	287.5	23.2	266	7	ABU62452 S. aureus
89	287.5	23.2	266	7	ABU62451 S. aureus
90	286.5	23.1	266	5	ABW79504 Staphyloc
91	286.5	23.1	266	6	ABU10084 Staphyloc
92	286.5	23.1	266	7	ABU62327 Staphyloc
93	286.5	23.1	266	7	AAE37679 Protein #
94	285.5	23.1	251	2	AAW12153 Streptoco
95	284.5	23.0	221	2	AAW13209 Streptoco
96	284.5	23.0	221	2	AAW45017 Staphyloc
97	284.5	23.0	221	5	ABW76240 Staphyloc
98	284.5	23.0	251	2	AAW12151 Streptoco

99 284.5 23.0 251 2 AAW12150
100 283 22.9 265 3 AAY70104 Staphyloc

ALIGNMENTS

RESULT 1
ABP58457
ID ABP58457 standard; protein; 233 AA.
XX AC ABP58457;
XX DT 14-APR-2003 (first entry)
XX XX Engineered superantigen SEA/E-18 for human cancer therapy.
XX DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
XX KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
XX OS Staphylococcus sp.
XX OS Synthetic.
XX PN WO2003002143-A1.
XX XX
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX XX (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX WPI; 2003-201467/19.
XX XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX XX Example 3; Fig 3; 102pp; English.
XX CC The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-18. The superantigen is based on staphylococcal
CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
CC to the N-terminal that were from enterotoxin A and one substitution in
CC the C-terminal part, D227A. Models of new superantigen variants were
CC constructed using the SEA/E-18 model as the template. These include the
CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
CC genetically fused to the Fab moiety of the tumour reactive antibody 5T4
CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
CC claimed example of novel conjugates of the invention comprising an
CC engineered bacterial superantigen and an antibody moiety. The conjugates
CC are designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)
XX SQ Sequence 233 AA;
Query Match 100.0%; Score 1238; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVGLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTCMYGVTLLHNNRLT 120
DB 61 HPWYNDLLVGLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTCMYGVTLLHNNRLT 120

QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKRVQ 180
DB 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKRVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLALVLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLALVLYTT 233

RESULT 2
AAW35375
ID AAW35375 standard; peptide; 245 AA.
XX AC AAW35375;
XX DT 20-APR-1998 (first entry)
XX XX Staphylococcus enterotoxin SEE modified superantigen.
XX DE SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX KW cancer; infection; autoimmune disease; antibody; modified.
XX OS Staphylococcus sp.
XX FH Key Location/Qualifiers
FT Misc-difference 20 /label= R20G
FT /note= "wild-type Arg is replaced by Gly"
FT Misc-difference 21 /label= N21T
FT /note= "wild-type Asn is replaced by Thr"
FT Misc-difference 24 /label= S24G
FT /note= "wild-type Ser is replaced by Gly"
FT Misc-difference 27 /label= R27K
FT /note= "wild-type Arg is replaced by Lys"
XX WO9736932-A1.
XX PN 09-OCT-1997.
XX PD 26-MAR-1997; 97WO-SE000537.
XX PF 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PHAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
XX Abrahamson L, Forsberg G;
XX WPI; 1997-503052/46.
XX DR Conjugate of target seeking moiety and modified superantigen - useful for
XX activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
PT Claim 5; Page; 58pp; English.
XX CC This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
CC type SEE superantigen is modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. This modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be
CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in Vbeta specific
CC manner) in which cysteines providing for interchain cysteine linkages in

CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 CC Note: this sequence is not provided in the specification. It has been
 CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
 CC 39 of the specification
 XX
 SQ Sequence 245 AA;

Query Match 98.2%; Score 1216; DB 2; Length 245;
 Best Local Similarity 94.7%; Pred. No. 1.8e-113;
 Matches 232; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

QY 1 SEKSEINEKDLRKSELGQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELGQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNRRLT 120
 DB 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNRRLT 120
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 DB 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIALYLYTT 228
 DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIALYLYTT 240
 QY 229 YLYTT 233
 DB 241 YLYTT 245

RESULT 3
 ABP58456
 ID ABP58456 standard; protein; 233 AA.
 AC ABP58456;
 XX
 DT 14-APR-2003 (first entry)
 DE Staphylococcal enterotoxin E.
 XX Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX Staphylococcus sp.
 OS WO2003002143-A1.
 PN 09-JAN-2003.
 PD 19-JUN-2002; 2002WO-SE001188.
 PF 28-JUN-2001; 2001SE-00002327.
 PR (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PI WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX Example 3; Fig 4; 102pp; English.

CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
 CC for human cancer therapy. These comprise an engineered bacterial
 CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
 CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
 CC superantigen is engineered to reduce seroreactivity whilst maintaining
 CC biological activity and production levels. The conjugates are designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 233 AA;

Query Match 97.7%; Score 1210; DB 6; Length 233;
 Best Local Similarity 97.9%; Pred. No. 6.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELGQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNRRLT 120
 DB 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNRRLT 120
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 DB 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIALYLYTT 233
 DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHIALYLYTT 233

RESULT 4
 AAU14103
 ID AAU14103 standard; peptide; 257 AA.
 XX AAU14103;
 AC AAU14103;
 XX
 DT 21-NOV-2001 (first entry)
 DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
 XX Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
 KW antitumorigenic; antiviral; HIV transmission.
 XX Staphylococcus aureus.
 OS WO200151673-A2.
 PN 19-JUL-2001.
 PD 05-JUL-2000; 2000WO-US035727.
 PF 09-JUL-1999; 99US-00350841.
 PR (TRIM-) TRIMERIS INC.
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 PI WPI; 2001-442157/47.
 DR
 XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitumorigenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX Disclosure; Fig 4; 259pp; English.

PS The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifeusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin type
 CC E
 XX
 SQ Sequence 257 AA;

Query Match 97.7%; Score 1210; DB 4; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSLOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSLOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLT 120
 DB 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLT 144
 QY 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENLHIALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENLHIALYLYTT 257

RESULT 5
 ABO10268
 ID ABO10268 standard; protein; 257 AA.
 XX ABO10268;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 DE *S. aureus* enterotoxin E.
 XX
 KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.

XX *Staphylococcus aureus*.

OS US6518013-B1.

PN 11-FEB-2003.

XX 07-JUN-1995; 95US-00485546.

XX 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX (TRIM-) TRIMERIS INC.

XX Barney SO, Lambert DM, Petteway SR;

XX WPI; 2003-465599/44.

XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting

PT the cell with a peptide consisting of a region of Epstein-Barr virus

PT protein.

XX Example; Fig 41; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 16-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLMOT15,
 CC 107x178x4 or PL2IP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxycarbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 SQ Sequence 257 AA;

Query Match 97.7%; Score 1210; DB 6; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSLOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSLOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLT 120
 DB 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLT 144
 QY 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENLHIALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENLHIALYLYTT 257

RESULT 6
 AAB67339
 ID AAB67339 standard; peptide; 230 AA.
 XX AAB67339;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE *Staphylococcus aureus* enterotoxin E protein.
 XX
 KW Tumour; cancer; immune; enterotoxin.
 XX
 OS *Staphylococcus aureus*.

XX US6180097-B1.

PN 30-JAN-2001.

XX 30-OCT-1998; 98US-00183437.

XX 03-OCT-1989; 89US-00416530.

PR 17-JAN-1990; 90US-00466577.

PR 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.

PR 02-MAR-1993; 93US-00025144.

PR 31-JAN-1994; 94US-00189424.

PR 19-JUN-1995; 95US-00491746.

PA (TERM/) TERVAN D S.
 XX Terman DS;
 PI
 XX
 DR WPI; 2001-158657/16.
 XX
 XX
 PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX
 XX
 PS Disclosure; Fig 2; 16pp; English.
 XX
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 96.6%; Score 1196; DB 4; Length 230;
 Best Local Similarity 97.8%; Pred. No. 1.7e-111;
 Matches 225; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTPG 63
 Db 1 SEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTPG 60
 QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
 Db 61 YNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
 Db 121 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
 QY 184 IVFHSSEGSTVSYDLFDAQGGYPTLLRIYRDNKTINSENHLIALYLYTT 233
 Db 181 IVFHSSEGSTVSYDLFDAQGGYPTLLRIYRDNKTINSENHLIALYLYTT 230
 RESULT 7
 AAW35374
 ID AAW35374 standard; peptide; 245 AA.
 AC AAW35374;
 XX
 XX 20-APR-1998 (first entry)
 XX
 XX Staphylococcus enterotoxin SEE wild-type superantigen.
 DE
 XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 XX cancer; infection; autoimmune disease; antibody.
 XX
 XX Staphylococcus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 20 /note= "can be mutated at this position"
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT
 XX W09736932-A1.
 PN
 XX
 XX 09-OCT-1997.
 PD
 XX
 XX 26-MAR-1997; 97WO-SE000537.
 PF

XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX
 PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abrahmsen L, Forsberg G;
 XX
 XX WPI; 1997-503052/46.
 XX
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX
 PS Claim 4; Page 38-39; 58pp; English.
 XX
 CC This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody, (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX
 SQ Sequence 245 AA;
 Query Match 96.4%; Score 1194; DB 2; Length 245;
 Best Local Similarity 93.1%; Pred. No. 2.9e-111;
 Matches 228; Conservative 1; Mismatches 4; Indels 12; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
 Db 121 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGGYPTLLRIYRDNK-----TINSENHLIAL 228
 Db 181 RGLIVFHSSEGSTVSYDLFDAQGGYPTLLRIYRDNK-----TINSENHLIAL 240
 QY 229 YLYTT 233
 Db 241 YLYTT 245
 RESULT 8
 ABU79072
 ID ABU79072 standard; protein; 248 AA.
 XX
 AC ABU79072;
 XX
 XX 18-JUN-2003 (first entry)
 DT
 XX
 DE S. aureus SEE (staphylococcus enterotoxin E) protein.

XX Superantigen; Shg: staphylococcal enterotoxin; tumour; cancer; apoptosis;
 XX gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
 XX T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 XX APC; antitumour.
 XX Staphylococcus aureus.
 XX US2002177551-A1.
 XX 28-NOV-2002.
 XX 30-MAY-2001; 2001US-00870759.
 XX 31-MAY-2000; 2000US-0208128P.
 XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 2003-361759/34.
 XX N-PSDB; ACA64698.
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 XX to tumor associated lipids where the binding induces anergy or apoptosis
 XX in T cells and antigen presenting cells.
 XX Disclosure; Page; 167pp; English.
 XX The invention relates to a mammalian cell receptor, useful in the
 XX treatment of cancer, which binds to tumour associated lipids and induces
 XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 XX Also included are a mammalian cell useful in the treatment of cancer
 XX where the receptor which binds tumour associated lipids and induces
 XX cellular inactivation or death is deleted or functionally deactivated,
 XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 XX (by allowing tumour associated lipids to contact immunocytes in which
 XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 XX sphingolipids, glycosphingolipids, phospholipids, gangliosides,
 XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 XX deleted), a construct useful in the treatment of cancer comprising a
 XX superantigen (Sg) nucleotide inserted into a virus, a mammalian T cell
 XX useful in the treatment of cancer (where an adaptor protein which
 XX inhibits T cell activation by tumour associated antigens is deleted or
 XX functionally deactivated), a composition useful in the treatment of
 XX cancer (comprising a lipid raft conjugated to a superantigen), producing
 XX (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 XX allowing tumour associated lipids to contact immunocytes, in which
 XX receptors for the lipids are inactivated or deleted to produce a
 XX tumouricidal immunocyte population, and administering the tumouricidally
 XX activated immunocytes to the host), producing (M3) a tumouricidal APC
 XX population ex vivo in a mammal (by allowing a tumour associated lipid to
 XX contact APCs, in which receptors for the tumour associated lipids are
 XX inactivated or deleted to produce a tumouricidally activated population,
 XX and administering APCs to the host), producing a tumouricidal T cell
 XX population ex vivo in a mammal (by allowing a tumour associated lipids to
 XX contact T cells, in which adaptor proteins, which inhibit T cell
 XX activation by tumour associated antigens, are deleted or functionally
 XX deactivated to produce a tumouricidal population of T cells, and
 XX administering the tumouricidally activated T cells to the host, or
 XX allowing a superantigen-lipid raft to contact T cells ex vivo, and
 XX administering the tumouricidally activated T cells to the host), treating
 XX (M5) cancer in a mammal (by administering a lipid binding molecule which
 XX binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 XX a tumouricidal T cell population in vivo in a mammal (by allowing a
 XX tumour associated antigen to contact immunocytes in which adaptor
 XX proteins which inhibit T cell activation by tumour associated antigens
 XX are deleted or functionally deactivated) and producing (M7) a
 XX tumouricidal T cell population ex vivo in a mammal comprising allowing a
 XX superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 XX receptors, methods and compositions are useful for treating cancers and
 XX tumours. Bacterial superantigens are co-administered or administered as
 XX fusion constructs with anti-tumour proteins or motifs. The present

CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic form from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 XX SQ Sequence 248 AA;
 XX
 XX Query Match 94.3%; Score 1168; DB 6; Length 248;
 XX Best Local Similarity 98.2%; Pred. No. 1.2e-108;
 XX Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOGTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFTG 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGVKVDLYGAYGYGQACGTPNKTACMYGGVTLHDNRLLT 120
 DB 85 HPWYNDLLVDLGSKDATNKYKGVKVDLYGAYGYGQACGTPNKTACMYGGVTLHDNRLLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQSQYPTDILLRYRDNKNTINSENL 224
 DB 205 RGLIVFHSSEGSVSYDLFDAQSQYPTDILLRYRDNKNTINSENL 248
 RESULT 9
 AAR45012
 ID AAR45012 standard; protein; 230 AA.
 XX
 AC AAR45012;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX
 DE Staphylococcal enterotoxin SEE.
 XX
 KW Staphylococcal enterotoxin; SE: cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 120 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 121 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123 /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124 /note= "Given in the specification as U, no further
 FT details given"
 XX
 W09324136-A1.
 XX
 PD 09-DEC-1993.
 XX
 PD 01-JUN-1993; 93WO-US005213.
 XX
 PD 01-JUN-1992; 92US-00891718.
 XX
 PA (TERM/) TERMAN D S.
 PA (STON/) STONE J L.
 XX
 PI Terman DS, Stone JL;
 XX
 XX WPI; 1993-405418/50.
 DR

XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX
 PS Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A pertussis system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 230 AA;

Query Match 93.0%; Score 1151; DB 2; Length 230;
 Best Local Similarity 93.9%; Pred. No. 5.5e-107;
 Matches 216; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 4 SEEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 DB 1 SEEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQVORGL 183
 DB 121 XVXXKXWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQVORGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQVDPDILLRIYRDNKTINSENHIALYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQVDPDILLRIYRDNKTINSENHIALYLYTT 230

RESULT 10
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 AC ABB76235;

DT 09-AUG-2002 (first entry)

DE Staphylococcus aureus enterotoxin E.

KW Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 therapy.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
 FH Misc-difference 120

FT /note= "given as 'J' in the specification"

FT Misc-difference 121

FT /note= "given as 'J' in the specification"

FT Misc-difference 123

FT /note= "given as 'O' in the specification"

FT Misc-difference 124

FT /note= "given as 'U' in the specification"

FT Misc-difference 125

FT /note= "given as 'V' in the specification"

XX US2002051765-A1.

XX 02-MAY-2002.

XX 19-DEC-2000; 2000US-00741503.

XX 03-OCT-1989; 89US-00416530.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2002-415198/44.

DR Reagent for treating cancer without the need for e.g. radiotherapy;
 XX comprises a specific V beta subset of T cells sensitized to a growing
 XX tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydrophathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumoricidal reaction

XX Sequence 230 AA;

Query Match 92.6%; Score 1147; DB 5; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.4e-106;

Matches 216; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 4 SEEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 DB 1 SEEINEKDLRKSELOGTALGNLKOIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 60

QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123

DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120

QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQVORGL 183

DB 121 XVXXKXWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQVORGL 180

QY 184 IVFHSSEGSTVSVDLFDAGQVDPDILLRIYRDNKTINSENHIALYLYTT 233

DB 181 IVFHSSEGSTVSVDLFDAGQVDPDILLRIYRDNKTINSENHIALYLYTT 230

RESULT 11

ABP58455

ID ABP58455 standard; protein; 233 AA.

XX ABP58455;

XX 14-APR-2003 (first entry)

XX Engineered superantigen SEA/E-120 for human cancer therapy.

XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;

XX cytostatic; vaccine; SEA/E-120; mutant; mutein.

XX Staphylococcus sp.

XX WO2003002143-A1.
 XX 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001188.
 XX 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX Claim 12; Fig 10; 102pp; English.
 XX The present sequence is a conjugate of a bacterial superantigen and an
 CC antibody moiety, and has been designed to target and destroy cancer
 CC cells. The bacterial superantigen is SEA/E-120 (see also AB58455), which
 CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
 CC of the following amino acid substitutions to reduce seroreactivity whilst
 CC maintaining production levels and biological activity: R20G, N21T, S24G,
 CC R27K, K79E, K81S, K83S and D227S. SEA/E-120 was genetically fused to the
 CC Fab moiety of the tumour reactive antibody 5T4. Substitutions were made
 CC in the 5T4 sequence to obtain higher yields: in the heavy chain, H41P,
 CC S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
 CC T77S, L78V and L63A. An expression vector comprising DNA encoding the
 CC conjugate can be used to transform host cells for recombinant production
 CC of the conjugate. The conjugate is useful for treating cancer, including
 CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
 CC cervix and prostate (claimed)
 XX Sequence 672 AA;
 SQ
 Query Match 91.3%; Score 1130; DB 6; Length 672;
 Best Local Similarity 91.4%; Pred. No. 3.2e-104;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELQGTALGNLQIYYYNKAITENKESDDQFLENTLLFKGFTG 60
 DB 226 SEKSEINEKDLRKSELQGTALGNLQIYYYNKAITENKESDDQFLENTLLFKGFTG 285
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 DB 286 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 458
 RESULT 13
 AAR13204
 ID AAR13204 standard; protein; 230 AA.
 XX AAR13204;
 AC AAR13204;
 XX 15-OCT-1991 (first entry)
 DT Staphylococcal enterotoxin E.
 DE Staphylococcal enterotoxin E.
 XX SEB; cancer treatment; pyrogen; tumouricide.
 KW
 XX

OS Staphylococcus aureus.
 XX WO9110680-A.
 XX 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 XX SEE was isolated and purified from S.aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX Sequence 230 AA;
 SQ
 Query Match 91.1%; Score 1128; DB 2; Length 230;
 Best Local Similarity 91.7%; Pred. No. 1.1e-104;
 Matches 211; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 QY 4 SEBINEKDLRKSELQGTALGNLQIYYYNKAITENKESDDQFLENTLLFKGFTGHPW 63
 DB 1 SEBINEKDLRKSELQGTALGNLQIYYYNKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQVGL 183
 DB 121 XVQXBKWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQVGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 230
 RESULT 14
 AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX AAR13203;
 AC AAR13203;
 XX 15-OCT-1991 (first entry)
 DT Staphylococcal enterotoxin A.
 DE Staphylococcal enterotoxin A.
 XX SEA; cancer treatment; pyrogen; tumouricide.
 KW
 XX Staphylococcus aureus.
 OS
 XX WO9110680-A.
 XX 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX

XX 17-JAN-1990; 90US-00466577.
 XX (TERM/) Terman D S.
 XX Terman DS;
 XX WPI; 1991-237994/32.
 XX
 XX Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity as
 PT *Staphylococcal* protein A without potential toxic reactions.
 XX
 XX Disclosure; Fig 1; 74pp; English.
 XX
 XX SEA was isolated and purified from *S. aureus*. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEA. Synthetic polypeptides having structural homology to
 CC *Staphylococcal* exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See also AAR13204-R13211
 XX
 XX Sequence 233 AA;
 SQ
 Query Match 84.7%; Score 1049; DB 2; Length 233;
 Best Local Similarity 84.1%; Pred. No. 9.7e-97;
 Matches 196; Conservative 16; Mismatches 21; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
 DB 61 HSWYNDLLVDLGSKDIDVKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 121 EEKVPINLMDGKQNTVPLETKNKNQNTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 QY 181 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
 DB 181 RGLIVHSTSTPSVNYDLFDAGQGYSNLLRIYRDNKTINSENHDIYLYTS 233
 RESULT 16
 ID AUP14104 standard; protein; 233 AA.
 AC ABP58458;
 AC ABP58458;
 DT 14-APR-2003 (first entry)
 DE *Staphylococcal* enterotoxin A.
 XX Superantigen; *staphylococcal* enterotoxin A; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX *Staphylococcus* sp.
 OS WO2003002143-A1.
 EN 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001188.
 XX 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PI

XX WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 XX Example 3; Fig 3; 102pp; English.
 XX
 XX The present sequence is the protein sequence of *staphylococcal*
 CC enterotoxin A (SEA). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 XX Sequence 233 AA;
 SQ
 Query Match 83.8%; Score 1037; DB 6; Length 233;
 Best Local Similarity 83.3%; Pred. No. 1.6e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
 DB 61 HSWYNDLLVDLGSKDIDVKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 121 EEKVPINLMDGKQNTVPLETKNKNQNTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 QY 181 RGLIVHSSSGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
 DB 181 RGLIVHSTSTPSVNYDLFDAGQGYSNLLRIYRDNKTINSENHDIYLYTS 233
 RESULT 16
 ID AUP14104 standard; peptide; 257 AA.
 XX
 XX AAU14104;
 XX
 XX 21-NOV-2001 (first entry)
 XX Peptide sequence from *Staphylococcus aureus* enterotoxin A.
 DE Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
 XX antiviral; HIV transmission.
 XX *Staphylococcus aureus*.
 OS WO200151673-A2.
 XX 19-JUL-2001.
 XX 05-JUL-2000; 2000WO-US035727.
 XX 09-JUL-1999; 99US-00350841.
 XX (TRIM-) TRIMERIS INC.
 XX Jeff's P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 XX WPI; 2001-442157/47.
 DR

XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 XX Disclosure; Fig 42; 259pp; English.
 XX
 XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin A
 XX
 XX Sequence 257 AA;

Query Match 83.8%; Score 1037; DB 4; Length 257;
 Best Local Similarity 83.3%; Pred. No. 1.8e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
 Db 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESHDDQFLOHTLLPKGFFTD 84
 QY 61 HPWYNDLLVDSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 Db 85 HSWYNDLLVDPDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144
 QY 121 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVNSDPSFGKVQ 180
 Db 145 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVNSDPSFGKVQ 204
 QY 181 RGLIVFHSSEGSTVSYDLDFAQQGYPTDILLRIYRDNKTINSENHLIALYLT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 17
 ABO10269
 ID ABO10269 standard; protein; 257 AA.
 XX
 AC ABO10269;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 XX *S. aureus* enterotoxin A.
 DE
 DE HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.
 XX
 XX *Staphylococcus aureus*.
 OS
 XX
 PN US6518013-B1.
 XX
 PD 11-FEB-2003.
 XX
 PF 07-JUN-1995; 95US-00485546.
 XX
 XX 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX

PA (TRIM-) TRIMERIS INC.
 XX
 XX Barney SO, Lambert DM, Petteway SR;
 XX WPI; 2003-465599/44.
 XX
 XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 XX
 XX Example; Fig 42; 716pp; English.
 XX
 XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 16-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLMOT15,
 CC 107x178x4 or PIZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 XX Sequence 257 AA;

Query Match 83.8%; Score 1037; DB 6; Length 257;
 Best Local Similarity 83.3%; Pred. No. 1.8e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
 Db 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESHDDQFLOHTLLPKGFFTD 84
 QY 61 HPWYNDLLVDSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 Db 85 HSWYNDLLVDPDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144
 QY 121 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVNSDPSFGKVQ 180
 Db 145 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVNSDPSFGKVQ 204
 QY 181 RGLIVFHSSEGSTVSYDLDFAQQGYPTDILLRIYRDNKTINSENHLIALYLT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 18
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX
 AC ADD44368;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX *Staphylococcus aureus* enterotoxin A protein.
 DE
 DE enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 KW ice cream.
 KW
 XX *Staphylococcus aureus*.
 OS
 XX
 PN WO2003080865-A1.
 XX

PD 02-OCT-2003.
 XX 26-MAR-2002; 2002WO-IB001150.
 PF 26-MAR-2002; 2002WO-IB001150.
 PR (COUL) COUNCIL SCI & IND RES.
 XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
 PI WPI; 2003-779273/73.
 DR N-PSDB; ADD44363.
 XX Novel oligonucleotide primers directed against enterotoxin A gene of
 PT Staphylococcus aureus and heat stable enterotoxin gene of *Yersinia*
 PT enterocolitica, useful for detecting food poisoning causing bacteria.
 XX Example 2; Page 14-15; 34pp; English.
 PS The invention relates to novel oligonucleotide primers directed against
 CC enterotoxin A gene (ent A) of *Staphylococcus aureus* and heat stable
 CC enterotoxin gene (yst) of *Yersinia enterocolitica*. The novel
 CC oligonucleotide primers are useful for simultaneously detecting food
 CC poisoning bacterial species *Staphylococcus aureus* and/or *Yersinia*
 CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
 CC without prior enrichment for preventing food poisoning outbreak. The PCR
 CC detection method is useful for detecting the bacteria strains in quantity
 CC as low as one cell. The method can be directly used for detecting
 CC bacterial strains. The oligonucleotide primers allow quick and highly
 CC sensitive detection of the food poisoning bacterial species. This
 CC sequence represents the protein derived from the enterotoxin A gene from
 CC *Staphylococcus aureus* of the invention.
 XX Sequence 257 AA;
 SQ

Query Match 83.8%; Score 1037; DB 7; Length 257;
 Best Local Similarity 83.8%; Pred. No. 1.8e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKKELOQTALGNLKOIYYNEKAITENKESHDFLOHTLLFKGFFTD 84
 Qy 61 HPYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 120
 Db 85 HSYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLT 144
 Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
 Db 145 EEKVPINLWIDGKQNTVPLETKNKQNTVPLETKNKQNTVPLETKNKQNTVPLETKNKQNTVP 204
 Qy 181 RGLIVFHSSGSGTSVYDLFDAQGQYPTLLRIYRDNKTINSENHLIALYTT 233
 Db 205 RGLIVFHTSTSPSVNYDLFDAQGQYNTLLRIYRDNKTINSENMHIDILYTS 257

RESULT 19
 AAW06738
 ID AAW06738 standard; protein; 233 AA.
 XX AAW06738;
 AC
 XX 08-MAR-1997 (first entry)
 DT
 XX Staphylococcus enterotoxin A.
 DE
 XX Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
 KW adjuvant.
 XX
 OS Staphylococcus sp.
 XX
 XX WO9636366-A1.
 PN

XX 21-NOV-1996.
 PD 20-MAY-1996; 96WO-US007432.
 XX 18-MAY-1995; 95US-00446918.
 PR 29-DEC-1995; 95US-00580806.
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX Dow SW, Elmelle RE, Potter TA;
 PI WPI; 1997-011857/01.
 DR N-PSDB; AAT45699.
 XX Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer.
 XX Example 1; Page 98-99; 131pp; English.
 PS A CDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
 CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
 CC AAW06739), esp. truncated forms of the superantigen lacking the leader
 CC peptide, can be used in the gene therapy of cancer, infectious diseases
 CC and immunological disorders. The nucleic acid, optionally in combination
 CC with cytokine or chemokine nucleic acids, is delivered to an animal using
 CC e.g. liposomes. It acts by controlling the activity of effector cells,
 CC such as T-cells, macrophages, monocytes and/or natural killer cells.
 CC Localised prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal
 XX Sequence 233 AA;
 SQ

Query Match 83.4%; Score 1033; DB 2; Length 233;
 Best Local Similarity 83.2%; Pred. No. 3.9e-95;
 Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKKELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
 Db 2 EKSEINEKDLRKKELOQTALGNLKOIYYNEKAITENKESHDFLOHTLLFKGFFTD 61
 Qy 62 PNYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLTE 121
 Db 62 SWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAQMGVTLHNNRLTE 121
 Qy 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 181
 Db 122 EKKVPINLWIDGKQNTVPLETKNKQNTVPLETKNKQNTVPLETKNKQNTVPLETKNKQNTVP 181
 Qy 182 GLIVFHSSGSGTSVYDLFDAQGQYPTLLRIYRDNKTINSENHLIALYTT 233
 Db 182 GLIVFHTSTSPSVNYDLFDAQGQYNTLLRIYRDNKTINSENMHIDILYTS 233

RESULT 20
 AAW35373
 ID AAW35373 standard; peptide; 233 AA.
 XX AAW35373;
 AC
 XX 20-APR-1998 (first entry)
 DT
 XX Staphylococcus enterotoxin SEA wild-type superantigen.
 DE
 XX SEA; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody.
 KW
 OS Staphylococcus sp.
 XX
 XX WO9736932-A1.
 XX
 XX 09-OCT-1997.
 PD

XX PF 26-MAR-1997; 97WO-SE000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PHAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kaalland T;
XX PI Abrahmsen L, Forsberg G;
XX DR WPI; 1997-503052/46.
XX PT Conjugate of target seeking moiety and modified superantigen - useful for
XX PT activating the immune system to treat cancer, viral infections, parasitic
XX PT infestations and autoimmune diseases.
XX PS Claim 8; Page 36-37; 58pp; English.
XX CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
XX CC SEA superantigen can be modified to be used in a novel conjugate. The
XX CC novel conjugate comprises a target seeking moiety and a modified wild
XX CC type superantigen. The modified superantigen retains its ability to
XX CC activate a subset of T cells, even though 1 or more wild-type amino acid
XX CC residues in at least 1 region which functions in determining binding to T
XX CC cell receptor (TCR) and activation of a subset of T cells has/have been
XX CC replaced. Such a modified superantigen can optionally be used as part of
XX CC a conjugate with a target seeking moiety, for activating the immune
XX CC system to treat a mammalian disease. A pharmaceutical composition can be
XX CC prepared comprising a modified antibody (preferably a Fab fragment fused
XX CC to a peptide moiety providing activation of T cells in Vbeta specific
XX CC manner) in which cysteines providing for interchain cysteine linkages in
XX CC the native antibody have been replaced (preferably by serine residues) to
XX CC prohibit cysteine formation. The modified wild-type superantigen is used
XX CC for treating cancer, viral infections, parasitic infestations and
XX CC autoimmune disease. The modified wild type superantigen has a lower
XX CC immunogenicity and reactivity with neutralising antibodies and has fewer
XX CC side-effects when used as a drug, compared to wild type superantigen

SQ Sequence 233 AA;

Query Match 83.2%; Score 1030; DB 2; Length 233;
Best Local Similarity 82.8%; Pred. No. 7.8e-95;
Matches 193; Conservative 16; Mismatches 24; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKVPINLWLDGKQNTVPLETVKTNKNTVQELDLQARRYLOEKXNLYNSDVDFGKVQ 180
QY 181 RGLIVFHSSGTSVYDLFPAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQGYNSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 21
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX AC AAB67338;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin A protein.
XX KW Tumour; cancer; immune; enterotoxin.

XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX PA (TERM/) Terman D S.
XX PI Terman DS;
XX DR WPI; 2001-158657/16.
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX SQ Sequence 233 AA;
Query Match 83.2%; Score 1030; DB 4; Length 233;
Best Local Similarity 82.8%; Pred. No. 7.8e-95;
Matches 193; Conservative 16; Mismatches 24; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLOHTLLFKGFFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKVPINLWLDGKQNTVPLETVKTNKNTVQELDLQARRYLOEKXNLYNSDVDFGKVQ 180
QY 181 RGLIVFHSSGTSVYDLFPAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQGYNSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 22
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX AC AAR45011;
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1994 (first entry)
XX DE Staphylococcal enterotoxin SEA.
XX KW Staphylococcal enterotoxin; SE; cancer; tumoricidal agent;
XX KW autoimmune disease; toxicity; Protein A; perfusion system.

XX OS Staphylococcus aureus.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 49
 XX FT /note= "Given in the specification as O, no further
 XX PN details Given"
 XX PN WO9324136-A1.
 XX PD 09-DEC-1993.
 XX PF 01-JUN-1993; 93WO-US005213.
 XX PR 01-JUN-1992; 92US-00891718.
 XX PA (TERM/) TERMAN D S.
 XX PA (STON/) STONE J L.
 XX PI Terman DS, Stone JL;
 XX DR WPI; 1993-405418/50.
 XX PS
 XX PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 XX PT in a patient or for the treatment of auto-immune diseases.
 XX PS Disclosure; Fig 1; 90pp; English.
 XX CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 XX CC which may be used in the methods of the invention for treating cancer in
 XX CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 XX CC agents for treating cancers and autoimmune disease. They exhibit
 XX CC tumouricidal activity and toxicity identical to that observed for the
 XX CC protein A perfusion system. They may be administered by i.v. injection.
 XX CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 233 AA;
 Query Match 83.0%; Score 1027; DB 2; Length 233;
 Best Local Similarity 82.8%; Pred. No. 1.6e-94;
 Matches 193; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
 OY 1 SEKSEENEDLRKXSELOQTALGNLQIYYNEKAITENKSDDOFLENTLLFKGFTG 60
 DB 1 SEKSEENEDLRKXSELOQTALGNLQIYYNEKAITENKSDDOFLENTLLFKGFTG 60
 OY 61 HPWYNLLVLDLGSKDATNKYKGRKVDLYGAYGYQYQAGGTPNKTACMYGGVTLHDNNRIT 120
 DB 61 HSWYNLLVDFDSKDIVDKYKGRKVDLYGAYGYQYQAGGTPNKTACMYGGVTLHDNNRIT 120
 OY 121 BEKVPINLMDGKQTTVPIDKVKTSKVTVOELQARHYLKGFGVNSDFGKQV 180
 DB 121 BEKVPINLMDGKQNTVPLETKNKGVTVQELDPQARRYLQEKINLYNSDVFQV 180
 OY 181 RGLIVFRSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLHLYLTT 233
 DB 181 RGLIVFHTSTEPSVYDLFGAQGYSTLLRLIYRDNKTINSENHDIYLYTS 233
 RESULT 23
 ABU79068
 ID ABU79068 standard; protein; 257 AA.
 AC ABU79068;
 XX AC
 XX DT 18-JUN-2003 (first entry)
 XX DE S. aureus SEA (staphylococcus enterotoxin A) protein.
 XX KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 XX KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
 XX KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 XX KW APC; antitumour.

XX OS Staphylococcus aureus.
 XX PN US2002177551-A1.
 XX XX 28-NOV-2002.
 XX PF 30-MAY-2001; 2001US-00870759.
 XX PR 31-MAY-2000; 2000US-0208128P.
 XX PA (TERM/) TERMAN D S.
 XX PI Terman DS;
 XX DR WPI; 2003-361759/34.
 XX DR N-PSDB; ACA64694.
 XX CC A mammalian cell receptor, useful in the treatment of cancer by binding
 XX CC to tumor associated lipids where the binding induces energy or apoptosis
 XX CC in T cells and antigen presenting cells.
 XX PS Disclosure; Page; 167pp; English.
 XX CC The invention relates to a mammalian cell receptor, useful in the
 XX CC treatment of cancer, which binds to tumour associated lipids and induces
 XX CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 XX CC Also included are a mammalian cell useful in the treatment of cancer
 XX CC where the receptor which binds tumour associated lipids and induces
 XX CC cellular inactivation or death is deleted or functionally deactivated,
 XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 XX CC (by allowing tumour associated lipids to contact immunocytes in which
 XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 XX CC deleted), a construct useful in the treatment of cancer comprising a
 XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 XX CC useful in the treatment of cancer (where an adaptor protein which
 XX CC inhibits T cell activation by tumour associated antigens is deleted or
 XX CC functionally deactivated), a composition useful in the treatment of
 XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 XX CC allowing tumour associated lipids to contact immunocytes, in which
 XX CC receptors for the lipids are inactivated or deleted to produce a
 XX CC tumouricidal immunocyte population, and administering the tumouricidal
 XX CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 XX CC contact APCs, in which receptors for the tumour associated lipids are
 XX CC inactivated or deleted to produce a tumouricidally activated population,
 XX CC and administering APCs to the host), producing a tumouricidal T cell
 XX CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 XX CC contact T cells, in which adaptor proteins, which inhibit T cell
 XX CC activation to produce a tumouricidal population of T cells, and
 XX CC administering the tumouricidally activated T cells to the host, or
 XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 XX CC administering the tumouricidally activated T cells to the host), treating
 XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 XX CC tumour associated antigen to contact immunocytes in which adaptor
 XX CC proteins which inhibit T cell activation by tumour associated antigens
 XX CC are deleted or functionally deactivated) and producing (M7) a
 XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 XX CC superantigen methods and compositions are useful for treating cancers and
 XX CC tumours. Bacterial superantigens are co-administered or administered as
 XX CC fusion constructs with anti-tumour proteins or motifs. The present
 XX CC sequence represents a bacterial superantigen protein (e.g. a
 XX CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 XX CC not form part of the printed specification, but was obtained in
 XX CC electronic format from the US patent office website at
 XX CC "seqdata.uspto.gov/sequence.html?docID=20020177551"

XX Sequence 257 AA;
SQ
Query Match 82.7%; Score 1024; DB 6; Length 257;
Best Local Similarity 82.4%; Pred. No. 3.6e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTN 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 BEKKVPINLWDGKQNTVPLETKNKNVTQVQELDQARHYLHGKGLYNSDSVDFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHIDIYLYTS 257
RESULT 24.
ID ABB76234 standard; protein; 233 AA.
XX ABB76234;
AC ABB76234;
XX
DT 09-AUG-2002 (first entry)
XX
DE Staphylococcus aureus enterotoxin A.
XX
KW Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
KW therapy.
XX
OS Staphylococcus aureus.
XX
PH Key Location/Qualifiers
FT Misc-difference 49
FT /note= "amino acid residue given as 'O' in the
FT specification"
XX
PN US2002051765-A1.
XX
PD 02-MAY-2002.
XX
PF 19-DEC-2000; 2000US-00741503.
XX
PR 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
XX WPI; 2002-415198/44.
DR
XX
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX
XX Disclosure; Fig 2; 17pp; English.
PS
XX
XX The present sequence is the protein sequence of enterotoxin A (SEA) of
CC Staphylococcus aureus. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic

CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydropathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX
SQ Sequence 233 AA;
Query Match 82.2%; Score 1018; DB 5; Length 233;
Best Local Similarity 82.4%; Pred. No. 1.3e-93;
Matches 192; Conservative 15; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKGLYNSDSFGKVKQ 180
DB 121 BEKKVPINLWDGKQNTVPLETKNKNVTQVQELDQARHYLHGKGLYNSDSVDFGKVKQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHIALYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHIDIYLYTS 233
RESULT 25
ID ABB79501 standard; protein; 257 AA.
XX ABB79501;
XX
DT 23-SEP-2002 (first entry)
XX
DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).
XX
KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;
KW attenuation; mutant; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..257
FT /label= Mature_protein
FT Misc-difference 72
FT /note= "wild-type Leu substituted by Arg"
FT Misc-difference 94
FT /note= "wild-type Asp substituted by Arg"
FT Misc-difference 116
FT /note= "wild-type Tyr substituted by Ala"
XX
XX US6399332-B1.
XX
XX 04-JUN-2002.
XX
XX 01-SEP-1998; 98US-00144776.
XX
XX

PR 25-JUN-1997; 97US-00882431.
 PA (USSA) US SEC OF ARMY.
 PI Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2002-546281/58.
 DR N-PSDB; ABN84222.
 XX
 PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 PS Claim 4; Col 33-35; 46pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The full-length expressed product is secreted into the periplasmic space
 CC of *Escherichia coli* host cells, and the leader peptide is recognised and
 CC cleaved by a native mechanism. The vaccine is used to protect against
 CC superantigen toxin infections. Superantigen attributes are absent, but
 CC the superantigen is effectively recognised by the immune system and an
 CC appropriate antibody response is produced. In examples from the
 CC invention, attenuated superantigen toxins were shown to protect animals
 CC against challenge with wild-type toxin. Methods of producing and using
 CC the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TSGT-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 5; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFROHTILFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWLDGKQNTVPLETKNKVNTVQELDLQARRYLQEKYLNYSDFDGKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHTSTEPSVNDLFGAQQQYNTLLRIYRDNKTINSENHMDIYLYTS 257
 RESULT 26
 ABU10081
 ID ABU10081 standard; protein; 257 AA.
 XX
 AC ABU10081;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin A #1.
 XX
 KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 KW superantigen toxin.
 XX
 OS Staphylococcus sp.
 XX
 PN US2003009015-A1.

XX 09-JAN-2003.
 PD
 XX 25-JUN-1997; 97US-00882431.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2003-401542/38.
 DR N-PSDB; ACA61177.
 XX
 PT New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 PS Claim 10; Page 18-19; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #1
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 6; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFROHTILFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWLDGKQNTVPLETKNKVNTVQELDLQARRYLQEKYLNYSDFDGKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHTSTEPSVNDLFGAQQQYNTLLRIYRDNKTINSENHMDIYLYTS 257
 RESULT 27
 ABU62324
 ID ABU62324 standard; protein; 257 AA.
 XX
 AC ABU62324;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE S. aureus periplasmic enterotoxin A mutant #1.
 XX
 KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX

```

OS Staphylococcus aureus.
XX Synthetic.
FH Key
FT Peptide
FT /label= Signal_peptide
FT Protein
FT 25..257
FT /label= Mature_SEA_mutant #1
FT Misc-difference
FT /note= "Wild-type Leu substituted by Glu"
FT Misc-difference
FT /note= "Wild-type Leu substituted by Arg"
FT Misc-difference
FT /note= "Wild-type Asp substituted by Arg"
FT Misc-difference
FT /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference
FT /note= "Wild-type Tyr substituted by Ala"
XX
FN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
XX
PF 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28894.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Disclosure; Page 22-23; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TST-1 superantigen toxin and an antibody which recognises altered TST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the
CC mature protein sequence) mutant of periplasmic SEA
XX
SQ Sequence 257 AA;
Query Match 81.9%; Score 1014; DB 7; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.6e-93;
Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLEQGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFFTG 60
DB 25 SEKSEINEKDLRKKSLEQGTALGNLKOIYYNEKAITENKESHDPQFQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDITVDKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLOEKYNLYNSDVFQKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAGQGYPDTLRIYRDKNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDVFAGQGYSENTLLRIYRDKNKTINSENMHIDIYLYTS 257

```

RESULT 28

AAE37676

ID AAE37676 standard; protein; 257 AA.

XX

AC AAE37676;

XX

DT 06-OCT-2003 (first entry)

XX

DE Protein #1 related to the invention.

XX

XW Superantigen toxin; vaccine; infection; gene therapy.

XX

OS Unidentified.

XX

XN WO2003056015-A1.

XX

PD 10-JUL-2003.

XX

PF 26-NOV-2001; 2001WO-US046540.

XX

PR 26-NOV-2001; 2001US-00002784.

XX

PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX

PI Ulrich RG;

XX

DR WPI; 2003-492125/46.

XX

DR N-PSDB; AAD56764.

XX

PT New superantigen toxin DNA fragment, useful for preparing a composition

PT

for treating or preventing bacterial infection.

XX

PS Disclosure; Page 108-109; 141pp; English.

XX

CC The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is a protein related to the
 CC invention

XX

SQ Sequence 257 AA;

XX

Query Match 81.9%; Score 1014; DB 7; Length 257;

XX

Best Local Similarity 82.0%; Pred. No. 3.6e-93;

XX

Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY

1 SEKSEINEKDLRKKSLEQGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFFTG 60

DB

25 SEKSEINEKDLRKKSLEQGTALGNLKOIYYNEKAITENKESHDPQFQHTILFKGFFTD 84

QY

61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 120

DB

85 HSWYNDLLVRFDSKDITVDKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 144

QY

121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180

DB

145 EEKKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLOEKYNLYNSDVFQKQV 204

QY

181 RGLIVFHSSEGSTVSYDLFDAGQGYPDTLRIYRDKNKTINSENHLIALYLYTT 233

XX

Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 29
 AAY54463
 ID AAY54463 standard; protein; 233 AA.
 AC AAY54463;
 XX
 XX
 XX 25-APR-2000 (first entry)
 XX
 XX Amino acid sequence of a mutant Staphylococcal enterotoxin A.
 XX
 XX Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
 KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
 KW Staphylococcal intoxication; Staphylococcus exotoxin.
 XX
 XX Staphylococcus aureus.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "Glu encoded by AGAA"
 FT Misc-difference 4
 FT Misc-difference 4 /note= "Ser encoded by C"
 FT
 FT
 XX WO200002523-A2.
 XX
 XX 20-JAN-2000.
 XX
 XX 09-JUL-1999; 99WO-US015569.
 XX
 XX 10-JUL-1998; 98US-0092416P.
 XX
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 PA
 XX Lee JS, Pushko P, Smith JF, Ulrich RG;
 PI
 XX WPI; 2000-160826/14.
 DR N-PSDB; AA245833.
 DR
 XX New DNA construct useful as vaccines against enterotoxins of
 FT Staphylococcus aureus which causes gastrointestinal distress, or toxic
 PT shock syndrome.
 PT
 XX Disclosure; Page 28; 30pp; English.
 PS
 XX The present sequence is represents a mutant Staphylococcal enterotoxin A.
 CC It is encoded by a mutant SEA gene. The mutant gene product is unable to
 CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes
 CC were inserted into a Venezuelan equine encephalitis (VEE) replicon
 CC vector, to produce vaccine vectors. The mutant gene product is unable to
 CC bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA
 CC derived from the recombinant VEE vectors can be used as a nucleic acid
 CC vaccine, or to transfect cells along with RNA from helper plasmids. The
 CC recombinant proteins produced are used as vaccines for providing immunity
 CC against Staphylococcal intoxication or as a diagnostic tool for detection
 CC of Staphylococcus exotoxin. The transformed host cells are used to
 CC analyse the effectiveness of drugs and agents which inhibit S. aureus
 CC exotoxins or release of exotoxins. Infectious alpha-virus particles
 CC comprising the mutant SEA or SEB genes are used for providing immunity
 CC against Staphylococcal exotoxins by generating a protective immune
 CC reaction in humans or animals. The vaccines are used to reduce disease
 CC symptoms or reduce severity of disease caused by enterotoxins of S.
 CC aureus
 XX
 XX Sequence 233 AA;
 SQ
 Query Match 81.6%; Score 1010; DB 3; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHDOFROHTILFKGFFTDH 61
 |||||

Db 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAKTENKESHDOFROHTILFKGFFTDH 61

Qy 62 PWYNDLLVLSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACWYGGVTLHDNNRLTE 121
 |||||
 Db 62 SWYNDLLVRFDSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTACWYGGVTLHDNNRLTE 121
 |||||
 Qy 122 EKVPINLWIDGKOTTPIDIKVTKSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
 |||||
 Db 122 EKVPINLWIDGKOTTPIDIKVTKSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
 |||||
 Qy 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHDIYLYTT 233
 |||||
 Db 182 GLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 233
 |||||

RESULT 30
 ABB79502
 ID ABB79502 standard; protein; 233 AA.
 XX
 XX ABB79502;
 XX
 XX 23-SEP-2002 (first entry)
 XX
 XX Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).
 DE Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
 KW attenuation; mutant; mutein.
 KW
 XX Staphylococcus sp.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "encoded by AT, apparent frameshift"
 FT Misc-difference 48
 FT Misc-difference 70 /note= "wild-type Leu substituted by Arg"
 FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
 FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
 FT
 XX US6399332-B1.
 PN
 XX 04-JUN-2002.
 PD
 XX 01-SEP-1998; 98US-00144776.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR (USSA) US SEC OF ARMY.
 PA
 XX Ulrich RG, Olson MA, Bavari S;
 PI
 XX WPI; 2002-546281/58.
 DR N-PSDB; ABN84223.
 DR
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 PT
 XX Claim 5; Col 37-39; 46pp; English.
 PS
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The protein is expressed as a nonsecreted product within host Escherichia
 CC coli cells. The vaccine is used to protect against superantigen toxin
 CC infections. Superantigen attributes are absent, but the superantigen is
 CC effectively recognised by the immune system and an appropriate antibody
 CC response is produced. In examples from the invention, attenuated
 CC superantigen toxins were shown to protect animals against challenge with

CC wild-type toxin. Methods of producing and using the altered superantigen
CC toxins as vaccines, and in diagnosis and therapy, are provided. A
CC multivalent vaccine consisting of altered superantigen toxins from SEA,
CC SEA, SEC-1, TSST-1 and streptococcal SPA is predicted to provide
CC protective immunity against the majority of bacterial superantigen toxins
XX
SQ Sequence 233 AA;

Query Match 81.6%; Score 1010; DB 5; Length 233;
Best Local Similarity 81.9%; Pred. No. 8e-93;
Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
QY 62 PWYNDLLVLDGSKDNTKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVYKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYNLYNSDVFQGVQR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHIDILYLYTS 233

RESULT 31
ABU10082
ID ABU10082 standard; protein; 233 AA.
XX
AC ABU10082;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcal enterotoxin A #2.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX
OS Staphylococcus sp.

Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by AT"
XX
XX US2003009015-A1.
XX
PD 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
FI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
DR N-PSDB; ACA61178.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.

Claim 11; Page 20-21; 50pp; English.
PS
XX
XX The invention relates to an isolated and purified superantigen toxin
CC

CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC A #2

XX
SQ Sequence 233 AA;
Query Match 81.6%; Score 1010; DB 6; Length 233;
Best Local Similarity 81.9%; Pred. No. 8e-93;
Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
QY 62 PWYNDLLVLDGSKDNTKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVYKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYNLYNSDVFQGVQR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHIDILYLYTS 233

RESULT 32
ABU62325
ID ABU62325 standard; protein; 233 AA.
XX
AC ABU62325;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus cytoplasmic enterotoxin A mutant #1.
XX
KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Staphylococcus aureus.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 1.2 /note= "Encoded by ATGAG"
FT Misc-difference 42 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 48 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 70 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 89 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 92 /note= "Wild-type Tyr substituted by Ala"
XX

US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-0002784.
XX
XX 25-JUN-1997; 97US-00882431.
PR

PR 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRICH R G.
 XX PI Ulrich RG;
 XX WPI; 2003-492125/46.
 XX DR N-PSDB; ACD28895.
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX Disclosure; Page 24-25; 68pp; English.
 XX The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SECL) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
 CC SEA
 XX SQ Sequence 233 AA;
 Query Match 81.6%; Score 1010; DB 7; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFETH 61
 DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFETH 61
 QY 62 PWYNDLLVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQABHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQABHYLHGKFLYNSDSFGKQVOR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDILYLYTS 233
 RESULT 33
 AAEE37677
 ID AAE37677 standard; protein; 233 AA.
 AC AAE37677;
 XX 06-OCT-2003 (first entry)
 DT Protein #2 related to the invention.
 DE Superantigen toxin; vaccine; infection; gene therapy.
 KW Unidentified.
 XX Location/Qualifiers
 XX Key

FT Misc-difference 1 /note= "Encoded by AT"
 XX W02003056015-A1.
 XX 10-JUL-2003.
 XX 26-NOV-2001; 2001WO-US046540.
 XX 26-NOV-2001; 2001US-00002784.
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX Ulrich RG;
 XX WPI; 2003-492125/46.
 XX N-PSDB; AAD56765.
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX Disclosure; Page 110-112; 141pp; English.
 XX The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is a protein related to the
 CC invention
 XX SQ Sequence 233 AA;
 Query Match 81.6%; Score 1010; DB 7; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFETH 61
 DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFETH 61
 QY 62 PWYNDLLVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQABHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDQABHYLHGKFLYNSDSFGKQVOR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDILYLYTS 233
 RESULT 34
 ABU10099
 ID ABU10099 standard; protein; 233 AA.
 AC ABU10099;
 XX 11-AUG-2003 (first entry)
 DT Staphylococcus enterotoxin A K14E substitution mutant.
 DE Staphylococcus enterotoxin A K14E substitution mutant.
 KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
 XX superantigen toxin; vaccine; mitein.
 OS Staphylococcus sp.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Misc-difference 14 /note= "Wild-type Lys substituted by Glu"
 FT

```

XX PN US2003009015-A1.
XX PD 09-JAN-2003.
XX PF 25-JUN-1997; 97US-00882431.
XX PR 25-JUN-1997; 97US-00882431.
XX PA (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX Example 7; Page; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the staphylococcus
XX enterotoxin A K4E mutant. Note: The present sequence is not present in
XX the specification but was created by the indexer from the wild-type
XX staphylococcus enterotoxin A sequence (see ACA61178)
XX SQ Sequence 233 AA;

Query Match 81.3%; Score 1006; DB 6; Length 233;
Best Local Similarity 81.5%; Pred. No. 2e-92;
Matches 189; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESHDPQHQHLLFKGFTDH 61

QY 62 PWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKKVPINLWDGKQTTVPLETVTNKKNVTVPQELDLQARRYLQEKYLYNSDVFQKQVOR 181

QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKNTINSENHLALVLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 35
ABU10098
ID ABU10098 standard; protein; 233 AA.
XX ABU10098;
XX AC
XX DT 11-AUG-2003 (first entry)
XX Staphylococcus enterotoxin A Y64A substitution mutant.
XX Enterotoxin A; superantigen-associated bacterial infection; mutant;

```

```

KW superantigen toxin; vaccine; mutain.
XX Staphylococcus sp.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
XX US2003009015-A1.
XX 09-JAN-2003.
XX 25-JUN-1997; 97US-00882431.
XX 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX Example 7; Page; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the staphylococcus
XX enterotoxin A Y64A mutant. Note: The present sequence is not present in
XX the specification but was created by the indexer from the wild-type
XX staphylococcus enterotoxin A sequence (see ACA61178)
XX SQ Sequence 233 AA;

Query Match 80.9%; Score 1001; DB 6; Length 233;
Best Local Similarity 81.5%; Pred. No. 6.4e-92;
Matches 189; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESHDPQHQHLLFKGFTDH 61

QY 62 PWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKKVPINLWDGKQTTVPLETVTNKKNVTVPQELDLQARRYLQEKYLYNSDVFQKQVOR 181

QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKNTINSENHLALVLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 36
AAV70102
ID AAY70102 standard; protein; 257 AA.

```

XX AAY70102;
 AC
 DT 05-JUN-2000 (first entry)
 XX
 DE Staphylococcal enterotoxin A.
 XX
 KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
 KW treatment; superantigen-associated bacterial infection.
 XX
 OS Staphylococcus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 2..25
 FT Protein /label= Leader_peptide
 FT 26..253
 FT /label= Mature Staphylococcal enterotoxin A
 FT /note= "Includes transcription start site residue, Met"
 FT Misc-difference 42
 FT /note= "Encoded by TTG"
 FT Misc-difference 125
 FT /note= "Encoded by CCA"
 FT
 FT WO200009154-A1.
 PN
 XX
 PD 24-FEB-2000.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 XX
 XX (REED-) REED ARMY INST RES WALTER.
 XX
 XX Ulrich RG, Olson MA, Bavari S;
 PI
 XX WPI; 2000-224177/19.
 DR
 DR N-PSDB; AA251105.
 XX
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections.
 PT
 XX Claim 7; Page 72-73; 118pp; English.
 XX
 XX The present amino acid sequence is the Staphylococcal enterotoxin A
 CC (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
 CC toxin when altered by site directed mutagenesis, results in disruption of
 CC binding of the toxin to both the MHC class II or T-cell antigen receptor.
 CC SEA has antibacterial and cytostatic activity. This sequence is useful
 CC for the production of SEA vaccines and specific antibodies. This vaccine
 CC overcomes the disadvantages of the chemically inactivated toxoids and is
 CC designed to protect individuals against one or several related
 CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
 CC treatment or amelioration of superantigen-associated bacterial
 CC infections
 XX
 XX Sequence 257 AA;
 SQ
 Query Match 80.5%; Score 997; DB 3; Length 257;
 Best Local Similarity 81.1%; Pred. No. 1.9e-91;
 Matches 189; Conservative 16; Mismatches 28; Indels 0; Gaps 0;
 1 SEKSEINEKDLKKSELOQTALGNLKQIYYNEKAITENKSDDDQFLENTLLFKGFFTG 60
 25 SEKSEINEKDLKKSEKQGTALGNLKQIYYNEKAITENKSHDQFROHTILFKGFFTD 84
 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTFNKTACMYGGVTLHNNRLT 144
 121 EEKKVPINLMDGKQTTVPIDKVKTSKKEVTVQELDQARRYLHGKFGLYNSDSFGKVKQ 180

Db 145 EEKKVPINLMDGKQNTVPLETVKTKNKNVTQELDQARRYLQEKYNLYNSDVFSGKVQ 204
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRLRYDRNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRLRYDRNKTINSENHLDIVLYTS 257
 RESULT 37
 AAY70103
 ID AAY70103 standard; protein; 233 AA.
 XX
 AC AAY70103;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Mutant Staphylococcal enterotoxin A for vaccine A489270P.
 XX
 KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
 KW treatment; superantigen-associated bacterial infection; A489270P.
 XX
 OS Staphylococcus sp.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..233
 FT /label= Mature Staphylococcal enterotoxin_A
 FT /note= "Mutant sequence without the leader peptide"
 FT Misc-difference 2
 FT /note= "Encoded by AG"
 FT
 FT Misc-difference 18
 FT /note= "Encoded by TTG"
 FT
 FT Misc-difference 48
 FT /note= "Wild type leu substituted with Arg"
 FT
 FT Misc-difference 70
 FT /note= "Wild type asp substituted with Arg"
 FT
 FT Misc-difference 92
 FT /note= "Wild type Tyr substituted with Ala"
 FT
 FT Misc-difference 157
 FT /note= "Encoded by CTT"
 FT
 FT Misc-difference 180
 FT /note= "Encoded by CAG"
 FT
 XX WO200009154-A1.
 PN
 XX
 PD 24-FEB-2000.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 XX
 XX (REED-) REED ARMY INST RES WALTER.
 XX
 XX Ulrich RG, Olson MA, Bavari S;
 PI
 XX WPI; 2000-224177/19.
 DR
 DR N-PSDB; AA251106.
 XX
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections.
 PT
 XX Claim 8; Page 74-76; 118pp; English.
 XX
 XX The present amino acid sequence is the mutant Staphylococcal enterotoxin
 CC A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
 CC of SEA vaccine A489270P. The coding region of this SAG toxin is altered
 CC by site directed mutagenesis, that results in disruption of binding of
 CC the toxin to both the MHC class II or T-cell antigen receptor. This
 CC altered SAG toxin has the leader peptide cleaved by native bacterial
 CC enzymatic mechanism and the first residue of the mature protein is
 CC encoded by the transcriptional start site (ATG). SEA has antibacterial
 CC and cytostatic activity. This sequence is useful for the production of
 CC SEA vaccines and specific antibodies. This vaccine overcomes the

CC disadvantages of the chemically inactivated toxoids and is designed to
 CC protect individuals against one or several related staphylococcal and
 CC streptococcal toxins. It is used for the diagnosis and treatment or
 CC amelioration of superantigen-associated bacterial infections
 XX
 SQ Sequence 233 AA;
 Query Match 80.1%; Score 992; DB 3; Length 233;
 Best Local Similarity 80.6%; Pred. No. 5.1e-91;
 Matches 187; Conservative 16; Mismatches 29; Indels 0; Gaps 0;
 QY 2 EKSEBINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 Db 2 EKSEBINEKDLRKSEKOGTALGNLKQIYYNEKAITENKESHQFROHTLLFKGFTDH 61
 QY 62 PWYNDLLVDSGSKDATNYKGGKVDLYGAYGYCAGGTPNKTCMYGGVTLHDNRILTE 121
 Db 62 SWYNDLLVDFSDIDYKGGKVDLYGAYGYCAGGTPNKTCMYGGVTLHDNRILTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHLYHGKFGLYNSDSFGKVQR 181
 Db 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHLYHGKFGLYNSDSFGKVQR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGQVPTLLRYRDNKTINSNLHIALYLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFDAQGQVPTLLRYRDNKTINSNMHIDIYLYTS 233
 RESULT 38
 ABU79071
 ID ABU79071 standard; protein; 258 AA.
 AC ABU79071;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE S. aureus SED (staphylococcus enterotoxin D) protein.
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW Gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 KW APC; antitumour.
 XX
 OS Staphylococcus aureus.
 XX
 FN US2002177551-A1.
 PN
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 XX
 PA (TERM//) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2003-361759/34.
 DR N-PSDB; ACA64697.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 PS Disclosure; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal

CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein is which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 258 AA;
 Query Match 53.6%; Score 663; DB 6; Length 258;
 Best Local Similarity 55.0%; Pred. No. 6.4e-58;
 Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;
 QY 1 SEKSEBINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
 Db 26 NENIDSVKELHKKSELSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKFFTD 85
 QY 61 HPWYNDLLVDSGSKDATNYKGGKVDLYGAYGYCAGGTPNKTCMYGGVTLHDNRILT 120
 Db 86 LINFEDLLINFNSKVAHQFKSNVDVPIRYSINCYGGEIDRTACTGYGVPFHEGNKILK 145
 QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHLYHGKFGLYNSDSFGKVQ 180
 Db 146 ERKIPINLWINGVQKESVLDKVDKQNTKQNTVQELDAQARRYLQKDLKLYNNDTLGGKIQ 205
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGQVPTLLRYRDNKTINSNLHIALYLY 231
 Db 206 RGIKIEPDSGSKVSYDLFDFVKGDFPEKQLRIYSNDKNTLSTSLHLDIYLY 256
 RESULT 39
 AAR45013
 ID AAR45013 standard; protein; 228 AA.
 XX
 AC AAR45013;
 XX
 DT 25-MAR-2003 (revised)

PN US2002051765-A1.
 XX 02-MAY-2002.
 XX 19-DEC-2000; 2000US-00741503.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 2002-415198/44.
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.
 XX The present sequence is the protein sequence of enterotoxin D (SED) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumoricidal reaction
 XX SQ Sequence 228 AA;
 Query Match 53.1%; Score 657; DB 5; Length 228;
 Best Local Similarity 56.0%; Pred. No. 2.2e-57;
 Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;
 QY 7 INEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTCGHPWYND 66
 Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGQDQFLENTLLYKKFFTDLINFED 61
 QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTGNKTACMYGGVTLHDNNRLTEKKVP 126
 Db 62 LLINFSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVGQRLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKKNVTQVELDAQRRYLQKDLKLYNNDTLGGKIQRGKIEF 181
 QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYDRNKNINSENHIALYLY 231
 Db 182 DSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTSLSTEHLHIDYLY 226
 RESULT 42
 AAR13205
 ID AAR13205 standard; protein; 228 AA.
 XX AAR13205;
 AC

XX 15-OCT-1991 (first entry)
 XX Staphylococcal enterotoxin D.
 XX SED; cancer treatment; pyrogen; tumouricide.
 XX Staphylococcus aureus.
 XX WO9110680-A.
 XX 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 1991-237984/32.
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 XX SED was isolated and purified from S. aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SED. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX SQ Sequence 228 AA;
 Query Match 52.4%; Score 649; DB 2; Length 228;
 Best Local Similarity 55.6%; Pred. No. 1.4e-56;
 Matches 125; Conservative 31; Mismatches 69; Indels 0; Gaps 0;
 QY 7 INEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTCGHPWYND 66
 Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGQDQFLENTLLYKKFFTDLINFED 61
 QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTGNKTACMYGGVTLHDNNRLTEKKVP 126
 Db 62 LLINFSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVGQRLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKKNVTQVELDAQRRYLQKDLKLYNNDTLGGKIQRGKIEF 181
 QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYDRNKNINSENHIALYLY 231
 Db 182 DSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTSLSTEHLHIDYLY 226
 RESULT 43
 ABP58459
 ID ABP58459 standard; protein; 203 AA.
 XX ABP58459;
 XX 14-APR-2003 (first entry)
 XX Staphylococcal enterotoxin D.
 XX Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
 KW cytostatic; vaccine.

XX OS Staphylococcus sp.
XX PN WC2003002143-A1.
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX PN WPI; 2003-201467/19.
XX DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX PT receptor and four regions to determine binding to class II major
XX PT histocompatibility complex, antibody to cancer associated cell surface
XX PT structure.
XX PS Example 3; Fig 3; 102pp; English.
XX CC The present sequence is the protein sequence of staphylococcal
XX CC enterotoxin D (SED). The invention provides novel conjugates (see
XX CC ABP58454) for human cancer therapy. These comprise an engineered
XX CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
XX CC antibody moiety, such as tumour reactive antibody 5T4. Bacterial
XX CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
XX CC modelling of the engineered superantigens. The superantigens were
XX CC engineered to reduce seroreactivity whilst maintaining biological
XX CC activity and production levels. The novel conjugates were designed to
XX CC target and destroy cancer cells, including cancer of the lung, breast,
XX CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX CC Sequence 203 AA;
XX SQ
Query Match 42.2%; Score 523; DB 6; Length 203;
Best Local Similarity 50.0%; Pred. No. 5.2e-44;
Matches 110; Conservative 23; Mismatches 67; Indels 20; Gaps 3;
QY 12 LRKSELSQGTALGNLQKQIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPWNLLVLDL 71
DB 2 LHKSELSSTALNNKHSYADANPIGANKSTGQFLENTLLYKAPF-----LLINF 53
QY 72 GSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWI 131
DB 54 NSAEQAQHPKSKNDVVAIRYAAAC-----RTACTYGGVTPHAGNALKARKKIPINLWI 107
QY 132 DGKQTTVPIDKVTSKKVTQVQLDLOARHYLHGKFLYNSDSFGKVGORGLIVFHSSEG 191
DB 108 IGQVKEVSLDKVTDKKNVTVQELDQAARYLOKDLKLYNA-----IORGKLEFDSAAA 161
QY 192 STVSYDLFDAQGOQPTLLRIYRDNKTINSENHLIALYLY 231
DB 162 SKVSYDLFDVAGDFPEKQLRIYSDNKTLSLHLDIYLY 201
RESULT 44
ABM70958
ID ABM70958 standard; protein; 250 AA.
XX AC
XX ABM70958;
XX DT 20-NOV-2003 (first entry)
XX DE Staphylococcus aureus protein #198.
XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
XX KW enzymatic assay; antibiotic target.
XX OS Staphylococcus aureus.

XX PN WO200294868-A2.
XX PD 28-NOV-2002.
XX PF 27-MAR-2002; 2002WO-IB002637.
XX PR 27-MAR-2001; 2001GB-00007661.
XX PA (CHIR-) CHIRON SPA.
XX PI Masignani V, Mora M, Scarselli M;
XX PN WPI; 2003-120786/11.
XX DR N-ESDB; ACF72519.
XX CC New Staphylococcus aureus protein, useful as a vaccine for treating or
XX CC preventing Staphylococcal infection, specifically an infection caused by
XX CC S. aureus, e.g. sepsis.
XX PS Claim 1; SEQ ID NO 396; 49pp; English.
XX CC The invention relates to novel genes and encoded proteins from
XX CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX CC nucleic acid encoding the protein, or an antibody to the protein, is
XX CC useful as a pharmaceutical, particularly as a vaccine for treating or
XX CC preventing infection due to Staphylococcus bacteria, specifically an
XX CC infection caused by S. aureus. The composition is particularly useful for
XX CC treating or preventing sepsis in a patient. The composition can also be
XX CC used for diagnostics. The protein is also used in an assay for enzymatic
XX CC studies and as a target for antibiotics. This sequence represents one of
XX CC the novel S. aureus proteins of the invention
XX CC Sequence 250 AA;
XX SQ
Query Match 39.1%; Score 483.5; DB 6; Length 250;
Best Local Similarity 39.4%; Pred. No. 6.5e-40;
Matches 91; Conservative 47; Mismatches 88; Indels 5; Gaps 3;
QY 1 SEKSEENEDLRKSELSQGTALGNLQKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 23 TNSASAEYSDLHHKSKFDSKRISNAK-MSFINPTQL-ENKNTINDRLKDLHLFHDNFVN 80
QY 61 HPWYNDDLVDLIGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
DB 81 DDWKKDFKVFENEALSKKFKINDIDIFAGNYGVGCHGATNKTQCSYGGVTLSDNNKYD 140
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKVTQVQLDLOARHYLHGKFLYNSDSFGKVKQ 180
DB 141 DYKNIPCNLWIDGHTQIEITAVTKKKKIYTIQELVQLENYLNEKYKLYEQ---GGDIV 197
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOQPTLLRIYRDNKTINSENHLIALYLY 231
DB 198 KGYVYNDDEQNVDFYNLNGEYGREVLKMYADNKTINSDKLHLDIYLF 248
RESULT 45
ABU10091
ID ABU10091 standard; protein; 82 AA.
XX AC
XX ABU10091;
XX DT 11-AUG-2003 (first entry)
XX DE Bacterial superantigen toxin SEE.
XX KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
XX KW SEE.
XX OS Unidentified.
XX PN US2003009015-A1.
XX SQ

PD 09-JAN-2003.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 XX (ULRI/) ULRICH R. G.
 PA (OLSO/) OLSON M. A.
 PA (BAVA/) BAVARI S.
 XX
 XX Ulrich RG, Olson MA, Bavari S;
 XX
 XX WPI; 2003-401542/38.
 XX
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 XX Example 1; Page 36; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEE
 XX
 XX Sequence 82 AA;
 SQ

Query Match 36.9%; Score 457; DB 6; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.1e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYOCAGGTPN 102
 DB 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 46
 ABU62338
 ID ABU62338 standard; protein; 82 AA.
 XX
 XX AC ABU62338;
 XX
 XX DT 27-AUG-2003 (first entry)
 XX
 XX DE S. aureus enterotoxin E, SEE, MHC binding region.
 XX
 XX KW SEE; staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC;
 XX superantigen-associated bacterial infection; bacterial infection;
 XX antibacterial.
 XX
 XX OS Staphylococcus aureus.
 XX
 XX PN US2003036644-A1.
 XX
 XX PD 20-FEB-2003.
 XX
 XX PF 26-NOV-2001; 2001US-00002784.
 XX
 XX PR 25-JUN-1997; 97US-00882431.
 XX
 XX PR 01-SEP-1996; 98US-00144776.

XX (ULRI/) ULRICH R. G.
 XX Ulrich RG;
 XX WPI; 2003-492125/46.
 XX
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 XX Disclosure; Fig 3; 68pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antisera isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SEB). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the S. aureus enterotoxin E, SEE, MHC binding region
 XX
 XX Sequence 82 AA;
 SQ

Query Match 36.9%; Score 457; DB 7; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.1e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYOCAGGTPN 102
 DB 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDLYGAYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 47
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 XX
 XX AC ABU10089;
 XX
 XX DT 11-AUG-2003 (first entry)
 XX
 XX DE Bacterial superantigen toxin SEA.
 XX
 XX KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 XX SEA.
 XX
 XX OS Unidentified.
 XX
 XX PN US2003009015-A1.
 XX
 XX PD 09-JAN-2003.
 XX
 XX PF 25-JUN-1997; 97US-00882431.
 XX
 XX PR 25-JUN-1997; 97US-00882431.
 XX
 XX PA (ULRI/) ULRICH R. G.
 XX (OLSO/) OLSON M. A.
 XX (BAVA/) BAVARI S.

XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX PT New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 1; Page 35; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEA
 XX SQ Sequence 82 AA;
 Query Match 32.2%; Score 399; DB 6; Length 82;
 Best Local Similarity 86.6%; Pred. No. 4.1e-32;
 Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 43 SDQFLENTLLFKGFFTHGHPWYNDLLVLDGSKDATNKYKGVLDLYGAYYGQCAGGTPN 102
 Db 1 SHDQFLQHTILFKGFFTHGHWYNDLLVDFDPSKDIDVKYKGVLDLYGAYYGQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 Db 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 48
 ABU62336
 ID ABU62336 standard; protein; 82 AA.
 XX AC ABU62336;
 XX DT 27-AUG-2003 (first entry)
 XX DE S. aureus enterotoxin A, SEA, MHC binding region.
 XX KW SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 XX OS Staphylococcus aureus.
 XX PH Staphylococcus aureus.
 XX FT US2003036644-A1.
 XX PN 20-FEB-2003.
 XX PD 26-NOV-2001; 2001US-00002784.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 01-SEP-1998; 98US-00144776.
 XX XX (ULRI/) ULRICH R G.
 XX PA Ulrich RG;
 XX PI WPI; 2003-492125/45.
 XX DR New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.

XX PS Disclosure; Fig 3; 68pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection,
 CC antisera isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
 XX SQ Sequence 82 AA;
 Query Match 32.2%; Score 399; DB 7; Length 82;
 Best Local Similarity 86.6%; Pred. No. 4.1e-32;
 Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLFKGFFTHGHPWYNDLLVLDGSKDATNKYKGVLDLYGAYYGQCAGGTPN 102
 Db 1 SHDQFLQHTILFKGFFTHGHWYNDLLVDFDPSKDIDVKYKGVLDLYGAYYGQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 Db 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 49
 AAW24299
 ID AAW24299 standard; protein; 91 AA.
 XX AC AAW24299;
 XX DT 14-APR-1998 (first entry)
 XX DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
 XX KW Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen;
 KW vaccine; disease; protection; isolation.
 XX OS Staphylococcus aureus.
 XX PH Staphylococcus aureus.
 XX FT Key Location/Qualifiers
 XX FT Misc-difference 29 /note= "Unspecified amino acid"
 XX PN WO9731114-A2.
 XX PD 28-AUG-1997.
 XX PF 25-FEB-1997; 97WO-GB000524.
 XX XX 26-FEB-1996; 96GB-00004045.
 XX PA (SMIX) SMITHKLINE BEECHAM PLC.
 XX PI Burnham MKR, Hodgson JE;
 XX DR WPI; 1997-435166/40.
 XX DR N-PSDB; AAV01865.
 XX PT New Staphylococcus aureus polynucleotide and polypeptide(s) - for

PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
 XX Claim 11; Page 33; 117pp; English.
 XX
 CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from *Staphylococcus aureus*. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds that
 CC bind and inhibit the activity of the polypeptide. Such compounds can be
 CC used as anti-bacterial compounds. The polypeptide may also be used as an
 CC immunogen to vaccinate an animal for protection against *Staphylococcus*
 CC *aureus* caused disease
 XX
 SQ Sequence 91 AA;
 Query Match 29.9%; Score 370; DB 2; Length 91;
 Best Local Similarity 76.9%; Pred. No. 3.8e-29;
 Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 107 MYGGVTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGK 166
 Db 1 MYGGVTLHNNRLTEKKVPINLWIDGKXNTVPLETKNTKNTVQVQLDQARRYLEK 60
 QY 167 FGLYNSDSFGGKVGQGLIVFHSSEGSTVSVD 197
 Db 61 YNLNSDVFVGKVGQGLIVFHTSTEPSVNYD 91
 RESULT 50
 ABP58460
 ID ABP58460 standard; protein; 217 AA.
 AC ABP58460;
 XX
 DT 14-APR-2003 (first entry)
 DE Staphylococcal enterotoxin H.
 DE Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX
 OS Staphylococcus sp.
 XX
 PN WO200302143-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX
 DR WPI; 2003-201467/19.
 XX
 CC Conjugate for therapy, has bacterial superantigen with a region in T-cell
 CC receptor and four regions to determine binding to class II major
 CC histocompatibility complex, antibody to cancer associated cell surface
 CC structure.
 XX
 PS Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin D (SED). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 5T4. Bacterial
 CC enterotoxins such as SEA, SED, SEB and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to

CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 217 AA;
 Query Watch 29.1%; Score 360; DB 6; Length 217;
 Best Local Similarity 37.5%; Pred. No. 1.3e-27;
 Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;
 QY 10 KDLRKSELOQPALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLV 69
 Db 1 EDLHKSELTDALAN--AYGQYHHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55
 QY 70 DLGSXDATNKYKGVLDLYGAYGYQCAGGTPNKTACWYGGVTLHNNRLTEKKVPINL 129
 Db 56 KPATADLAQKFNKNDIYGASFYKKEKISENISECLYGGTLL-NSEKLAQERVIGANV 114
 QY 130 WIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 189
 Db 115 WVDGKQKTEL--INTNKNVTLOELDIKIRKILSDKYKIYKDS--EISKGLIEPDMK 169
 QY 190 EGSITSYDLFDAQGYPTTLRIYRDNKTINSENL-HIALVLYT 232
 Db 170 TPRDSYFDIYDLKGENYEDIKIYEDNKTLSKSDDISHIDVNLVT 213
 RESULT 51
 ABP29357
 ID ABP29357 standard; protein; 259 AA.
 XX
 AC ABP29357;
 XX
 DT 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 7890.
 DE Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB004789.
 XX
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN69988.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX
 CC Claim 1; Page 3920; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FRI99

XX SQ Sequence 240 AA;

Query Match 25.1%; Score 310.5; DB 6; Length 240;
 Best Local Similarity 35.0%; Pred. No. 1.4e-22;
 Matches 82; Conservative 46; Mismatches 87; Indels 19; Gaps 9;

QY 11 DLKXSELOQTALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLIYNINDKLNNDYKVT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVVDVYGSVYVNCYFSSKDNVGVTSKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 127 NLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHIALYLT 232
 DB 183 TGYIKFIESNGTFTWYDMMPAGDKFDQSKYLMYKDMYDVSXKVEIHLTT 236

RESULT 54
 AAY06253
 ID AAY06253 standard; protein; 239 AA.
 AC AAY06253;

XX 23-AUG-1999 (first entry)
 DE Staphylococcal group C enterotoxin SEC3-FRI913.
 XX Enterotoxin; SEC3-FRI913; toxin; disulphide loop; protein engineering.
 XX Staphylococcus aureus.

Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX WO9927889-A2.
 XX 10-JUN-1999.
 XX 01-DEC-1998; 98WO-US025107.
 XX 02-DEC-1997; 97US-0067357P.
 XX (IDAH-) IDAHO RES FOUND INC.
 XX Bohach GI;
 XX WPI; 1999-358008/30.

Non-toxic modified staphylococcal enterotoxins.
 PT Disclosure; Page 17; 25pp; English.
 XX This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI913. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.

CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold.
 CC while LB50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX Sequence 239 AA;

Query Match 24.7%; Score 305.5; DB 2; Length 239;
 Best Local Similarity 33.8%; Pred. No. 4.5e-22;
 Matches 79; Conservative 47; Mismatches 89; Indels 19; Gaps 9;

QY 11 DLKXSELOQTALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLIYNISDKLKNYDKVT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVVDVYGSVYVNCYFSSKDNVGVTSKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 127 NLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHIALYLT 232
 DB 183 TGYIKFIENNGTFTQDMMPAGDKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 55
 ABG71369
 ID ABG71369 standard; protein; 240 AA.
 AC ABG71369;

XX 29-JAN-2003 (first entry)
 DE Staphylococcal enterotoxin SEC3-FRI913.

XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC3-FRI913.

XX Staphylococcus aureus.
 XX Key Location/Qualifiers
 FT Misc-difference 240 /label= unknown

XX WO200283169-A1.
 XX 24-OCT-2002.
 XX 11-APR-2002; 2002WO-US011619.
 XX 13-APR-2001; 2001US-0283720P.
 XX (IDAH-) IDAHO RES FOUND INC.

XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.

XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.

XX Disclosure; Fig 15; 67pp; English.

Db 260 YLTT 263

RESULT 59
AAW64647
ID AAW64647 standard; peptide; 239 AA.
XX AC AAW64647;
XX DT 23-OCT-1998 (first entry)
XX DE Synthetic SEB protein fragment.
XX KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
XX KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
XX KW therapeutic; vaccine; food poisoning.
XX OS Synthetic.
XX OS Staphylococcus aureus.
XX PN WO9829444-A1.
XX PD 09-JUL-1998.
XX PF 30-DEC-1997; 97WO-IL000438.
XX PR 30-DEC-1996; 96IL-00119938.
XX PA (YISS) YISSUM RES & DEV CO.
XX PI Kaempfer R, Arad G;
XX DR WPI; 1998-388042/33.
XX PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
XX PT antagonising toxin-mediated activation of T cells and prevention or
XX PT treatment of toxic shock caused by exotoxin(s).
XX PS Example 8; Page 41; 68pp; English.
XX CC AAW64636-M64657 are peptides homologous to the amino acid sequence of a
XX CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
XX CC capable of eliciting protective immunity against toxic shock induced by
XX CC PET or by a mixture of PETs. Such peptides are also capable of
XX CC antagonising toxin-mediated activation of T-cells, inhibiting expression
XX CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or INF-
XX CC beta genes. The peptides may be used to prepare therapeutics or vaccines
XX CC for the treatment of prophylaxis of toxin-mediated activation of T cells
XX CC and eliciting protective immunity against toxic shock induced by PETs.
XX CC They can also be used for the treatment of harmful effects (especially
XX CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides
XX CC can also be used for alleviating toxic shock induced by PET
XX CC

Sequence 239 AA;
Query Match 24.5%; Score 303.5; DB 2; Length 239;
Best Local Similarity 34.6%; Pred. No. 7.2e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTTGH 61
Db 1 ESQDPKPELHKSCKFTG-LMENKVLVYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGV 111
Db 59 GNYDNRVFEFNKDLADKYKVDVFGANYYYQCVFSKKTNDINSHQTDKRTKTCMYGGV 118
QY 112 TLHDNRLTEKKVPINLWIDGKQTVPIDKVTSKKVTVOELDLQARHLYHGKFLYN 171
Db 119 TEHNGNQLDKYRSITRVFEDCK-NLLSFD-VQNNKKKVTQAQELDLTRHLYVKNKLYE 176
QY 172 SDSFGCKVQRLGLIVFHSESGTGVSYDLFDAQGVDP--TLRLRYRNKNTINSENHLIAY 229

177 FNN--SPYETGYIKFIENENS-FWYDMFAPGDKFQSKYLQMYNDNKKVDSKDKVIEVY 233

QY 230 LYT 232
Db 234 LTT 236

RESULT 60
AAB67341
ID AAB67341 standard; peptide; 239 AA.
XX AC AAB67341;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin B protein.
XX KW Tumour; cancer; immune; enterotoxin.
XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00691718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2001-158657/16.
XX CC Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX CC in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX CC costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX CC

Sequence 239 AA;
Query Match 24.5%; Score 303.5; DB 4; Length 239;
Best Local Similarity 34.6%; Pred. No. 7.2e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTTGH 61
Db 1 ESQDPKPELHKSCKFTG-LMENKVLVYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGV 111
Db 59 GNYDNRVFEFNKDLADKYKVDVFGANYYYQCVFSKKTNDINSHQTDKRTKTCMYGGV 118
QY 112 TLHDNRLTEKKVPINLWIDGKQTVPIDKVTSKKVTVOELDLQARHLYHGKFLYN 171
Db 119 TEHNGNQLDKYRSITRVFEDCK-NLLSFD-VQNNKKKVTQAQELDLTRHLYVKNKLYE 176

QY 172 SDSFGKVGORGLIVHSESGSTVSYDLFDAOGQYPD--TLRIYRDNKTINSENHLIALY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFQSKYLMYNDNRKVDKVKIEVY 233
QY 230 LYT 232
DB 234 LTT 236
RESULT 61
AAW06737
ID AAW06737 standard; protein; 255 AA.
XX
AC AAW06737;
XX
DT 08-MAR-1997 (first entry)
XX
DE Staphylococcus enterotoxin B.
XX
KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT /label= Sig_peptide
XX
PN W09636366-Al.
XX
PD 21-NOV-1996.
XX
PF 20-MAY-1996; 96WO-US007432.
XX
PR 18-MAY-1995; 95US-00446918.
PR 29-DEC-1995; 95US-00580806.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Dow SW, Elmslie RE, Potter TA;
XX
DR WPI; 1997-011857/01.
DR N-PSDB; AAT45698.
XX
PT Recombinant molecule encoding super:antigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX
PS Example 1; Page 96-97; 131pp; English.
XX
CC A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
CC superantigen. Nucleic acids encoding superantigens (see also AAW06738-
CC 39), esp. truncated forms of the superantigen lacking the leader peptide,
CC can be utilised in the gene therapy of cancer, infectious diseases and
CC immunological disorders. The nucleic acid, optionally in combination with
CC cytokine or chemokine nucleic acids, is delivered to an animal using e.g.
CC liposomes. It acts by controlling the activity of effector cells, such as
CC T-cells, macrophages, monocytes and/or natural killer cells. Localised
CC prodn. of an effective but non-toxic amount of encoded proteins allows
CC safe treatment of the animal
XX
SQ Sequence 255 AA;
Query Match 24.5%; Score 303.5; DB 2; Length 255;
Best Local Similarity 34.6%; Pred. No. 7.9e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 61
DB 17 ESQDPKPKDELKSKSRFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKOTRL 74
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGVQC-----AGTTPNKTACWGGV 111

DB 75 GNYDNVRFKKKDLADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCWGGV 134
QY 112 TLHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYN 171
DB 135 TEHNGQLDKYRSITVRVFECDGK-NLLSFD-VQTNKKKVTAGELDYLTTRHYLVKNKKLYE 192
QY 172 SDSFGKVGORGLIVHSESGSTVSYDLFDAOGQYPD--TLRIYRDNKTINSENHLIALY 229
DB 193 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFQSKYLMYNDNRKVDKVKIEVY 249
QY 230 LYT 232
DB 250 LTT 252
RESULT 62
AAW06255
ID AAW06255 standard; protein; 239 AA.
XX
AC AAW06255;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin SEC-MNCopeland.
XX
KW Enterotoxin; SEC-MNCopeland; toxin; disulfide loop; protein engineering.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 93..110
XX
PN W09927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025107.
XX
PR 02-DEC-1997; 97US-0067357P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI; 1999-358008/30.
XX
PT Non-toxic modified staphylococcal enterotoxins.
XX
PS Disclosure; Page 17; 25pp; English.
XX
CC This protein represents the Staphylococcus aureus type C enterotoxin SEC-
CC MNCopeland. The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulfide loop region.
CC Typically, the modification involves deletions within the disulfide loop
CC region of SEC (see AAW06261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine production,
CC but have substantially reduced toxicity compared to the corresponding
CC unmodified native toxin. Emetic response inducing activity and fever
CC inducing activity are typically decreased by at least about 100-fold,
CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
CC native toxin
XX
SQ Sequence 239 AA;
Query Match 24.4%; Score 302.5; DB 2; Length 239;
Best Local Similarity 32.9%; Pred. No. 9.1e-22;
Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENK-ESDDOFLNTLLFKGFFTG 60
DB 1 ESQDPDDELKSKSEFTGT-MGNMK--LYDDHYVSATKSVKVDKFLADLIYNISDKK 57

QY 61 HPWYNDLLVLSKSDATNKYKGVLDLYGAYGYQC-----AGTTPNKATCMYGGVTL 113
 Db 58 LKNYDKVKTLLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVTKGKTCMYGGITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
 Db 118 HEGNHFDNGNLQNVLIIRY-ENKNTISFE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGKQVQRLIVFHSSEGSTVSYDLFDAQGGYPD--TLRIYRDNKTINSENHIALY 229
 Db 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFQDSKYLWYNDNKTVDSEKVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 63
 ABG71371
 ID ABG71371 standard; protein; 240 AA.
 XX
 AC ABG71371;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-MNCopeland.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-MNCopeland.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 FT /label= unknown
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 PT New modified staphylococcal enterotoxin derived from a native disulphide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 PS Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-MNCopeland
 XX
 SQ Sequence 240 AA;

Query Match 24.4%; Score 302.5; DB 6; Length 240;

Best Local Similarity 32.9%; Pred. No. 9.1e-22;
 Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKSSELOQTALGNLKOIYYNKAITENK-ESDDQFLENTLLPFKFFTG 60
 Db 1 ESQPDPTDELHKSEFTGT-MGNWK--LYDDHYVSATKVKSDVKFLAHDLIYNSDKK 57
 QY 61 HPWYNDLLVLSKSDATNKYKGVLDLYGAYGYQC-----AGTTPNKATCMYGGVTL 113
 Db 58 LKNYDKVKTLLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVTKGKTCMYGGITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
 Db 118 HEGNHFDNGNLQNVLIIRY-ENKNTISFE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGKQVQRLIVFHSSEGSTVSYDLFDAQGGYPD--TLRIYRDNKTINSENHIALY 229
 Db 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFQDSKYLWYNDNKTVDSEKVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 64
 AAY06252
 ID AAY06252 standard; protein; 239 AA.
 XX
 AC AAY06252;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC2.
 XX
 KW Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 PT WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin
 CC SEC2. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the
 CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06261). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 24.3%; Score 300.5; DB 2; Length 239;

Best Local Similarity 32.9%; Pred. No. 1.4e-21;
Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHLIYNISDKK 57
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTNPNTACMYGGVTL 113
DB 58 LKNYDKVKTLLNELAKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGGTKMYGGITK 117
QY 114 HDNNLTTEE--KKVPINLWIDGKQTVTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
DB 118 HEGNHFNDGNLQNLIRVY-ENKRNITISFE-VQTDKKSVTQAELDIKARNFLINKNLYE 175
QY 172 SDSFGKVQGLIVFHSSEGSTVSYDLFDAQGOYPD--TLRIYRDNKTINSENHLIALY 229
DB 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFQSKYLMYNDNKTVDKSVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 65
ABG71368
ID ABG71368 standard; protein; 240 AA.
XX AC ABG71368;
XX DT 29-JAN-2003 (first entry)
XX DE Staphylococcal enterotoxin SEC2.
XX KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
XX KW emetic response-inducing activity; staphylococcal enterotoxin; SEC2;
XX KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
XX OS Staphylococcus aureus.
XX PH Key Location/Qualifiers
XX FT Peptide 1. .26
XX FT Misc-difference 240 /label= unknown
XX FT
XX WO200283169-A1.
XX PD 24-OCT-2002.
XX PF 11-APR-2002; 2002WO-US011619.
XX PR 13-APR-2001; 2001US-0283720P.
XX PA (IDAH-) IDAHO RES FOUND INC.
XX PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX WPI; 2003-058608/05.
XX DR
XX PT New modified staphylococcal enterotoxin derived from a native disulfide
XX PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
XX PT immune function and as a vaccine against toxic shock syndrome or food
XX PT poisoning.
XX PS Disclosure; Fig 15; 67pp; English.
XX CC The invention relates to a modified pyrogenic toxin derived from a native
XX CC disulphide loop-containing pyrogenic toxin where the modified toxin
XX CC comprises a disulphide loop having no more than 10 amino acids. The
XX CC modified toxin has a fever-inducing activity or an emetic response-
XX CC inducing activity decreased by about 100-fold in comparison to a native
XX CC toxin. The modified pyrogenic toxin, that is a staphylococcal
XX CC enterotoxin, is useful for non-specifically enhancing an immune function
XX CC and for vaccination against diseases such as toxic shock syndrome and

CC food poisoning. This sequence represents the staphylococcal enterotoxin,
CC SEC2
XX SQ Sequence 240 AA;
Query Match 24.3%; Score 300.5; DB 6; Length 240;
Best Local Similarity 32.9%; Pred. No. 1.4e-21;
Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHLIYNISDKK 57
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTNPNTACMYGGVTL 113
DB 58 LKNYDKVKTLLNELAKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGGTKMYGGITK 117
QY 114 HDNNLTTEE--KKVPINLWIDGKQTVTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
DB 118 HEGNHFNDGNLQNLIRVY-ENKRNITISFE-VQTDKKSVTQAELDIKARNFLINKNLYE 175
QY 172 SDSFGKVQGLIVFHSSEGSTVSYDLFDAQGOYPD--TLRIYRDNKTINSENHLIALY 229
DB 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFQSKYLMYNDNKTVDKSVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 66
ABU62455
ID ABU62455 standard; protein; 266 AA.
XX AC ABU62455;
XX DT 27-AUG-2003 (first entry)
XX DE S. aureus periplasmic enterotoxin B mutant Y94A.
XX KW SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine;
XX KW superantigen toxin; MHC; superantigen-associated bacterial infection;
XX KW bacterial infection; antibacterial.
XX OS Staphylococcus aureus.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT Peptide 1. .26
XX FT Protein /label= Signal_peptide
XX FT 27. .266 /label= Mature_SEB_mutant
XX FT Misc-difference 121 /note= "Wild-type Tyr substituted by Ala"
XX FT
XX US2003036644-A1.
XX PD 20-FEB-2003.
XX PF 26-NOV-2001; 2001US-00002784.
XX PR 25-JUN-1997; 97US-00882431.
XX PR 01-SEP-1998; 98US-00144776.
XX PA (ULRI/) ULRICH R G.
XX PI Ulrich RG;
XX DR WPI; 2003-492125/46.
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.

PS XX Example 3; Page; 68pp; English.

CC The invention relates to an isolated and purified superantigen toxin DNA

CC fragment is altered so that binding of the encoded altered toxin to

CC either the MHC class II or T cell antigen receptor is altered. Also

CC included are a recombinant DNA construct (comprising a vector and an

CC isolated and purified altered superantigen toxin DNA fragment), a host

CC cell transformed with the recombinant DNA construct, producing altered

CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial

CC infection, a vaccine (comprising an altered superantigen toxin for

CC producing antigenic and immunogenic response resulting in the protection

CC of a mammal against superantigen-associated bacterial infection),

CC treating/ameliorating a superantigen-associated bacterial infection, an

CC antiserum isolated from individuals immunised with one or more altered

CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,

CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and

CC SPEb). The superantigen toxin DNA fragment is useful for preparing a

CC composition for treating or preventing bacterial infection. The present

CC sequence represents the 194A (with reference to the mature protein

CC sequence) mutant of SEB. Note: The present sequence is not shown in the

CC specification but was created by the indexer using the wild-type sequence

CC and the information in the specification

XX SQ Sequence 266 AA;

Query Match 24.3%; Score 300.5; DB 7; Length 266;

Best Local Similarity 34.0%; Pred. No. 1.7e-21;

Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKRLKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60

DB 27 AESQPPKPEDELKSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84

QY 61 HPWYNLLVDLGSKDNTNKGKVDLYGAYGYQCAGG-----TPNKTACMYGG 110

DB 85 LGDYDNVRVEFNKDLADKYKVDVFGANYYYQCAFESKNTDINSHQTDKRTKCMYGG 144

QY 111 VTLHDNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY 170

DB 145 VTEHNGQLDKYRSITVRVEDGK-NLFSFD-VQTNKKVTAQELDLTRHVLVKNKLY 202

QY 171 NSDSFGGKVQGLIVFHSSSGSTVSYDLFDAQQG--YPDTLLRIYRDNKTINSENHLIAL 228

DB 203 EFN--SPYETGYIKFIENENS-FWIDMMPAPGDKFAQSKYLMYNDNKNVDKDKVIEV 259

QY 229 YLYT 232

DB 260 YLTT 263

RESULT 67

AAR45016

ID AAR45016 standard; protein; 238 AA.

XX AC AAR45016;

XX XX 25-MAR-2003 (revised)

DT 08-JUN-1994 (first entry)

XX XX Staphylococcal enterotoxin SEC3.

XX XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;

XX KW auto-immune disease; toxicity; Protein A; perfusion system.

XX OS Staphylococcus aureus.

XX XX WO9324136-A1.

XX FN 09-DEC-1993.

XX PD 01-JUN-1993; 93WO-US005213.

XX PF

XX XX 01-JUN-1992; 92US-00891718.

XX PR (TERM/) TERNAN D S.

PA (STON/) STONE J L.

XX XX Terman DS, Stone JL;

PI WPI; 1993-405418/50.

XX DR Use of staphylococcal enterotoxin(s) and homologues - for treating cancer

XX PT in a patient or for the treatment of auto-immune diseases.

XX PS Disclosure; Fig 1; 90pp; English.

XX XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)

CC which may be used in the methods of the invention for treating cancer in

CC a patient. These SEs, and homologues of them, can be used as tumouricidal

CC agents for treating cancers and autoimmune disease. They exhibit

CC tumouricidal activity and toxicity identical to that observed for the

CC Protein A perfusion system. They may be administered by i.v. injection.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 238 AA;

Query Match 24.1%; Score 298.5; DB 2; Length 238;

Best Local Similarity 34.2%; Pred. No. 2.3e-21;

Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLRKSLQGTALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHFWYNDLLV 69

DB 9 ELHKSSEFTGT-MGNK--LYDDHYVSATKWSVDKFLAHDLIYNSDKLKNYDKVKT 65

QY 70 DLGSKDATNKGKVDLYGAYGYQC-----AGTPNKTACMYGGVTLHDNRLTEE 122

DB 66 ELLNEDLAKYKDEVDVGVSNYYVNCYFSSKDNVGVGTGKTCMYGKITKEGHNFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGVNSDSFGKQV 180

DB 126 NLQWNLRIYV-ENKRNITSE-VQTDKSVTAQELDKARFNLINKNLYEFS--SPYE 181

QY 181 RGLIVFHSSSGSTVSYDLFDAQQGYPD--TLRLIYRDNKTINSENHLIALYLT 232

DB 182 TGYIKFIENNGNTFWIDMMPAPGDKPDQSKYLMYNDNKNVDKSVKIEVHLAT 235

RESULT 68

AAB67343

ID AAB67343 standard; peptide; 238 AA.

XX AC AAB67343;

XX XX 23-APR-2001 (first entry)

DT Staphylococcus aureus enterotoxin C3 protein.

XX XX Tumour; cancer; immune; enterotoxin.

XX OS Staphylococcus aureus.

XX PN US6180097-B1.

XX PD 30-JAN-2001.

XX XX 30-OCT-1998; 98US-00183437.

XX PR 03-OCT-1989; 89US-00416530.

XX PR 17-JAN-1990; 90US-00466577.

XX PR 17-JAN-1991; 91WO-US000342.

XX PR 01-JUN-1992; 92US-00891718.

XX PR 02-MAR-1993; 93US-00025144.

XX PR 31-JAN-1994; 94US-00189424.

XX PR 19-JAN-1995; 95US-00491746.


```

XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2001-158657/16.
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX The present invention relates to a tumour cell capable of stimulating
XX antitumor immune reactivity in vitro or in vivo contains and expresses an
XX exogenous nucleic acid molecule encoding a superantigen or its active
XX fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX molecule that activates T cells in conjunction with an antigenic
XX stimulus. The invention may be used for cancer therapy by stimulating an
XX anticancer immune response in vivo or ex vivo
XX Sequence 238 AA;
XX
XX Query Match 23.9%; Score 296.5; DB 4; Length 238;
XX Best Local Similarity 33.8%; Pred. No. 3.6e-21;
XX Matches 79; Conservative 46; Mismatches 90; Indels 19; Gaps 9;
XX
XX QY 11 DLKSKSELTGALGNLQIYYVNEKAITENK-ESDDOFLNTLFGFTGHPWYNDLLV 69
XX Db 9 ELHKSSEFTGT-MGNMK--LYDDHYVSATKVMVDRLAHLIYINISDKLKNYDKVKT 65
XX
XX QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHNNRLTEE 122
XX Db 66 ELLNEDLAKKYDEVVDVYGSNVCYFSSKDNVGVTKGTCMYGGITKEGHNFDNG 125
XX
XX QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
XX Db 126 NLQNVLIIRY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKNLYEFNS--SPYE 181
XX
XX QY 181 RGLIVFHSSEGSTVSVDLFDAGQVDP--TLRIYRDNKTINSENHIALYLYT 232
XX Db 182 TGYIKFIENNGNTFWYDMAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
XX
XX RESULT 69
XX ABB76239
XX ID ABB76239 standard; protein; 238 AA.
XX AC ABB76239;
XX
XX XX 09-AUG-2002 (first entry)
XX DE Staphylococcus aureus enterotoxin C3.
XX KW Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer; antitumour;
XX therapy.
XX
XX Staphylococcus aureus.
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 208
XX FT /note= "given as 'O' in the specification"
XX
XX US2002051765-A1.
XX
XX 02-MAY-2002.
XX
XX 19-DEC-2000; 2000US-00741503.
XX
XX 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US0000342.
XX PR 01-JUN-1992; 92US-00891718.

```

```

PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2002-415198/44.
XX
XX Reagent for treating cancer without the need for e.g. radiotherapy,
XX comprises a specific V beta subset of T cells sensitized to a growing
XX tumor and stimulated with superantigens.
XX Disclosure; Fig 2; 17pp; English.
XX
XX The present sequence is the protein sequence of enterotoxin C3 (SEC3) of
XX Staphylococcus aureus. Similarity is shown, in several stretches of
XX sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
XX exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
XX present invention, synthetic polypeptides useful in tumour therapy and in
XX blocking or destroying autoreactive T and B lymphocyte populations are
XX characterised by substantial structural homology to staphylococcal
XX enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
XX exotoxins, with statistically significant sequence homology and
XX similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
XX analysis exceeding 6) to include alignment of cysteine residues and
XX similar hydrophathy profiles. These superantigens are used to treat solid
XX tumours, including their metastases, without radiation, surgery or
XX standard chemotherapeutic agents. A claimed method of human cancer
XX treatment involves contacting haematopoietic cells from a patient with
XX one or more superantigens ex vivo to generate stimulated cells, selecting
XX a specific V beta subset of cells, and reintroducing these cells into the
XX patient to induce an in vivo therapeutic, tumouricidal reaction
XX
XX Sequence 238 AA;
XX
XX Query Match 23.9%; Score 296.5; DB 5; Length 238;
XX Best Local Similarity 33.8%; Pred. No. 3.6e-21;
XX Matches 79; Conservative 45; Mismatches 91; Indels 19; Gaps 9;
XX
XX QY 11 DLKSKSELTGALGNLQIYYVNEKAITENK-ESDDOFLNTLFGFTGHPWYNDLLV 69
XX Db 9 ELHKSSEFTGT-MGNMK--LYDDHYVSATKVMVDRLAHLIYINISDKLKNYDKVKT 65
XX
XX QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHNNRLTEE 122
XX Db 66 ELLNEDLAKKYDEVVDVYGSNVCYFSSKDNVGVTKGTCMYGGITKEGHNFDNG 125
XX
XX QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
XX Db 126 NLQNVLIIRY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKNLYEFNS--SPYE 181
XX
XX QY 181 RGLIVFHSSEGSTVSVDLFDAGQVDP--YPTLLRIYRDNKTINSENHIALYLYT 232
XX Db 182 TGYIKFIENNGNTFWYDMAPGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
XX
XX RESULT 70
XX AARI3206
XX ID AARI3206 standard; protein; 239 AA.
XX AC AARI3206;
XX
XX 15-OCT-1991 (first entry)
XX DE Staphylococcal enterotoxin B.
XX KW SEB; cancer treatment; pyrogen; tumouricide.
XX
XX Staphylococcus aureus.
XX OS
XX WO9110680-A.

```

XX PD 25-JUL-1991.
 XX PF 17-JAN-1990; 90US-00466577.
 XX PR 17-JAN-1990; 90US-00466577.
 XX PA (TERM/) TERMAN D S.
 XX PI Terman DS;
 XX DR WPI; 1991-237984/32.
 XX PT Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity as
 PT *Staphylococcal* protein A without potential toxic reactions.
 XX PS Disclosure; Fig 1; 74pp; English.
 XX CC SEB was isolated and purified from *S. aureus*. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEB. Synthetic polypeptides having structural homology to
 CC *Staphylococcal* exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See AAR13203-R13211
 XX SQ Sequence 239 AA;
 Query Match 23.9%; Score 296.5; DB 2; Length 239;
 Best Local Similarity 34.9%; Pred. No. 3.6e-21;
 Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
 Db 1 ESQDPKPDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
 QY 62 PWYNDLVLGSKDATNKYKGVLDLYGAYGVQC-----AGGTPNKTCMYGGV 111
 Db 59 GNYDNVRFVKKDLADKYKVDVFGVANYCYCFYSKKTNDINSHQTDKRTCMYGGV 118
 QY 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFLYN 171
 Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHYLVKNKKLYE 176
 QY 172 SDSFGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
 Db 177 FNN--SPYETGYIKFIENENS-FWYDIMPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
 QY 230 L 230
 Db 234 L 234
 RESULT 71
 AAR45014
 ID AAR45014 standard; protein; 239 AA.
 XX AC AAR45014;
 XX AC AAR45014;
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX STaphylococcal enterotoxin SEB.
 XX STaphylococcal enterotoxin; SE; cancer; tumoricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX STaphylococcus aureus.
 XX WO9324136-A1.
 XX

PD 09-DEC-1993.
 XX 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 XX (TERM/) TERMAN D S.
 XX (STON/) STONE J L.
 XX Terman DS, Stone JL;
 XX WPI; 1993-405418/50.
 XX PT Use of *staphylococcal* enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX PS Disclosure; Fig 1; 90pp; English.
 XX CC The sequences given in AAR45011-21 are *Staphylococcal* enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumoricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumoricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 239 AA;
 Query Match 23.9%; Score 296.5; DB 2; Length 239;
 Best Local Similarity 34.9%; Pred. No. 3.6e-21;
 Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
 Db 1 ESQDPKPDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
 QY 62 PWYNDLVLGSKDATNKYKGVLDLYGAYGVQC-----AGGTPNKTCMYGGV 111
 Db 59 GNYDNVRFVKKDLADKYKVDVFGVANYCYCFYSKKTNDINSHQTDKRTCMYGGV 118
 QY 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFLYN 171
 Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHYLVKNKKLYE 176
 QY 172 SDSFGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
 Db 177 FNN--SPYETGYIKFIENENS-FWYDIMPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
 QY 230 L 230
 Db 234 L 234
 RESULT 72
 AAY92319
 ID AAY92319 standard; protein; 266 AA.
 XX AC AAY92319;
 XX AC AAY92319;
 DT 10-AUG-2000 (first entry)
 XX Plant-optimized mutant *staphylococcal* enterotoxin B.
 DE Rep; replicase; rescue; replication; vector; gene expression;
 KW recombinant protein production; plant; intronless; enterotoxin B.
 XX Staphylococcus sp.
 OS Synthetic.
 XX WO200020557-A2.
 XX PN WO200020557-A2.
 XX PD 13-APR-2000.
 XX

XX PN US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX PA (ULRI/) ULRI R G.
 XX PA (OLSC/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX DR N-PSDB; ACA61175.
 XX PT New superantigen toxin and/or DNA fragment with an altered binding of the
 XX PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 XX PT useful for treating or ameliorating superantigen-associated bacterial
 XX PT infection.
 XX PS Claim 12; Page 23-24; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 XX CC and/or DNA fragment, which has been altered so that the binding of the
 XX CC encoded toxin to either major histocompatibility complex (MHC) class II
 XX CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 XX CC fragments, and vaccines are useful for treating or ameliorating
 XX CC superantigen-associated bacterial infection. The DNA fragments are
 XX CC particularly useful for producing vaccine against superantigen toxin
 XX CC infections. The transformed host cells are useful for analysing the
 XX CC effectiveness of drugs and agents that affect the binding of
 XX CC superantigens to MHC class II or T-cell antigen receptors. The present
 XX CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 XX CC B #1
 XX SQ Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 6; Length 266;
 Best Local Similarity 33.6%; Pred. No. 4.2e-21;
 Matches 32; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 27 AESQDPKPDHLKSSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYDLYSIKDTK 84
 QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGANYGYOC-----AGTPNKTKCMYGG 110
 DB 85 LGDYDNVRVEFNKDLADKYDKYDVFGANYGYOCYFSKNTDINSHTQDKRKTCTMYGG 144
 QY 111 VTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202
 QY 171 NDSFGGKVGQRLIVPHSSEGSTVSVDLPDAQO--YPTLLRIYRDKNINSENHLAL 228
 DB 203 EFPN--SPYETGYIKFIENENS-FWYDMNPAPGDKFAQSKLYMYNDNKNQVDSKDVLE 259
 QY 229 YLYT 232
 DB 260 YLTT 263
 RESULT 75
 ABU62326
 ID ABU62326 standard; protein; 266 AA.
 XX AC ABU62326;
 XX DT 27-AUG-2003 (first entry)
 XX

DE SE, staphylococcal enterotoxin B; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 XX OS Staphylococcus aureus.
 XX PH Key Location/Qualifiers
 FT Peptide 1..27
 FT Protein 28..266
 FT /label= Signal_peptide
 FT /label= Mature_SEB
 XX PN US2003036644-A1.
 XX PD 20-FEB-2003.
 XX PT 26-NOV-2001; 2001US-00002784.
 XX PT 25-JUN-1997; 97US-00882431.
 XX PR 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRI R G.
 XX PI Ulrich RG;
 XX WPI; 2003-492125/46.
 XX DR N-PSDB; ACD28896.
 XX PT New superantigen toxin DNA fragment, useful for preparing a composition
 XX PT for treating or preventing bacterial infection.
 XX PS Disclosure; Page 26-27; 68pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin DNA
 XX CC fragment is altered so that binding of the encoded altered toxin to
 XX CC either the MHC class II or T cell antigen receptor is altered. Also
 XX CC included are a recombinant DNA construct (comprising a vector and an
 XX CC isolated and purified altered superantigen toxin DNA fragment), a host
 XX CC cell transformed with the recombinant DNA construct, producing altered
 XX CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 XX CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 XX CC infection, a vaccine (comprising an altered superantigen toxin for
 XX CC producing antigenic and immunogenic response resulting in the protection
 XX CC of a mammal against superantigen-associated bacterial infection),
 XX CC treating/ameliorating a superantigen-associated bacterial infection,
 XX CC antisera isolated from individuals immunised with one or more altered
 XX CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 XX CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C (SEA,
 XX CC SEB, SEC) and streptococcal pyrogenic enterotoxin A and B (SPEA and
 XX CC SPEB). The superantigen toxin DNA fragment is useful for preparing a
 XX CC composition for treating or preventing bacterial infection. The present
 XX CC sequence represents wild-type SEB
 XX SQ Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 7; Length 266;
 Best Local Similarity 33.6%; Pred. No. 4.2e-21;
 Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 27 AESQDPKPDHLKSSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYDLYSIKDTK 84
 QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGANYGYOC-----AGTPNKTKCMYGG 110
 DB 85 LGDYDNVRVEFNKDLADKYDKYDVFGANYGYOCYFSKNTDINSHTQDKRKTCTMYGG 144
 QY 111 VTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202

QY 171 NSDSFGKVKQGLIIVFHSSGSGTVSYDLFDAQGO--YFDTLLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNWVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

Search completed: August 12, 2004, 13:30:04
Job time : 32.2786 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:32:36 ; Search time 24.7742 Seconds
(without alignments)
2952.472 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEINEKLRKKSELOG.....RDKNKTENSENHIALYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	10	US-09-900-766-3
2	1210	97.7	233	10	US-09-900-766-7
3	1210	97.7	233	14	US-10-283-838-8
4	1210	97.7	257	12	US-10-267-682-112
5	1210	97.7	257	12	US-10-267-748-112
6	1168	94.3	248	9	US-09-870-759-16
7	1168	94.3	248	10	US-09-751-708A-16
8	1130	91.3	233	10	US-09-900-766-2
9	1130	91.3	672	10	US-09-900-766-4
10	1037	83.8	233	10	US-09-900-766-4
11	1037	83.8	233	14	US-10-283-838-7
12	1037	83.8	257	12	US-10-267-682-113
13	1037	83.8	257	12	US-10-267-748-113
14	1033	83.4	233	12	US-10-354-948-4
15	1024	82.7	257	9	US-09-870-759-8
Sequence 3, Appli					
Sequence 7, Appli					
Sequence 8, Appli					
Sequence 112, App					
Sequence 16, Appl					
Sequence 16, Appl					
Sequence 2, Appli					
Sequence 4, Appli					
Sequence 7, Appli					
Sequence 113, App					
Sequence 4, Appli					
Sequence 8, Appli					

16	1024	92.7	257	10	US-09-751-708A-8	Sequence 8, Appli
17	1014	81.9	257	14	US-10-002-784A-2	Sequence 2, Appli
18	1010	81.6	233	14	US-10-002-784A-4	Sequence 4, Appli
19	997	80.5	257	8	US-08-882-431-2	Sequence 2, Appli
20	992	80.1	233	8	US-08-882-431-4	Sequence 4, Appli
21	663	53.6	233	9	US-09-870-759-14	Sequence 14, Appli
22	663	53.6	258	10	US-09-751-708A-14	Sequence 14, Appli
23	523	42.2	203	10	US-09-900-766-5	Sequence 5, Appli
24	457	36.9	82	14	US-10-002-784A-34	Sequence 34, Appli
25	399	32.2	82	14	US-10-002-784A-32	Sequence 32, Appli
26	360	29.1	217	10	US-09-900-766-6	Sequence 6, Appli
27	304.5	24.6	266	9	US-09-870-759-10	Sequence 10, Appli
28	304.5	24.6	286	9	US-09-751-708A-10	Sequence 10, Appli
29	303.5	24.5	239	9	US-09-150-947B-12	Sequence 12, Appli
30	303.5	24.5	239	14	US-10-172-425B-12	Sequence 12, Appli
31	303.5	24.5	255	12	US-10-354-948-2	Sequence 2, Appli
32	296.5	23.9	266	14	US-10-002-784A-6	Sequence 6, Appli
33	296.5	23.9	266	14	US-10-151-336-8	Sequence 8, Appli
34	291.5	23.5	239	14	US-10-002-784A-10	Sequence 10, Appli
35	280.5	23.1	239	9	US-08-882-431-10	Sequence 10, Appli
36	286.5	23.1	266	14	US-10-002-784A-8	Sequence 8, Appli
37	283	22.9	265	8	US-08-882-431-6	Sequence 6, Appli
38	282.5	22.8	251	8	US-08-973-391A-13	Sequence 13, Appli
39	282.5	22.8	251	12	US-09-308-830-13	Sequence 13, Appli
40	280	22.6	265	8	US-08-882-431-8	Sequence 8, Appli
41	277.5	22.4	251	8	US-08-882-431-16	Sequence 16, Appli
42	277.5	22.4	251	14	US-10-002-784A-16	Sequence 16, Appli
43	270.5	21.8	266	9	US-09-870-759-12	Sequence 12, Appli
44	270.5	21.8	266	10	US-09-751-708A-12	Sequence 12, Appli
45	262.5	21.2	266	14	US-08-882-431-14	Sequence 14, Appli
46	262.5	21.2	266	14	US-10-002-784A-14	Sequence 14, Appli
47	244.5	19.7	220	14	US-10-002-784A-26	Sequence 26, Appli
48	244.5	19.7	468	14	US-10-002-784A-27	Sequence 27, Appli
49	234	18.9	250	9	US-09-870-759-20	Sequence 20, Appli
50	234	18.9	250	10	US-09-751-708A-20	Sequence 20, Appli
51	215	17.4	82	14	US-10-002-784A-33	Sequence 33, Appli
52	175.5	14.2	235	12	US-09-308-829-2	Sequence 2, Appli
53	175.5	14.2	235	12	US-09-336-036-2	Sequence 2, Appli
54	137.5	11.1	89	14	US-10-002-784A-35	Sequence 35, Appli
55	121	9.8	79	14	US-10-002-784A-39	Sequence 39, Appli
56	112.5	9.1	89	14	US-10-002-784A-37	Sequence 37, Appli
57	112.5	9.1	89	14	US-10-002-784A-38	Sequence 38, Appli
58	105.5	8.5	89	14	US-10-002-784A-36	Sequence 36, Appli
59	105.5	8.5	234	9	US-09-870-759-18	Sequence 18, Appli
60	105.5	8.5	234	10	US-09-751-708A-18	Sequence 18, Appli
61	105.5	8.5	234	12	US-10-267-682-111	Sequence 11, App
62	105.5	8.5	234	12	US-10-267-748-111	Sequence 11, App
63	105	8.5	233	8	US-08-882-431-12	Sequence 12, Appli
64	104.5	8.4	232	12	US-10-282-122A-70242	Sequence 70242, A
65	104.5	8.4	234	14	US-10-002-784A-12	Sequence 12, Appli
66	103.5	8.4	194	10	US-09-465-714-3	Sequence 3, Appli
67	103.5	8.4	194	12	US-10-354-948-6	Sequence 6, Appli
68	103.5	8.4	234	12	US-10-282-122A-70241	Sequence 70241, A
69	103.5	8.4	238	10	US-09-465-714-1	Sequence 1, Appli
70	101	8.2	1634	15	US-10-435-766-23	Sequence 23, Appli
71	100	8.1	226	9	US-09-815-242-5900	Sequence 5900, Ap
72	100	8.1	226	9	US-09-815-242-13156	Sequence 13156, A
73	99	8.0	621	12	US-10-424-559-264720	Sequence 264720, A
74	99	8.0	621	12	US-10-425-114-57792	Sequence 57792, A
75	98.5	8.0	231	12	US-10-282-122A-70240	Sequence 70240, A
76	98	7.9	631	14	US-10-043-344-111	Sequence 111, App
77	97.5	7.9	232	12	US-10-282-122A-70241	Sequence 70241, A
78	95.5	7.7	616	15	US-10-431-273-59	Sequence 59, Appli
79	94	7.6	227	12	US-10-283-122A-70243	Sequence 70243, A
80	94	7.6	622	12	US-10-425-114-39433	Sequence 39433, A
81	94	7.6	622	12	US-10-283-838-20	Sequence 60523, A
82	93	7.5	16	14	US-10-283-838-20	Sequence 20, Appli
83	93	7.5	306	12	US-10-425-114-54166	Sequence 54166, A
84	93	7.5	643	15	US-10-431-273-60	Sequence 60, Appli
85	93	7.5	616	12	US-10-425-114-38468	Sequence 38468, A
86	93	7.5	653	12	US-10-425-114-62449	Sequence 62449, A
87	92.5	7.5	291	12	US-10-282-122A-52208	Sequence 52208, A
88	90.5	7.3	460	12	US-10-425-114-38886	Sequence 38886, A

Sequence 489, App
Sequence 59134, A
Sequence 63660, A
Sequence 43957, A
Sequence 115, App
Sequence 19630, A
Sequence 70244, A
Sequence 5435, Ap
Sequence 173518, A
Sequence 52842, A
Sequence 50103, A
Sequence 57915, A

89 90.5 7.3 12 US-10-183-687-489
90 90 7.3 12 US-10-282-122A-59134
91 89.5 7.2 12 US-10-425-114-63660
92 89 7.2 12 US-10-282-122A-43957
93 89 7.2 12 US-10-043-344-115
94 89 7.2 14 US-10-369-493-19630
95 88.5 7.1 15 US-10-282-122A-70244
96 88.5 7.1 15 US-10-369-493-5435
97 88 7.1 12 US-10-424-599-173518
98 88 7.1 12 US-10-425-114-52842
99 88 7.1 12 US-10-425-114-50103
100 88 7.1 12 US-10-425-114-57915

ALIGNMENTS

RESULT 1
US-09-900-766-3
Sequence 3, Application US/09900766
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 3
LENGTH: 233
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: peptide
LOCATION: (1)..(233)
OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 100.0%; Score 1238; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.4e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Qy 61 HPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRILT 120
Db 61 HPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRILT 120

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 2
US-09-900-766-7
Sequence 7, Application US/09900766
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

Query Match 100.0%; Score 1238; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.4e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
LENGTH: 233
TYPE: PRT
ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 97.7%; Score 1210; DB 10; Length 233;
Best Local Similarity 97.9%; Pred. No. 1.5e-112;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Qy 61 HPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRILT 120
Db 61 HPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRILT 120

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 3
US-10-283-838-8
Sequence 8, Application US/10283838
Publication No. US20030092894A1
GENERAL INFORMATION:
APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsteden,
Johan Hansson, Terje Kalland, Lars
Abrahamson and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
AND THEIR USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:


```
/
/   LENGTH: 233 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/   MOLECULE TYPE: peptide
/   SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match          97.7%;   Score 1210;   DB 14;   Length 233;
Best Local Similarity 97.9%;   Pred. No. 1.5e-112;
Matches 228;   Conservative 1;   Mismatches 4;   Indels 0;   Gaps 0;

QY  1  SEKSEINEKDLRKSELOCTALGNLQIYYIYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db  1  SEKSEINEKDLRKSELOCTALGNLQIYYIYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY  61  HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGOCAGGTPNKTACMYGGVTLHDNNRLT 120
Db  61  HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY  121  BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db  121  BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY  181  RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db  181  RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 4
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;           Matthews, Thomas J.
;           Wild, Carl T.
;           Barney, Shawn O.
;           Lambert, Dennis M.
;           Petteway, Stephen R.
;           Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
```

```
/
/   LENGTH: 257 amino acids
/   TYPE: amino acid
/   STRANDEDNESS: <Unknown>
/   TOPOLOGY: unknown
/   MOLECULE TYPE: protein
/   SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match          97.7%;   Score 1210;   DB 12;   Length 257;
Best Local Similarity 97.9%;   Pred. No. 1.7e-112;
Matches 228;   Conservative 1;   Mismatches 4;   Indels 0;   Gaps 0;

QY  1  SEKSEINEKDLRKSELOCTALGNLQIYYIYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db  25  SEKSEINEKDLRKSELOCTALGNLQIYYIYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY  61  HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGOCAGGTPNKTACMYGGVTLHDNNRLT 120
Db  85  HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGOCAGGTPNKTACMYGGVTLHDNNRLT 144
QY  121  BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db  145  BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY  181  RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db  205  RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 5
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
;           Matthews, Thomas J.
;           Wild, Carl T.
;           Barney, Shawn O.
;           Lambert, Dennis M.
;           Petteway, Stephen R.
;           Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
```

SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:
 US-10-267-748-112

Query Match 97.7%; Score 1210; DB 12; Length 257;
 Best Local Similarity 97.9%; Pred. No. 1.7e-112;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 6

US-09-870-759-16

Sequence 16, Application US/09870759
 Publication No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-870-759-16

Query Match 94.3%; Score 1168; DB 9; Length 248;
 Best Local Similarity 98.2%; Pred. No. 2.6e-108;
 Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSEN 224
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSEN 248

RESULT 7

US-09-751-708A-16

Sequence 16, Application US/09751708A
 Publication No. US20030157113A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 751708
 CURRENT APPLICATION NUMBER: US/09/751,708A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: US 60/173,371
 PRIOR FILING DATE: 1999-12-28
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-751-708A-16

Query Match 94.3%; Score 1168; DB 10; Length 248;
 Best Local Similarity 98.2%; Pred. No. 2.6e-108;
 Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSEN 224
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSEN 248

RESULT 8

US-09-900-766-2
 Sequence 2, Application US/09900766
 Publication No. US20030039655A1
 GENERAL INFORMATION:
 APPLICANT: FORSBERG, GORAN
 APPLICANT: ERLANDSSON, EVA
 APPLICANT: ANTONSSON, PER
 APPLICANT: WALSE, BJORN
 TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 FILE REFERENCE: P02188USO;10104199
 CURRENT APPLICATION NUMBER: US/09/900,766
 CURRENT FILING DATE: 2001-07-06
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 LENGTH: 233
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: (1)..(233)
 OTHER INFORMATION: Chimeric Protein
 US-09-900-766-2

Query Match 91.3%; Score 1130; DB 10; Length 233;
 Best Local Similarity 91.4%; Pred. No. 1.5e-104;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

```
Db 61 HPWYNDLLVDLGSSTAAATSEYSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTKNTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTTISSTLSISLYLYTT 233
```

RESULT 9

```
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1
```

```
Query Match 91.3%; Score 1130; DB 10; Length 672;
Best Local Similarity 91.4%; Pred. No. 6,5e-104;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKELOGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db 226 SEKSEINEKDLRKKELOGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 285
QY 61 HPWYNDLLVDLGSSTAAATSEYSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
Db 286 HPWYNDLLVDLGSSTAAATSEYSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 345
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
QY 181 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTKNTINSENHLIALYLYTT 233
Db 406 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTTISSTLSISLYLYTT 458
```

RESULT 10

```
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
```

```
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4
Query Match 93.8%; Score 1037; DB 10; Length 233;
Best Local Similarity 83.3%; Pred. No. 3e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKELOGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKELOGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSSTAAATSEYSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSSTAAATSEYSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTKNTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLYFDAQGYPTDLLRIYRDNTKNTINSENHLIALYLYTT 233
```

RESULT 11

```
US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030032894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
```

US-10-283-838-7

Query Match 83.8%; Score 1037; DB 14; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

QY 61 HPWYNDLLVLSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 61 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWIDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 DB 121 EEKVPINLWIDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180

QY 181 RGLIVFHSSSGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 181 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHMDIYLYTS 233

RESULT 12

US-10-267-682-113
 ; Sequence 113, Application US/10267682
 ; Publication No. US2004003235A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; Matthews, Thomas J.
 ; Wild, Carl T.
 ; Barney, Shawn O.
 ; Lambert, Dennis M.
 ; Petteway, Stephen R.
 ; Langlois, Alphonse J.
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION

NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,682
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:
 US-10-267-682-113

Query Match 83.8%; Score 1037; DB 12; Length 257;
 Best Local Similarity 83.3%; Pred. No. 3.4e-95;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84

QY 61 HPWYNDLLVLSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHNNRLT 144

QY 121 EEKVPINLWIDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 DB 145 EEKVPINLWIDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204

QY 181 RGLIVFHSSSGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 13

US-10-267-748-113
 ; Sequence 113, Application US/10267748
 ; Publication No. US20040052820A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; Matthews, Thomas J.
 ; Wild, Carl T.
 ; Barney, Shawn O.
 ; Lambert, Dennis M.
 ; Petteway, Stephen R.
 ; Langlois, Alphonse J.
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION

NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,748
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELE: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113;
US-10-267-748-113

Query Match 83.8%; Score 1037; DB 12; Length 257;
Best Local Similarity 83.3%; Pred. No. 3.4e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKOIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGOYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 14
US-10-354-948-4
Sequence 4, Application US/10354948
Publication No. US20030202962A1
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
Emslie, Robyn E.
Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match 83.4%; Score 1033; DB 12; Length 233;
Best Local Similarity 83.2%; Pred. No. 7.6e-95;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
DB 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTDH 61
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKOIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 122 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 181
DB 122 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGOYNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 15
US-09-870-759-8
Sequence 8, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 257
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 82.7%; Score 1024; DB 9; Length 257;
Best Local Similarity 82.4%; Pred. No. 6.9e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTN 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKOIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLOARHYLHGKGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGOYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 16
US-09-751-708A-8
Sequence 8, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1

```
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match      82.7%; Score 1024; DB 10; Length 257;
Best Local Similarity 82.4%; Pred. No. 6.9e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLOHTILFKGFTN 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETVKTNKKNVTVOELDLQARRYLQEKYNYNSDVFDEGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 17
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match      81.9%; Score 1014; DB 14; Length 257;
Best Local Similarity 82.0%; Pred. No. 6.9e-93;
Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFROHTILFKGFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETVKTNKKNVTVOELDLQARRYLQEKYNYNSDVFDEGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 18
US-10-002-784A-4
```

```
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match      81.6%; Score 1010; DB 14; Length 233;
Best Local Similarity 81.9%; Pred. No. 1.5e-92;
Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFROHTILFKGFTD 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 121
DB 62 SWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRILT 121
QY 122 EKVPIINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 181
DB 122 EKVPIINLWIDGKQTTVPLETVKTNKKNVTVOELDLQARRYLQEKYNYNSDVFDEGKVKQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 19
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```

; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match      80.5%; Score 997; DB 8; Length 257;
Best Local Similarity 81.1%; Pred. No. 3.4e-91;
Matches 189; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSEKQGTALGNLKOIYYNEKAITENKESHQDQFQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWDGKQTTVPLETVKTNKXNVTVQELDLQARRYLQEKYLNLYNSDVGDKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 257

```

RESULT 20

```

US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson,
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street WCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714

```

; INFORMATION FOR SEQ ID NO: 4:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match      80.1%; Score 992; DB 8; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.5e-91;
Matches 187; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSEKQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSEKQGTALGNLKOIYYNEKAITENKESHQDQFQHTILFKGFFTDH 61
QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db 122 EKKVPINLWDGKQTTVPLETVKTNKXNVTVQELDKQARYLQEKYLNLYNSDVFQKVAR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 233

```

RESULT 21

```

US-09-870-759-14
; Sequence 14, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-14

```

```

Query Match      53.6%; Score 663; DB 9; Length 258;
Best Local Similarity 55.0%; Pred. No. 8.6e-58;
Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 ENIDSVKREKELHKSELSSTALNNKHSYADKNPIIGENKSTGQDQFLENTLLYKFFTD 85
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 86 LNFEDLLNFNSKEMAHFKSKNVDPYRYSINCYGGEIDRTACTYGVTPHEGKULK 145
QY 121 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 146 ERKIPINLWINGVQKESVLDKQVTDKKNVTYQELDAQARYLQKDLKLYNNDTLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLY 231
Db 206 RGLIEFDSSDGSKVSYDLFDVKGFPEKQLRIYSNKNLTSTEHLDIYLY 256

```

RESULT 22

```

US-09-751-708A-14

```

```

; Sequence 14, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-14

Query Match      53.6%; Score 663; DB 10; Length 258;
Best Local Similarity 55.0%; Pred. No. 8.6e-58;
Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

QY      1 SEKSEINERKLRKSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB      26 NENIDSVKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKKFTD 85

QY      61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNRLT 120
DB      86 LINFEDLLNFNSKEMAOHFKSKNVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNLKL 145

QY      121 EEKQVPINLWIDQKQTPVDKVKTSKEVTYQVLDLQARHYLHGKFLYNSDSFGKQV 180
DB      146 ERKIPINLWINGQVEVSLDKVQTKNVTYQVLDLQARHYLQXLDLKLNNYDNLGKQI 205

QY      181 RGLIVFHSSEGSTVSDLDFAQQGYPTLLRIYRDNKTINSENHLIALYLY 231
DB      206 RGKIEFSDSGSVSYDLDFVKGDFPEKQIRIYSDNKTLSLSTLHEHLDIYLY 256

RESULT 23
US-09-900-766-5
; Sequence 5, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-5

Query Match      42.2%; Score 523; DB 10; Length 203;
Best Local Similarity 50.0%; Pred. No. 6.1e-44;
Matches 110; Conservative 23; Mismatches 67; Indels 20; Gaps 3;

QY      12 LRKXSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVDL 71
DB      2 LHKXSELSTALNNMKHSYADANPIIGANKSTGQFLENTLLYKAF-----LLINF 53

QY      72 GSKDATNKYKGGVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNRLTEKKVPINLWI 131
DB      54 NSAEAMQHFKSKNVDPYAIRYAAAC-----RTACTYGGVTPHAGNALKARKKIPINLWI 107

QY      132 DGKQTPIDKVKTSKEVTYQVLDLQARHYLHGKFLYNSDSFGKQVQRGLIVFHSSEG 191

```

```

DB      108 IGQKEVSLDKVQTKNVTYQVLDLQARHYLQXLDLKLNYA-----IQGKLEFDSAAA 161
QY      192 STVSYDLFDAQGQYPTLLRIYRDNKTINSENHLIALYLY 231
DB      162 SKVSYDLFDVAGDFPEKQIRIYSDNKTLSLSTLHEHLDIYLY 201

RESULT 24
US-10-002-784A-34
; Sequence 34, Application US/10002784A
; Publication No. US2003003664A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 34
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin E
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-34

Query Match      36.9%; Score 457; DB 14; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.9e-38;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGTGN 102
DB      1 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGTGN 60

QY      103 KTACMYGGVTLHDNRLTEKK 124
DB      61 KTACMYGGVTLHDNRLTEKK 82

RESULT 25
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; Publication No. US2003003664A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match      32.2%; Score 399; DB 14; Length 82;
Best Local Similarity 86.6%; Pred. No. 4.4e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY      43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGTGN 102

```


Db 1 SHDQFLQHTLTKGFFTDHSTWNTDILLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPN 60
QY 103 KTACMYGGVTLHDNNRLTEEXK 124
Db 61 KTACMYGGVTLHDNNRLTEEXK 82

RESULT 26

US-09-900-766-6
; Sequence 6, Application US/09900766
; Publication No. US2003039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P0218US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 6
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-6

Query Match 29.1%; Score 360; DB 10; Length 217;
Best Local Similarity 37.5%; Pred. No. 1.3e-27;
Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;
QY 10 KDLRKSLOGTALGNLQIYYNEKAITENKESDDQFLNTLLPKGFFTHPWNDLLV 69
Db 1 EDLHXSBLTALAN--AYGYNHPFKENIKSDEISGEKDLIFRN--QDQSG-NDLRV 55
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEXKVPINL 129
Db 56 KFATADLAQKFKNKVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114
QY 130 WIDGKQTVPIDKVTSKEVTQVQLDQARHYLHGKGLNSDSFGKVGORGLIVFHS 189
Db 115 WVDGQKTELE--IRTNKKVNTLQELDIKIKILSDKYIKYKDS---EISKGLIEFDMK 169
QY 190 EGSTVSYDLFDAQGYQPTLLRIYRDNKTINSNL-HIALYLT 232
Db 170 TPRDVSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 27
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match 24.6%; Score 304.5; DB 9; Length 266;
Best Local Similarity 34.4%; Pred. No. 6.2e-22;
Matches 84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSKSELOGTALGNLQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 27 AESQPPKPDDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGYNDNVRFVFNKDLADKYKVDVFGANYYYQCYFYSKKTNDINSHQTDKRTCTMYGG 144
QY 111 VTLDNNRLTEKKVPINLWIDGKQTVPIDKVTSKEVTQVQLDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTVSYDLFDAQGYQPD--TLRIYRDNKTINSNLHIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 28

US-09-751-708A-10
; Sequence 10, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-10

Query Match 24.6%; Score 304.5; DB 10; Length 266;
Best Local Similarity 34.4%; Pred. No. 6.2e-22;
Matches 84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSKSELOGTALGNLQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 27 AESQPPKPDDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGYNDNVRFVFNKDLADKYKVDVFGANYYYQCYFYSKKTNDINSHQTDKRTCTMYGG 144
QY 111 VTLDNNRLTEKKVPINLWIDGKQTVPIDKVTSKEVTQVQLDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTVSYDLFDAQGYQPD--TLRIYRDNKTINSNLHIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNQVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 29

US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila

;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30
;; PRIOR APPLICATION NUMBER: ISRAEL 119938
;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 12
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 24.5%; Score 303.5; DB 9; Length 239;
Best Local Similarity 34.6%; Pred. No. 6.8e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 1 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNDLLVLDGSKDANKYKGVKVDLYGAYGYQC-----AGGTPNKTAQWYGV 111
Db 59 GNYDNVRVEFKNDLADKYKVDVFGANYYYQCYFSKKTNDINSHETDKRTQWYGV 118
QY 112 TLHNNRLTEKKVPINLWDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTIENSENLHIALY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWVDSKDKVIEVY 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 30
US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12

Query Match 24.5%; Score 303.5; DB 14; Length 239;
Best Local Similarity 34.6%; Pred. No. 6.8e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61

Db 1 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNDLLVLDGSKDANKYKGVKVDLYGAYGYQC-----AGGTPNKTAQWYGV 111
Db 59 GNYDNVRVEFKNDLADKYKVDVFGANYYYQCYFSKKTNDINSHETDKRTQWYGV 118
QY 112 TLHNNRLTEKKVPINLWDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTIENSENLHIALY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWVDSKDKVIEVY 233
QY 230 LYT 232
Db 234 LTT 236
RESULT 31
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmalie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match 24.5%; Score 303.5; DB 12; Length 255;
Best Local Similarity 34.6%; Pred. No. 7.4e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 17 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 74

```

QY 62 PWYNDLLVGLSKDATNKYKGGKVDLYGAYYGYOC-----AGSTPNKTKACMYGGV 111
Db 75 GNYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCTMYGGV 134
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYSITVRVFEDEGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 192
QY 172 SDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPD--TLRIYRDNKTINSENHLIALY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMKNQVDSKDVKIEVY 249
QY 230 LYT 232
Db 250 LTT 252

```

```

RESULT 32
US-10-002-784A-6
; Sequence 6, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 6
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B
US-10-002-784A-6

```

```

Query Match 23.9%; Score 296.5; DB 14; Length 266;
Best Local Similarity 33.6%; Pred. No. 3.9e-21;
Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPKPDELHKSSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYYGYOC-----AGSTPNKTKACMYGG 110
Db 85 LGYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCTMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYSITVRVFEDEGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQ--YPTDLLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFQAQSKYLMYNDNMKNQVDSKDVKIEV 259
QY 229 LYT 232
Db 260 LTT 263

```

```

RESULT 33
US-10-151-336-8
; Sequence 8, Application US/10151336
; Publication No. US20030079248A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen

```

```

; APPLICANT: Mor, Tsafirir
; APPLICANT: Anttzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/10/151,336
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/414,276
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-10-151-336-8

```

```

Query Match 23.9%; Score 296.5; DB 14; Length 266;
Best Local Similarity 34.0%; Pred. No. 3.9e-21;
Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPKPDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQSLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYYGYOC-----AGSTPNKTKACMYGG 110
Db 85 LGYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCTMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYSITVRVFEDEGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPD--TLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMKNQVDSKDVKIEV 259
QY 229 LYT 232
Db 260 LTT 263

```

```

RESULT 34
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

```

```

Query Match 23.5%; Score 291.5; DB 14; Length 239;
Best Local Similarity 35.0%; Pred. No. 1.1e-20;
Matches 82; Conservative 42; Mismatches 91; Indels 19; Gaps 8;

QY 11 DLKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 10 ELKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFDFDIYSIKOTLGNNDNRVE 67
QY 71 LGSKDATNKYKGGKVDLYGAYYGYOCAGG-----TPNKTKACMYGGVTLHDNNRLT 120

```

```

Db 68 FKNKDLADKYKDYVDFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGGVTEHNGQLD 127
Qy 121 EKKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGFLYNSDSFGKVQ 180
Db 128 KYRSITVRVEDGK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNNKLYEFNN--SPYE 183
Qy 181 RGLIVFHSSEGSTVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIALYLT 232
Db 184 TGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMWYNDNKNMVDKDKVIEVYLT 236

```

RESULT 35

```

US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

```

```

Query Match 23.5%; Score 290.5; DB 8; Length 239;
Best Local Similarity 35.0%; Pred. No. 1.4e-20;
Matches 82; Conservative 42; Mismatches 91; Indels 19; Gaps 8;
Qy 11 DLKSKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPYNDLLVD 70
Db 10 ELHKSSKFTG-KMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVRVE 67
Qy 71 LGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNRLT 120
Db 68 FKNKDLADKYKDYVDFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGGVTEHNGQLD 127
Qy 121 EKKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGFLYNSDSFGKVQ 180
Db 128 KYRSITVRVEDGK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNNKLYEFNN--SPYE 183

```

```

Qy 181 RGLIVFHSSEGSTVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIALYLT 232
Db 184 TGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMWYNDNKNMVDKDKVIEVYLT 236

```

RESULT 36

```

US-10-002-784A-8
; Sequence 8, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 266
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
US-10-002-784A-8

```

```

Query Match 23.1%; Score 286.5; DB 14; Length 266;
Best Local Similarity 33.6%; Pred. No. 3.9e-20;
Matches 82; Conservative 44; Mismatches 99; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPKPELHKSSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGG 110
Db 85 LGNYDNVRVEFKNKDLADKYKDYVDFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGG 144
Qy 111 VTLHNNRLTEKKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFLY 170
Db 145 VTEHNGQLDKYRSITVRVEDGK-NLLSFD-VQYNKKKVTAGELDLTRHYLVKNNKLY 202
Qy 171 NSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMWYNDNKNMVDKDKVIEV 259
Qy 229 YLYT 232
Db 260 YLYT 263

```

RESULT 37

```

US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:

```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
;
US-08-882-431-6

Query Match 22.9%; Score 283; DB 8; Length 265;
Best Local Similarity 32.4%; Pred. No. 8.8e-20;
Matches 79; Conservative 46; Mismatches 99; Indels 20; Gaps 8;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYVNEKAITENKESDDOFLNTLLFKGFTG 60
DB 27 AESQDPKPELHKSSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYFLLIYSIKDTK 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTPTNKATACMYGG 110
DB 85 LGDYDNVRFKNDLADKDKYVDVEGANYYYQCYFYSKTTDINSHQTDKRTOMYGG 144
QY 111 VTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLY 170
DB 145 VTEHNGNLDKRSITVRVFDGK-NLLSFD-VQYNKKKVTQAQELDYLTRHYLVNKKLY 202
QY 171 NSDSFGGVORGLIVFHSSEGSTVSYDLFDAQGG--YPTTLRIYRDNKNTINSNLHIAL 228
DB 203 EFNN--SPYEIGYKFE--LENQNFYDMMPAGDKFAQSKYLMYNDNKVDSKDVKLEV 258
QY 229 YLYT 232
DB 259 YLTT 262

RESULT 38
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorff, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251

; MEDIUM TYPE: Streptococcus pyogenes
; ORGANISM: Streptococcus pyogenes
; US-08-973-391A-13

Query Match 22.8%; Score 282.5; DB 8; Length 251;
Best Local Similarity 33.8%; Pred. No. 9.1e-20;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOQTAL-GNLKOIYY-YNEKAIT-ENKESDDOFLNTLLFKGFTG 60
DB 25 SQEVPAAQDPDPSQLHRSSLVKNLQNTIYFLYEGDPVTHENVKSVQDLLSHLIYN---VS 81
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTPTNKATACMYGGVTLHNNRL 119
DB 82 GPYDKLTTELXNQEMATLFDKRNVDIYGVYTHLYCLENARSACIYGVGVNHEGHL 141
QY 120 TEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGGKV 179
DB 142 EIPKKIVKVSIDGIQ-SLSFD-IETNKQWVTAQELDYKVKYLTDNKQLYTNGP--SKY 197
QY 180 QRLIVFHSSEGSTVSYDLFD----AQGYPTTLRIYRDNKNTINSNLHIALYLT 232
DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 250

RESULT 39
US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Verchanch & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
;
US-09-308-830-13
```

Query Match	22.8%	Score 282.5	DB 12	Length 251
Best Local Similarity	33.8%	Pred. No. 9,1e-20		
Matches 80	Conservative 44	Mismatches 20	Indels 19	Gaps 10

QY	4	SEENEKDLRKSELOCTAL-GNLKQIYY-YNEKAIT-ENKESDDQFTLENTLLFKGFPFTG	60
Db	25	SQEVFAQQDPFSQILHRSSILVKNLQNIYIEGDPVTHENKVSVDLLSHLLIYN---VS	81
QY	61	HPWNDLLVDLGSKDATNKYKGVKVDLYGAYGYQC-AGGTENKTCACMYGVTLHDNNRL	119
Db	82	GFNDYDKLTELKNQEMATLFDKNVDIYIGVEYHLLCYLCENASACIYGVVTHREGNHL	141
QY	120	TEEEKVPIINLWIDGQTTVPIDVKVTSKKEVTVQELDLQARHYLHGKGLYNSDFSGKV	179
Db	142	BIPKKIVVKVSDIGIQ-SLSFD-IETNKNVTAQELDYKRVKLYLDNFKQLYTNGP--SKY	197
QY	190	ORGILVIFHSSEGSVSYDLFD---AQGVDPDLLRIYRDNKTINSENHLIALVLT	232
Db	198	ETGVIKFTPKNKSEFWDFPEPEFTOSKY----EWYKDNFTDSNTSOIEVILTT	250

RESULT 40
 US-08-882-431-8
 ; Sequence 8, Application US/08882431
 ; Publication No. US20030009015A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; APPLICANT: Mark A. Olson
 ; APPLICANT: Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; TITLE OF INVENTION: Vaccines
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John Moran
 ; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND

Query Match 22.6%; Score 280; DB 8; Length 265;
Best Local Similarity 32.8%; Pred. No. 1.7e-19;
Matches 80; Conservative 44; Mismatches 100; Indels 20; Gaps 8;
QY 1 SEKSEEINEKDLRKKSLEQTAGLNKQIYYNKEAITENKESDDQFLENTLLFKGFTG 60

27	Db	AESQDPKPELHKSSKFTG--LMENMKVYDDNHVSAI--NVKSIDQFRFYDILYISIKUTK	84
61	QY	HPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACTMYG	110
85	Db	LGDYDNRVVFKNGLADKYDKYVDVFGANAYYQCAFSSKKTNDINSHQTDKRKTCMYG	144
111	QY	VTLDHNRLTEEKVPINLWIDGQQTIVPIDKVYTSKKEVTVQELDLQARHVLHCKPGLY	170
145	Db	VTENGNGLDKYRSITVRFVEDGK--NLLSFD--VQYNKKGVTAQELDYLTRHYLVYNNKKLY	202
171	QY	NSDFGCKVGORGLIVPHSSSGSVSYDLFDAQQYPD--TLRIYRDNKTINSENLIHAL	228
203	Db	EFNN--SPYETGYIKP--IENQNFYDMMPAPGCKFQDSKYLMMYNDNKNVDSKDVKLEV	258
229	QY	YLTY	232
259	Db	YLTY	262

RESULT 41
US-08-882-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavati
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MWRMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012

```

Query Match      22.4%; Score 277.5; DB 8; Length 251;
Best Local Similarity 33.3%; Pred. NO. 2.9e-19;
Matches 79; Conservative 44; Mismatches 95; Indels 19; Gaps 10;

4 SEINEKDLKKSELQGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLNTLLFKGFTTG 60
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
25 SQEFAQQDDPPQSRLHSLVKNLQNIYFLREGDPVTHENKVSQDLRSHLIYN---VS 81
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

```

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKNOEMATLFDKNVDIYGVYVHLCVLCENABRSACIYGGVTHNHNH 141
QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGVNSDFGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKMVTAEQELDYKVKYLTDNKQLYTNGP--SKY 197
QY 180 QRLIVFHSSSGSTVSVDLFD-AGQYQPDTLRLIYRDNKTINSNHLIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLT 250

```

```

RESULT 42
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRN
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

```

```

Query Match 22.4%; Score 277.5; DB 14; Length 251;
Best Local Similarity 33.3%; Pred. No. 2.9e-19; Indels 19; Gaps 10;
Matches 79; Conservative 44; Mismatches 95;
QY 4 SEENKDLRKSELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SOEVFAQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKNOEMATLFDKNVDIYGVYVHLCVLCENABRSACIYGGVTHNHNH 141
QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGVNSDFGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKMVTAEQELDYKVKYLTDNKQLYTNGP--SKY 197
QY 180 QRLIVFHSSSGSTVSVDLFD-AGQYQPDTLRLIYRDNKTINSNHLIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLT 250

```

```

RESULT 43
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12

```

```

; LENGTH: 266
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-09-870-759-12
Query Match 21.8%; Score 270.5; DB 9; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.6e-18; Indels 17; Gaps 8;
Matches 76; Conservative 49; Mismatches 101;
QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQPDPTDELHKASKFTG-LMENMKVLYDDHYVSATKVK-SVDFLAHDLIYNISDKK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTL 113
Db 85 LKNYDKVKTELLNEGLAKYKDEVDVYGSNYYVNCYFSSKDNVKGKVTGGKTCMYGGITK 144
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGVLYN 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKKNLYE 202
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDQAQGYPD--TLLRIYRDNKTINSNHLIALY 229
Db 203 FNS--SPYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLLMMYNDNKTVDSSKVKIEVH 260
QY 230 LYT 232
Db 261 LTT 263

```

```

RESULT 44
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12
Query Match 21.8%; Score 270.5; DB 10; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.6e-18; Indels 17; Gaps 8;
Matches 76; Conservative 49; Mismatches 101;
QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQPDPTDELHKASKFTG-LMENMKVLYDDHYVSATKVK-SVDFLAHDLIYNISDKK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTL 113
Db 85 LKNYDKVKTELLNEGLAKYKDEVDVYGSNYYVNCYFSSKDNVKGKVTGGKTCMYGGITK 144
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGVLYN 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKKNLYE 202
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDQAQGYPD--TLLRIYRDNKTINSNHLIALY 229
Db 203 FNS--SPYETGYIKFTIENNGNTFWYDMMPAPGDKFQSKYLLMMYNDNKTVDSSKVKIEVH 260
QY 230 LYT 232
Db 261 LTT 263

```



```
Matches 75; Conservative 42; Mismatches 87; Indels 21; Gaps 12;
QY 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKTLEK 64
QY 73 SKDATNKYKGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWI 131
Db 65 NQEMATLFDKKNIDYGVYHLCVLCENAESACI-GGVNREGNHLIEIPKIVVKVSI 123
QY 132 DKGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEG 191
Db 124 DGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTNDKNQLYTNGP--SKYETGYIKFIPKQK 179
QY 192 STVSYDLEFD---AQGOYPTDLLRIYRDKNKTINSENHLIALYLT 232
Db 180 ESFWDFDFPEPEFTQSKY----LMIYKDNETLDS-NTQIEVYLT 219

RESULT 48
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant-SpeB fusion
US-10-002-784A-27

Query Match 19.7%; Score 244.5; DB 14; Length 468;
Best Local Similarity 33.3%; Pred. No. 1.4e-15;
Matches 75; Conservative 42; Mismatches 87; Indels 21; Gaps 12;
QY 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SQLHRSSLVKLNQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKTLEK 64
QY 73 SKDATNKYKGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWI 131
Db 65 NQEMATLFDKKNIDYGVYHLCVLCENAESACI-GGVNREGNHLIEIPKIVVKVSI 123
QY 132 DKGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEG 191
Db 124 DGIQ-SLSFD-IETNKKWMTAQELDYKVRKYLTNDKNQLYTNGP--SKYETGYIKFIPKQK 179
QY 192 STVSYDLEFD---AQGOYPTDLLRIYRDKNKTINSENHLIALYLT 232
Db 180 ESFWDFDFPEPEFTQSKY----LMIYKDNETLDS-NTQIEVYLT 219

RESULT 49
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
```

```
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20

Query Match 18.9%; Score 234; DB 9; Length 250;
Best Local Similarity 30.3%; Pred. No. 6.4e-15;
Matches 69; Conservative 41; Mismatches 96; Indels 22; Gaps 9;
QY 14 KXSELQGTALGNLKQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQQRNSLVTKFIYIFFMRVTLVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKT 91
QY 71 LGSKDATNKYKGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKQEMATLFDKKNVDIYGVYHLCVLCENAESACLYGGVTHHGNHLEIPKIVVKV 151
QY 130 WIDGKQT-TVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
Db 152 SIDGIQSLSPDIEQIKNG---NCSRIYTVRKYLTDKNQLYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSYDLEFD---AQGOYPTDLLRIYRDKNKTINSENHLIALYLT 232
Db 206 KNKESFWDFDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 249

RESULT 50
US-09-751-708A-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20

Query Match 18.9%; Score 234; DB 10; Length 250;
Best Local Similarity 30.3%; Pred. No. 6.4e-15;
Matches 69; Conservative 41; Mismatches 96; Indels 22; Gaps 9;
QY 14 KXSELQGTALGNLKQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQQRNSLVTKFIYIFFMRVTLVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKT 91
QY 71 LGSKDATNKYKGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINL 129
Db 92 LKQEMATLFDKKNVDIYGVYHLCVLCENAESACLYGGVTHHGNHLEIPKIVVKV 151
QY 130 WIDGKQT-TVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
Db 152 SIDGIQSLSPDIEQIKNG---NCSRIYTVRKYLTDKNQLYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSYDLEFD---AQGOYPTDLLRIYRDKNKTINSENHLIALYLT 232
Db 206 KNKESFWDFDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 249

RESULT 51
US-09-751-708A-20
```

```

US-10-002-784A-33
; Sequence 33, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 33
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin D
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-33

Query Match      17.4%; Score 215; DB 14; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.1e-13;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy      45 DQLENTLLPKGFTGHPWNLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTGPKT 104
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3- DQLENTLLPKGFTDLINEFDLINFNSKEMAQHFKSKNDVPIPIRYINCYGGIDRT 62

Qy      105 ACYGGVTLHDNNRLTEBK 124
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 ACTYGGVTPHEGNKLERKK 82

RESULT 52
US-09-308-829-2
; Sequence 2, Application US/09308829
; Publication No. US20020039585A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Ohlendorf, Douglas
; APPLICANT: Mitchell, David T.
; APPLICANT: Gahr, Pamela J.
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
; FILE REFERENCE: 600.347USW0
; CURRENT APPLICATION NUMBER: US/09/308,829
; CURRENT FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/US97/22125
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US 60/033,251
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-308-829-2

Query Match      14.2%; Score 175.5; DB 12; Length 235;
Best Local Similarity 25.4%; Pred. No. 4.2e-09;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

Qy      47 FLENTLLPKGFTGCH-----KVDLYGAYGYQCAGGTGPKTKACMYGVTLHDNNRL 79
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 FIITVILISTVFTYHQSDSKDISNVKSDLLYAVTIPIYDKCRVNFSTHTLNIDTQK 70

Qy      80 YKKG-----KVDLYGAYGYQCAGGTGPKTKACMYGVTLHDNNRL 119
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 YRGKDYIISSEMSYEASQKFRDDHVDVFGLFYILNSHTG-----EYIYGGITPAQNNKV 125

Qy      120 TEKKVPINLWIDGKQTTPIDVKTSKEVTVQELDQARHYLHGKFLYNSDS--FGG 177
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      126 NH--KLGNLFISGESQONLNKILKDIIVTFQEIPIKIRKYLMDNYKIYDATSPYVSG 183

Qy      178 KVORGLIVFHSSEGSTVSYDLFDA--QGQVPTDLLRIYRDNKTINSENL-HIALYL 230
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 RIEIG-----TKDGKHEQIDLFDSPNEGTRSDIFAK-YKONRIINMKNFSHFDIYL 233

RESULT 54
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
US-10-002-784A-35

Query Match      14.2%; Score 175.5; DB 12; Length 235;
Best Local Similarity 25.4%; Pred. No. 4.2e-09;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

Qy      47 FLENTLLPKGFTGCH-----KVDLYGAYGYQCAGGTGPKTKACMYGVTLHDNNRL 79
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 FIITVILISTVFTYHQSDSKDISNVKSDLLYAVTIPIYDKCRVNFSTHTLNIDTQK 70

Qy      80 YKKG-----KVDLYGAYGYQCAGGTGPKTKACMYGVTLHDNNRL 119
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 YRGKDYIISSEMSYEASQKFRDDHVDVFGLFYILNSHTG-----EYIYGGITPAQNNKV 125

Qy      120 TEKKVPINLWIDGKQTTPIDVKTSKEVTVQELDQARHYLHGKFLYNSDS--FGG 177
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      126 NH--KLGNLFISGESQONLNKILKDIIVTFQEIPIKIRKYLMDNYKIYDATSPYVSG 183

Qy      178 KVORGLIVFHSSEGSTVSYDLFDA--QGQVPTDLLRIYRDNKTINSENL-HIALYL 230
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 RIEIG-----TKDGKHEQIDLFDSPNEGTRSDIFAK-YKONRIINMKNFSHFDIYL 233

```

```
; SEQ ID NO 35
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin B
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-35

Query Match          11.1%; Score 137.5; DB 14; Length 89;
Best Local Similarity 39.1%; Pred. No. 6.8e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQC----- 96
Db 1 SIDQFLYFDLIYSIKDTKLGNVDYRVEFKNDLADKYDKYDVDFGANY-YQCYFSKKT 59

QY 97 ----AGGTENKTACMYGGVTLHDNNRL 119
Db 60 NDNINSHQTDKRTKTCMYGGVTEHNGNQL 86

RESULT 55
US-10-002-784A-39
; Sequence 39, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 39
; LENGTH: 79
; TYPE: PRT
; ORGANISM: streptococcal pyrogenic enterotoxin a
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-39

Query Match          9.8%; Score 121; DB 14; Length 79;
Best Local Similarity 34.6%; Pred. No. 0.00026;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQC-AGGTP 101
Db 1 SVDQLLSHLIYN---VSGPNYDKLTKELKNQEMATLPKDKNVDLYGVEYYHLVLCENA 57

QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 56
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
```

```
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

Query Match          9.1%; Score 112.5; DB 14; Length 89;
Best Local Similarity 31.7%; Pred. No. 0.0022;
Matches 26; Conservative 14; Mismatches 35; Indels 7; Gaps 1;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQC----- 96
Db 1 SVDFLAHDLIYINISDKKLNKYDKVTELLNEDLAKKYKDEVDVYGSNYVVCYFSSKD 60

QY 97 -AGGTPNKTCMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITKHEGN 82

RESULT 57
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

Query Match          9.1%; Score 112.5; DB 14; Length 89;
Best Local Similarity 31.7%; Pred. No. 0.0022;
Matches 26; Conservative 14; Mismatches 35; Indels 7; Gaps 1;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQC----- 96
Db 1 SVDFLAHDLIYINISDKKLNKYDKVTELLNEDLAKKYKDEVDVYGSNYVVCYFSSKD 60

QY 97 -AGGTPNKTCMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITKHEGN 82

RESULT 58
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
```

```
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match      8.5%; Score 105.5; DB 14; Length 89;
Best Local Similarity 30.5%; Pred. No. 0.011;
Matches 25; Conservative 14; Mismatches 36; Indels 7; Gaps 1;

QY 43 SDDQFLENTLLFKGFFGTHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYOC-----96
Db 1 SVDRFLADHLIYNISDKLKNYDKVKTTELLNEGLAKKYKDEVVDVYGSNYVNCYFSSKD 60

QY 97 -AGGTPNKTACMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITRHEGN 82

RESULT 59
US-09-870-759-18
; Sequence 18, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION: David S
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-18

Query Match      8.5%; Score 105.5; DB 9; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 DLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFGTHPWYNDLLVD 70
Db 58 DTFNTEVLDNSLGSMT-----IKNTDGSF--SLIIFPS-----PYSPAF-- 97

QY 71 LGSKDATNKYKGGKVDL-----YGAYYGYOCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKTKSQTSGTYIHFGISGVT-----NTEK 133

QY 119 LTEKKVPIINLWIDGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKHKGDSPLKYGK-KFDKKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGG 192

QY 178 --KVQRGLIVFHSSEGSTVSVDL---FDAQGYEDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKEFYNTKPPINI---DEIKTIEAE 232

RESULT 60
US-09-751-708A-18
; Sequence 18, Application US/09751708A
; Patent No. US20030157113A1
; GENERAL INFORMATION: David S
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-18

Query Match      8.5%; Score 105.5; DB 10; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 DLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFGTHPWYNDLLVD 70
Db 58 DTFNTEVLDNSLGSMT-----IKNTDGSF--SLIIFPS-----PYSPAF-- 97

QY 71 LGSKDATNKYKGGKVDL-----YGAYYGYOCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKTKSQTSGTYIHFGISGVT-----NTEK 133

QY 119 LTEKKVPIINLWIDGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKHKGDSPLKYGK-KFDKKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGG 192

QY 178 --KVQRGLIVFHSSEGSTVSVDL---FDAQGYEDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKEFYNTKPPINI---DEIKTIEAE 232

RESULT 61
US-10-267-682-111
; Sequence 111, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteaway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-682-111

Query Match      8.5%; Score 105.5; DB 12; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 LDRKSELOCTALGNLKLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 58 DTFTNSEVLNLSGSMR-----IKNTDGSII-SLIIFPS-----PYSPAFI- 97
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGVCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDKTGG 192
QY 178 --KVQEGLVFHSSEGSTVSVDL---FDAQGOYPTDLLRIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFEYNTKPPINI---DEIKTIEAE 232

RESULT 62
US-10-267-748-111
; Sequence 111, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-748-111

Query Match      8.5%; Score 105.5; DB 12; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 LDRKSELOCTALGNLKLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 58 DTFTNSEVLNLSGSMR-----IKNTDGSII-SLIIFPS-----PYSPAFI- 97
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGVCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDKTGG 192
QY 178 --KVQEGLVFHSSEGSTVSVDL---FDAQGOYPTDLLRIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFEYNTKPPINI---DEIKTIEAE 232

RESULT 63
US-08-882-431-12
; Sequence 12, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
```

MOLECULE TYPE: Peptide

US-08-882-431-12

Query Match 8.5%; Score 105; DB 8; Length 233;

Best Local Similarity 26.4%; Pred. No. 0.046;

Matches 42; Conservative 25; Mismatches 50; Indels 42; Gaps 8;

QY 81 KGKVDL-----YGAAYGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPINL 129
 DB 98 KGEKVDLNTKTKKSQTSYTHFQISGVT-----NTEKLPTEIPLKV 143
 QY 130 WIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRLIVF 186
 DB 144 KVHGKDSPLKVP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGKWKIT-----196
 QY 187 HSSSEGSTVSVDL---FPAQCGQYPTLLRIYRDNKNTINSE 222
 DB 197 -MNDGSTYQSDLSKKFYNTEKPPINI---DEIKTIEAE 231

RESULT 64

US-10-282-122A-70242

; Sequence 70242, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282.122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 70242

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-10-282-122A-70242

Query Match 8.4%;

Best Local Similarity 24.1%; Pred. No. 0.051;

Matches 61; Conservative 31; Mismatches 80; Indels 81; Gaps 14;

QY 10 KDLRKSEKLOCTA---LGNLKQIYYNEKAITENK---ESDDOFLENTL-----LFK 55
 DB 26 KAVHAKVELDETORKYINMLHQ--YSESEFSTNISVSEDIYGSNVLNFORNKTFF 83
 QY 56 GFTTGHWPYNLLVDLGSKDATNKYKGGK-----VDLYGAYGYOCAGGTPNKT 104
 DB 84 VFLLG-----DDKNKYKEKTHGLDVFAVPELIDIKGGI--YSGGCTTKQNV 127
 QY 105 ACMYGGVTLHNNRLTEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHVL 164
 DB 128 RSVFGFV---SNPSLQVKV-----DAKGFISINELFFQKEEVSLEKELDFKIRKMLV 177
 QY 165 GKFGLYNSDSFGKVGQRLIVFHSSE-----GSTVSYD-LFDAQCGYPTLLRIYRD 215
 DB 178 EKRYLYK-----GASDKGRIVNNKDEKKYVIDLSEKLSFDRMFDVM-----D 220
 QY 216 NKTINSENHLIAL 228
 DB 221 SKQI--KNIEVNL 231

RESULT 65

US-10-002-784A-12

; Sequence 12, Application US/10002784A

; Publication No. US20030036644A1

; GENERAL INFORMATION:

; /33

; APPLICANT: Ulrich, Robert G.

; TITLE OF INVENTION: Bacterial Superantigen Vaccines

; FILE REFERENCE: 003/233/SAP

; CURRENT APPLICATION NUMBER: US/10/002.784A

; CURRENT FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776

; PRIOR FILING DATE: 97-06-25; 98-09-01

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Apple Macintosh Microsoft Word 6.0

; SEQ ID NO 12

; LENGTH: 234

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: toxin shock syndrom toxin-1 mutant

US-10-002-784A-12

Query Match 8.4%;

Best Local Similarity 26.2%; Pred. No. 0.052;

Matches 42; Conservative 25; Mismatches 50; Indels 43; Gaps 8;

QY 81 KGKVDL-----YGAAYGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPI 128
 DB 98 KGEKVDLNTKTKKSQTSYTHFQISGVT-----NTEKLPTEIPLK 143
 QY 129 LWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRLIV 185
 DB 144 KVHGKDSPLKVP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGKWKIT-----197
 QY 186 PHSSEGSTVSVDL---FPAQCGYPTLLRIYRDNKNTINSE 222
 DB 198 -MNDGSTYQSDLSKKFYNTEKPPINI---DEIKTIEAE 232

RESULT 66

US-09-465-714-3

; Sequence 3, Application US/09465714

; Publication No. US20030032582A1

; GENERAL INFORMATION:

; APPLICANT: Wahlsten, Jennifer L.

; APPLICANT: Ramakrishnan, S.

; APPLICANT: Schlievert, Patrick M.

; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION

; FILE REFERENCE: 09531/003001

; CURRENT APPLICATION NUMBER: US/09/465,714

```
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Bacterial Sequence
US-09-465-714-3

Query Match      8.4%; Score 103.5; DB 10; Length 194;
Best Local Similarity 22.7%; Pred. No. 0.05; Mismatches 65; Indels 79; Gaps 13;
Matches 53; Conservative 36;

QY 11 DLKKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 18 DFTNSELVDSLGMRL-----IKNTDGS1-SLIIFPS-----PYSPAPT- 57
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGQACGTPNKTACMYGGVTLHDNRR 118
Db 18 DFTNSELVDSLGMRL-----IKNTDGS1-SLIIFPS-----PYSPAPT- 57
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGQACGTPNKTACMYGGVTLHDNRR 118
Db 58 -----KGEKVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 93
QY 119 LTEKKVPINLWIDGQITV---PIDKVKTSKEVTVQELDLOARHYLHGKFGLY-NSDS 174
Db 58 -----KGEKVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 93
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGQACGTPNKTACMYGGVTLHDNRR 118
Db 94 LPTPIELPLKVKVHGKDSPLKYWP---KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDX 149
QY 175 FGG--KVQGLIVFHSSEGSTVSYDL---FDAQQGYPTLLRIYRDNKTINSE 222
Db 150 TGGYWKIT-----MNDGSTYQSDLSKKFEYNTKPPINI---DEIKTIEAE 192

RESULT 67
US-10-354-948-6
; Sequence 6, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-354-948-6

Query Match      8.4%; Score 103.5; DB 12; Length 194;
Best Local Similarity 22.7%; Pred. No. 0.05; Mismatches 65; Indels 79; Gaps 13;
Matches 53; Conservative 36;

QY 11 DLKKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 18 DFTNSELVDSLGMRL-----IKNTDGS1-SLIIFPS-----PYSPAPT- 57
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGQACGTPNKTACMYGGVTLHDNRR 118
Db 58 -----KGEKVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 93
QY 119 LTEKKVPINLWIDGQITV---PIDKVKTSKEVTVQELDLOARHYLHGKFGLY-NSDS 174
Db 94 LPTPIELPLKVKVHGKDSPLKYWP---KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDX 149
QY 175 FGG--KVQGLIVFHSSEGSTVSYDL---FDAQQGYPTLLRIYRDNKTINSE 222
Db 150 TGGYWKIT-----MNDGSTYQSDLSKKFEYNTKPPINI---DEIKTIEAE 192

RESULT 68
US-10-282-122A-70390
; Sequence 70390, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 70390
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
```



```

; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5900
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5900

Query Match
Best Local Similarity 24.1%; Score 100; DB 9; Length 226;
Matches 48; Conservative 42; Mismatches 79; Indels 30; Gaps 8;

QY 8 NEKLRKXSELOCTALGNLKOIYYNE-----KAITENKESDD--QFLENTLLFKGFTG 60
Db 24 NVQSVQAKAEVQKQSESELK--HYNKPILERKNVTGFKYTDGKHYLEVTV----- 73
QY 61 HPWYNDLLVDLGS-KDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRL 119
Db 74 -GQHSRITLLGSDKDKFKDGENSNIDVF-----ILREGDSRCATNYSIGVTKNSVQY 127
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 128 IDYINTPI-LEIKKDNEDVLKDFYISKEDISLKELDYLRERAIKQHGLYSNG----- 181
QY 180 QRGGLIVFHSSEGSTVSVDL 198
Db 182 KQGITITMNDGTTHTIDL 200

RESULT 72
US-09-815-242-13156
; Sequence 13156, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Hasebeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13156
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13156

Query Match
Best Local Similarity 24.1%; Score 100; DB 9; Length 226;
Matches 48; Conservative 42; Mismatches 79; Indels 30; Gaps 8;

QY 8 NEKLRKXSELOCTALGNLKOIYYNE-----KAITENKESDD--QFLENTLLFKGFTG 60
Db 24 NVQSVQAKAEVQKQSESELK--HYNKPILERKNVTGFKYTDGKHYLEVTV----- 73
QY 61 HPWYNDLLVDLGS-KDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRL 119
Db 74 -GQHSRITLLGSDKDKFKDGENSNIDVF-----ILREGDSRCATNYSIGVTKNSVQY 127
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 128 IDYINTPI-LEIKKDNEDVLKDFYISKEDISLKELDYLRERAIKQHGLYSNG----- 181
QY 180 QRGGLIVFHSSEGSTVSVDL 198
Db 182 KQGITITMNDGTTHTIDL 200

RESULT 73
US-10-424-599-264720
; Sequence 264720, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264720
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Glycine max
; FEATUERE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81062C.1.pap
US-10-424-599-264720

Query Match
Best Local Similarity 22.8%; Score 99; DB 12; Length 621;
Matches 50; Conservative 40; Mismatches 77; Indels 52; Gaps 11;

QY 24 GNLKQIYYN--EKAITEN-KESDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNK 79
Db 155 NGTDTVYQKGDSSSTLTDSEESDSSVNN---YSGFSRNG---SDLGIRRMIMELETE 208
QY 80 YKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 209 LREVKELWQEEHA-----DGSRTSRNENTEDVYTKINAY---EQELMT 252
QY 140 I-DKVTKSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGGLIVFHSSEGST----- 193
Db 253 VNEKLRSEBEITKQKIELQ-----KYRLFNTENLEAGFESLSLTKKHINEGGEAHKMI 305
QY 194 -----VSVDLFDAGQYPTILLRIYRDNKTKINSEN 224
Db 306 EVEGSDIDGVDELFDQNGEI-ETLARELR-----ITKENL 339

RESULT 74

```

```

US-10-425-114-57792
; Sequence 57792, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57792
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC107B05_FLI.pep
US-10-425-114-57792

Query Match      8.0%; Score 99; DB 12; Length 628;
Best Local Similarity 22.8%; Pred. No. 0.72;
Matches 50; Conservative 40; Mismatches 77; Indels 52; Gaps 11;

QY 24 GNLKQIYYVN---EKAITEN-KESDDQFLENTLLFKGFFTGHPWYNDLLVLDLGSKDATNK 79
Db 162 GNGTDVQKQDSESTLTDSEESDDSVNN---YSGFSRNG---SDLGINRIMELETE 215
QY 80 YGKKVDLYGAYGYQCAGGTPNKTCWYGVTHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 216 LREVEKELMQEBEHA-----DGSTRGSNENTEDLYTKINAY---EQELMT 259
QY 140 I-DKVTKSKTEVTQELDLQARVHLHGKFGLYNSDSPGGKVQVORGLIVFHSSEGST---- 193
Db 260 VNEKLRLSEETIKQKLEQ-----KYRLFNTENLEAGFESLTKKHINEGGEAHKMI 312
QY 194 -----VSVDLEDAQGQYPTDLLRIYRDNKNTINSEN 224
Db 313 EVEGSDGVDKELFDQNGEI-ETLARELR-----ITKENL 346

RESULT 75
US-10-282-122A-70240
; Sequence 70240, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsuo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335

```

```

; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70240
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-282-122A-70240

Query Match      8.0%; Score 98.5; DB 12; Length 231;
Best Local Similarity 23.6%; Pred. No. 0.2;
Matches 55; Conservative 29; Mismatches 96; Indels 53; Gaps 10;

QY 2 EKSEBINE-----KDLRKSELOQTALGNL--KQIYYNEKAITENKESDDQFLENTLLFK 55
Db 32 EKQERVQHLVDIKOLYRYYSSEFEFNSGKVENYNGSNVVRFNQEK-----QNHQLF- 85
QY 56 GFETGHPWYNDLLVDLGSKDATNKYK---GKKYVDLYGAYGYQCAGGTPNKTCMYGGV 111
Db 86 -----LLGKD-KDKYKKGLEQNVVVKELI-----DPNGRLSTVGGV 122
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTKSKTEVTQELDLQARVHLHGKFGLYN 171
Db 123 TKKNNKSSETNTHLFVNK-VYGGNLDASIDSFLINKBEVSLKELDFKIRKOLVKEGYLYK 181
QY 172 SDSFGKVQVORGLIVFHSSEGSTVSVYDLFDAQGQYPTDLLRIYRDNKNTINSEN 224
Db 182 -----GTTKYKITINLKDEKKEVIDLGDK-----LQFERMGDVNLNSKDI 221

Search completed: August 12, 2004, 13:46:23
Job time : 27.7742 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 9.21353 Seconds
(without alignments)

Title: US-09-900-766-3
Perfect score: 1238
Sequence: 1 SEKSEEINEKDLRKKSLEQ.....RDNKTINSENHLIALYLYTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs. 51625971 residues

Total number of hits satisfying chosen parameters: 389414

```
Minimum, DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: * -

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/iaa/BCTUS_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1210	97.7	233	4	US-08-695-693B-8	Sequence 8, Appli
2	1210	97.7	257	3	US-08-486-099-112	Sequence 112, App
3	1210	97.7	257	3	US-08-360-107A-122	Sequence 122, App
4	1210	97.7	257	3	US-08-424-223B-112	Sequence 112, App
5	1210	97.7	257	3	US-08-919-597-112	Sequence 112, App
6	1210	97.7	257	3	US-08-475-668A-112	Sequence 112, App
7	1210	97.7	257	3	US-08-485-551A-112	Sequence 112, App
8	1210	97.7	257	3	US-08-471-913A-112	Sequence 112, App
9	1210	97.7	257	3	US-08-485-264A-112	Sequence 112, App
10	1210	97.7	257	3	US-08-474-349A-112	Sequence 112, App
11	1210	97.7	257	4	US-08-470-896-112	Sequence 112, App
12	1210	97.7	257	4	US-08-485-546A-112	Sequence 112, App
13	1143	92.3	226	3	US-08-896-933-24	Sequence 24, Appl
14	1143	92.3	226	4	US-09-314-235-24	Sequence 24, Appl
15	1037	83.8	233	4	US-08-695-692B-7	Sequence 7, Appli
16	1037	83.8	257	3	US-08-486-099-113	Sequence 113, App
17	1037	83.8	257	3	US-08-360-107A-123	Sequence 123, App
18	1037	83.8	257	3	US-08-484-223B-113	Sequence 113, App
19	1037	83.8	257	3	US-08-919-597-113	Sequence 113, App
20	1037	83.8	257	3	US-08-475-668A-113	Sequence 113, App
21	1037	83.8	257	3	US-08-485-551A-113	Sequence 113, App
22	1037	83.8	257	3	US-08-471-913A-113	Sequence 113, App
23	1037	83.8	257	3	US-08-485-264A-113	Sequence 113, App
24	1037	83.8	257	4	US-08-474-349A-113	Sequence 113, App
25	1037	83.8	257	4	US-08-470-896-113	Sequence 113, App
26	1037	83.8	257	4	US-08-485-546A-113	Sequence 113, App
27	1033	83.4	233	1	US-08-446-919A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-695-692B-8
 ; Sequence 8, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692B
 ; FILING DATE: August 12, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-695-692B-8

Query Match 97.7%; Score 1210; DB 4; Length 233;
 Best Local Similarity 97.9%; Pred. No. 4.6e-117;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60
DB	1	SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60
QY	61	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT	120
DB	61	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT	120
QY	121	EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180
DB	121	EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180
QY	181	RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDNKTINSENHLIALYLYTT	233
DB	181	RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDNKTINSENHLIALYLYTT	233

RESULT 2

US-08-486-099-112

; Sequence 112, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barrey, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,099
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-031
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-486-099-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
 Best Local Similarity 97.9%; Pred. No. 5.3e-117;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60
DB	25	SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	84
QY	61	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT	120
DB	85	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT	144
QY	121	EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180
DB	145	EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	204
QY	181	RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDNKTINSENHLIALYLYTT	233
DB	205	RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDNKTINSENHLIALYLYTT	257

RESULT 3

US-08-360-107A-122
 ; Sequence 122, Application US/08360107A
 ; Patent No. 6017536
 ; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDQFLENTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 4
US-08-484-223B-112
Sequence 112, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDQFLENTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 5
US-08-919-597-112
Sequence 112, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.

```

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 780-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 6
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION

```

```

; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELEPHONE: (212) 780-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 7
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;

Best Local Similarity 97.9%; Pred. No. 5.3e-117;

Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGAIIYGYOCAGTGNKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDYGAIIYGYOCAGTGNKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHLYHGKFGLYNSDSFGKVKQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHLYHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 8

US-08-471-913A-112

; Sequence 112, Application US/08471913A

; Patent No. 6093794

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

; TRANSMISSION

; NUMBER OF SEQUENCES: 214

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;

Best Local Similarity 97.9%; Pred. No. 5.3e-117;

Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGAIIYGYOCAGTGNKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDYGAIIYGYOCAGTGNKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHLYHGKFGLYNSDSFGKVKQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHLYHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 9

US-08-485-264A-112

; Sequence 112, Application US/08485264A

; Patent No. 6228983

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING

; RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION

; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/485,264A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-021
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 869-9741/8864
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-485-264A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
 Best Local Similarity 97.9%; Pred. No. 5.3e-117;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	SEKSEENEKDLRKKSGLQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60
DB	25	SEKSEENEKDLRKKSGLQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	84
QY	61	HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT	120
DB	85	HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT	144
QY	121	EEKVPIINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV	180
DB	145	EEKVPIINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV	204
QY	181	RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENLHIALYLYTT	233
DB	205	RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENLHIALYLYTT	257

RESULT 10
 US-08-474-349A-112
 ; Sequence 112, Application US/08/474349A
 ; Patent No. 633395
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
 ; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
 ; TITLE OF INVENTION: VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 517
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/474,349A
 FILING DATE: 07-JUN-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-024
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-474-349A-112

Query Match 97.7%; Score 1210; DB 4; Length 257;
 Best Local Similarity 97.9%; Pred. No. 5.3e-117;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	SEKSEENEKDLRKKSGLQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	60
DB	25	SEKSEENEKDLRKKSGLQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG	84
QY	61	HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT	120
DB	85	HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT	144
QY	121	EEKVPIINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV	180
DB	145	EEKVPIINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV	204
QY	181	RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENLHIALYLYTT	233
DB	205	RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENLHIALYLYTT	257

RESULT 11
 US-08-470-896-112
 ; Sequence 112, Application US/08470896
 ; Patent No. 647955
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 ; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; TITLE OF INVENTION: TRANSMISSION
 ; NUMBER OF SEQUENCES: 273
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,896


```

; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112

Query Match 97.7%; Score 1210; DB 4; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 144
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 97.7%; Score 1210; DB 4; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 144
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 13
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-24

Query Match 92.3%; Score 1143; DB 3; Length 226;
Best Local Similarity 93.5%; Pred. No. 3.7e-110;
Matches 215; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 4 SESEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTGHWP 63
DB 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTTGHWP 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEEX 123
DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEE - 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQVQRL 183
DB 120 ---VBKWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQVQRL 176

```

QY 184 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 177 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 226

RESULT 14
 US-09-314-235-24
 ; Sequence 24, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09623/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 226
 ; TYPE: PRP
 ; ORGANISM: Staphylococcus aureus

US-09-314-235-24

Query Match 92.3%; Score 1143; DB 4; Length 226;
 Best Local Similarity 93.5%; Pred. No. 3.7e-110;
 Matches 215; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 4 SEBINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEBINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60

QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLTEK 123
 Db 61 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLTEK 119

QY 124 KVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVGQRL 183
 Db 120 ---VBKWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVGQRL 176

QY 184 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 177 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 226

RESULT 15
 US-08-695-692B-7
 ; Sequence 7, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston

US-08-695-692B-7

Query Match 92.3%; Score 1143; DB 4; Length 226;
 Best Local Similarity 93.5%; Pred. No. 3.7e-110;
 Matches 215; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 4 SEBINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEBINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60

QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLTEK 123
 Db 61 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLTEK 119

QY 124 KVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVGQRL 183
 Db 120 ---VBKWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVGQRL 176

QY 184 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 177 IVFHSSEGSTVSVDLFDQAQGYDPTLLRIYRDNKTINSENHIALYLYTT 226

RESULT 16
 US-08-486-099-113
 ; Sequence 113, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA

US-08-486-099-113

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHNNRLT 120

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGKVG 180

QY 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLDFAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233

US-08-695-692B-7

ZIP: 10036-2711
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486.099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDNTNKKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETKINKNTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKTINSENHIDYLYTS 257

RESULT 17
US-08-360-107A-123
Sequence 123, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123
Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDNTNKKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETKINKNTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKTINSENHIDYLYTS 257

RESULT 18
US-08-484-223B-113
Sequence 113, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```
/
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-484-223B-113

Query Match      83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDAFNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLMDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGYNSDSFGKVKQ 180
Db 145 EEKVPINLMDGKQNTVPLETVKTKNKNVTVOELDQARRYLQEKYNYNSDVFSGKVKQ 204
QY 181 RGLIVFHSSGSGTVSYDLFDQAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTPSVNYDLFQAQGYSNLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 19
US-08-919-597-113
; Sequence 113, Application US/08/919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Biocognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:

/
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,896
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-919-597-113

Query Match      83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDAFNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLMDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGYNSDSFGKVKQ 180
Db 145 EEKVPINLMDGKQNTVPLETVKTKNKNVTVOELDQARRYLQEKYNYNSDVFSGKVKQ 204
QY 181 RGLIVFHSSGSGTVSYDLFDQAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTPSVNYDLFQAQGYSNLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 20
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
```

REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEXKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEXKAITENKESHDOFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQTPLETVTKNKNVTVOELDQARRYLQEKYLNLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 21
US-08-485-551A-113
Sequence 113, Application US/0848551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEXKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEXKAITENKESHDOFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQTPLETVTKNKNVTVOELDQARRYLQEKYLNLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 22
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: protein
; QUERY MATCH: 83.8%; Score 1037; DB 3; Length 257;
; US-08-471-913A-113
;
; BEST LOCAL SIMILARITY 83.3%; Pred. No. 4.1e-99;
; MATCHES 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
;
; QUERY MATCH
; BEST LOCAL SIMILARITY 83.3%; Pred. No. 4.1e-99;
; MATCHES 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
;
; QY 1 SEKSEEEINEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
; DB 25 SEKSEEEINEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
;
; QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 120
; DB 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 144
;
; QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
; DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
;
; QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
; DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHIDIYLYTS 257
;
; RESULT 24
; US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
; QUERY MATCH
; BEST LOCAL SIMILARITY 83.8%; Score 1037; DB 3; Length 257;
; MATCHES 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
;
; QY 1 SEKSEEEINEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
; DB 25 SEKSEEEINEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
;
; QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 120
; DB 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 144
;
; QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
; DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
;
; QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
; DB 205 RGLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHIDIYLYTS 257
;
; RESULT 23
; US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
```

US-08-474-349A-113

Query Match
Best Local Similarity 83.8%; Score 1037; DB 4; Length 257;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 BEKKVPINLWLDGKQNTVPLETVKTNKKNVTVOELDLQARYLQEKYKLYNSDVDFGKVKQ 204
QY 181 RGLIVFHSSGTSVYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 25
US-08-470-896-113
Sequence 113, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
NUMBER OF SEQUENCES: 273
TITLE OF INVENTION: TRANSMISSION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-113

Query Match 83.8%; Score 1037; DB 4; Length 257;

Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESHDFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 BEKKVPINLWLDGKQNTVPLETVKTNKKNVTVOELDLQARYLQEKYKLYNSDVDFGKVKQ 204
QY 181 RGLIVFHSSGTSVYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 26
US-08-485-546A-113
Sequence 113, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 83.8%; Score 1037; DB 4; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESHQDFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIYDKYTKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSSGSTVSYDLFDAQGYPTDILLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVHSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 27
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmali, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 83.4%; Score 1033; DB 1; Length 233;
Best Local Similarity 83.2%; Pred. No. 9.1e-99;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESHQDFLOHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYDKYTKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181

QY 182 GLIVFHSSSGSTVSYDLFDAQGYPTDILLRIYRDNKTINSENHIALYLYTT 233
DB 182 GLIVHSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 28
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmali, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Conell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match 83.4%; Score 1033; DB 2; Length 233;
Best Local Similarity 83.2%; Pred. No. 9.1e-99;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESHQDFLOHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYDKYTKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181

QY 182 GLIVFHSSSGSTVSYDLFDAQGYPTDILLRIYRDNKTINSENHIALYLYTT 233
DB 182 GLIVHSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 29
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-08-896-933-23

Query Match 82.2%; Score 1017.5; DB 3; Length 232;
 Best Local Similarity 82.8%; Pred. No. 3.6e-97;
 Matches 193; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFL-HTILFKGFTD 59
 QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 DB 60 HSWYNDLLVDFSKDIYDKYKGVLDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 120 EEKVPINLWLDGKQNTVPLETKNKXNVTVQELDPQARRYLQEKYKLYNSDVDFGKVQ 179
 QY 181 RGLIVFHSSEGSTVSYDLFDAQOYPTLLRIYRDNKTINSENHLIALYTT 233
 DB 180 RGLIVFHTSTEPSVNYDLFQAQOYSNTLLRIYRDNKTINSENHIDIYLYTS 232

RESULT 30
 US-09-314-235-23
 ; Sequence 23, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-23

Query Match 82.2%; Score 1017.5; DB 4; Length 232;
 Best Local Similarity 82.8%; Pred. No. 3.6e-97;
 Matches 193; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60

DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFL-HTILFKGFTD 59
 QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 DB 60 HSWYNDLLVDFSKDIYDKYKGVLDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 120 EEKVPINLWLDGKQNTVPLETKNKXNVTVQELDPQARRYLQEKYKLYNSDVDFGKVQ 179
 QY 181 RGLIVFHSSEGSTVSYDLFDAQOYPTLLRIYRDNKTINSENHLIALYTT 233
 DB 180 RGLIVFHTSTEPSVNYDLFQAQOYSNTLLRIYRDNKTINSENHIDIYLYTS 232

Query Match 81.9%; Score 1014; DB 4; Length 257;
 Best Local Similarity 82.0%; Pred. No. 9.7e-97;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFRQHTLLFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120

Db 85 HSWNDLLVRFDSKIDVYKGGKVDLYGAYAGYQACAGTGNKATACMYGGVTLHNNRLT 144
 QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYINLYNSDVPDGRKVQ 204
 QY 181 RGLIVHSSSEGSTVSYDLFDAQGYQPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 205 RGLIVHSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHIDIVLYTS 257

RESULT 32
 US-09-144-776B-4
 ; Sequence 4, Application US/09144776B
 ; Patent No. 639932
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army NRC - 504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-144-776B-4

Query Match 81.6%; Score 1010; DB 4; Length 233;
 Best Local Similarity 81.9%; Pred. No. 2,2e-96;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDKRKSELOGTALGNLKIYYNEKAITENKESDDQLENTLLFKGFTGH 61
 Db 2 EKSEINEKDKRKSELOGTALGNLKIYYNEKAITENKESDDQLENTLLFKGFTGH 61
 QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYAGYQACAGTGNKATACMYGGVTLHNNRLTE 121
 Db 62 SWYNDLLVRFDSKIDVYKGGKVDLYGAYAGYQACAGTGNKATACMYGGVTLHNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 181
 Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYINLYNSDVPDGRKVQ 181
 QY 182 GLIVPHSSEGSTVSYDLFDAQGYQPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 182 GLIVPHSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHIDIVLYTS 233

RESULT 33
 US-08-896-933-25
 ; Sequence 25, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 228
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-08-896-933-25

Query Match 53.1%; Score 657; DB 3; Length 228;
 Best Local Similarity 56.0%; Pred. No. 6.5e-60;
 Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;
 QY 7 INEKLKRSLOGTALGNLKIYYNEKAITENKESDDQLENTLLFKGFTGH 66
 Db 2 VKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDDQLENTLLFKGFTGH 61
 QY 67 LLVDLGSKDATNKYKGGKVDLYGAYAGYQACAGTGNKATACMYGGVTLHNNRLTEKKVP 126
 Db 62 LLINFSKEMAQHFKSKNVDVPIYSINCYGGIDTACTYGGVTPHGNKLERKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNVTVOELDLQARRYLQEKYINLYNSDVPDGRKIEF 181
 QY 187 HSSEGSTVSYDLFDAQGYQPTLLRIYRDNKTINSENHIALYLY 231
 Db 182 DSSDGSKVSYDLFVKGDFPEKRLIYSDNKTILSTEHLHIDIVLY 226

RESULT 34
 US-09-314-235-25
 ; Sequence 25, Application US/09314235
 ; Patent No. 633845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530

```
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match
Best Local Similarity 53.1%; Score 657; DB 4; Length 228;
Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;

QY 7 INEXDLRKKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFTHPWN 66
DB 2 VZEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGDFLENTLLYKFFTDLINF 61
QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTPTACMYGGVTLHDNNRLTEKKVP 126
DB 62 LLINFSNKEMAQHFKSKNDVVPYIRSYNCYGGEDTACTYGGVTPHEGNKLERKKIP 121
QY 127 INLWDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKGLYNSDSFGKQVORGLIV 186
DB 122 INLWINGQVSEVSLDKVQDKKNVTQBELDAQRYLQDKLYNNNDTLGGKIQRKIEF 181
QY 187 HSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSENLHIALYLY 231
DB 182 DSSDGSKVSYDLFDVKGDPEKQLRIYSNKTSLSTEHLHIDILYLY 226

RESULT 35
US-09-144-776B-19
; Sequence 19, Application US/091444776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19

Query Match
Best Local Similarity 56.0%; Score 657; DB 4; Length 228;
Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;

QY 7 INEXDLRKKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLIFKGFTHPWN 66
DB 2 VZEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGDFLENTLLYKFFTDLINF 61
QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTPTACMYGGVTLHDNNRLTEKKVP 126
DB 62 LLINFSNKEMAQHFKSKNDVVPYIRSYNCYGGEDTACTYGGVTPHEGNKLERKKIP 121
QY 127 INLWDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKGLYNSDSFGKQVORGLIV 186
DB 122 INLWINGQVSEVSLDKVQDKKNVTQBELDAQRYLQDKLYNNNDTLGGKIQRKIEF 181
QY 187 HSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSENLHIALYLY 231
DB 182 DSSDGSKVSYDLFDVKGDPEKQLRIYSNKTSLSTEHLHIDILYLY 226

RESULT 36
US-09-144-776B-17
; Sequence 17, Application US/091444776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match
Best Local Similarity 32.2%; Score 399; DB 4; Length 82;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGT 102
```

```
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19

Query Match
Best Local Similarity 36.9%; Score 457; DB 4; Length 82;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGT 102
DB 1 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGT 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 36
US-09-144-776B-17
; Sequence 17, Application US/091444776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match
Best Local Similarity 86.6%; Score 399; DB 4; Length 82;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGT 102
```

Db 1 SHDQFLOHTLTKGFFTHSHWYNDLVDFOSKDIVDKYKGGKVDLYGAYIGYCCAGGTEN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 37

US-08-446-918A-2
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-446-918A-2
Query Match 24.5%; Score 303.5; DB 1; Length 255;
Best Local Similarity 34.6%; Pred. No. 2.7e-23;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61

Db 17 ESQDPKPEDELHKSSKFTG-LMENKVKLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 74

QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYIGYCC-----AGTPTNKTCMYGGV 111

Db 75 GNYDNVRVEFNKDLADKYDKYDVFEGANYYYQCYFSKKTNDINSHQTDKRTKTCMYGGV 134

QY 112 TLHDNNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYN 171

Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQNKKKVTAQELDYLTRHLYVKNKKLYE 192

QY 172 SDSFGKVGQRLIVFHSSEGSTVSIDLFDAGQGYPD--TLRIYRDNKTINSENHLIY 229

Db 193 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 249

QY 230 LYT 232

Db 250 LTT 252

RESULT 38

US-08-580-806-2
Sequence 2, Application US/08580806
Patent No. 5935568
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
APPLICANT: Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-580-806-2
Query Match 24.5%; Score 303.5; DB 2; Length 255;
Best Local Similarity 34.6%; Pred. No. 2.7e-23;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61

Db 17 ESQDPKPEDELHKSSKFTG-LMENKVKLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 74

QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYIGYCC-----AGTPTNKTCMYGGV 111

Db 75 GNYDNVRVEFNKDLADKYDKYDVFEGANYYYQCYFSKKTNDINSHQTDKRTKTCMYGGV 134

QY 112 TLHDNNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHLYHGKFGLYN 171

Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQNKKKVTAQELDYLTRHLYVKNKKLYE 192

QY 172 SDSFGKVGQRLIVFHSSEGSTVSIDLFDAGQGYPD--TLRIYRDNKTINSENHLIY 229

Db 193 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 249

QY 230 LYT 232

Db 250 LTT 252

RESULT 39

US-08-896-933-28
Sequence 28, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

;; FILE REFERENCE: 09629/005002

;; CURRENT APPLICATION NUMBER: US/08/896,933

;; CURRENT FILING DATE: 1997-07-18

;; EARLIER APPLICATION NUMBER: 08/252,978

;; EARLIER FILING DATE: 1994-06-02

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 28

;; LENGTH: 238

;; TYPE: PRT

;; ORGANISM: Staphylococcus aureus

US-08-896-933-28

Query Match . 24.1%; Score 298.5; DB 3; Length 238;

Best Local Similarity 34.2%; Pred. No. 7.9e-23;

Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNISDKLKNYDKVKT 65

QY 70 DLGSDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGVTLHDNNRLTEE 122

Db 66 ELINEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITKEGHNFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180

Db 126 NLQNVLIQVY-ENKENTISFE-VOTDKKSVTAQELDIKARNFLINKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKVTDSKVIEVHLTT 235

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKVTDSKVIEVHLTT 235

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKVTDSKVIEVHLTT 235

RESULT 40

US-09-314-235-28

;; Sequence 28, Application US/09314235

;; Patent No. 6338845

;; GENERAL INFORMATION:

;; APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

;; FILE REFERENCE: 09629/005004

;; CURRENT APPLICATION NUMBER: US/09/314,235

;; CURRENT FILING DATE: 1999-05-18

;; EARLIER APPLICATION NUMBER: 08/896,933

;; EARLIER FILING DATE: 1997-07-18

;; EARLIER APPLICATION NUMBER: 08/252,978

;; EARLIER FILING DATE: 1994-06-02

;; EARLIER APPLICATION NUMBER: 07/891,718

;; EARLIER FILING DATE: 1992-06-01

;; EARLIER APPLICATION NUMBER: US91/00342

;; EARLIER FILING DATE: 1991-01-17

;; EARLIER APPLICATION NUMBER: 07/466,577

;; EARLIER FILING DATE: 1990-01-17

;; EARLIER APPLICATION NUMBER: 07/416,530

;; EARLIER FILING DATE: 1989-10-03

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 28

;; LENGTH: 238

;; TYPE: PRT

;; ORGANISM: Staphylococcus aureus

US-09-314-235-28

Query Match . 24.1%; Score 298.5; DB 4; Length 238;

Best Local Similarity 34.2%; Pred. No. 7.9e-23;

Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNISDKLKNYDKVKT 65

QY 70 DLGSDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGVTLHDNNRLTEE 122

Db 66 ELINEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITKEGHNFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180

Db 126 NLQNVLIQVY-ENKENTISFE-VOTDKKSVTAQELDIKARNFLINKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKVTDSKVIEVHLTT 235

RESULT 41

US-08-896-933-26

;; Sequence 26, Application US/08896933

;; Patent No. 6221351

;; GENERAL INFORMATION:

;; APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

;; FILE REFERENCE: 09629/005002

;; CURRENT APPLICATION NUMBER: US/08/896,933

;; CURRENT FILING DATE: 1997-07-18

;; EARLIER APPLICATION NUMBER: 08/252,978

;; EARLIER FILING DATE: 1994-06-02

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 26

;; LENGTH: 239

;; TYPE: PRT

;; ORGANISM: Staphylococcus aureus

US-08-896-933-26

Query Match

Best Local Similarity 23.9%; Score 296.5; DB 3; Length 239;

Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 61

Db 1 ESQDPKPEDELHKSSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFLYDLIYSIKDTKL 58

QY 62 PWYNDLLVGLSGDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGV 111

Db 59 GYDNRVRFNKDLADKYKDVDFGANYCYCYFSKKTNDINSHQTDKRTCMYGV 118

QY 112 TLHDNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYN 171

Db 119 TEHNGNQLDKYRSLTVRVPEDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKLYE 176

QY 172 SDSFGGKVGRLIVFHSSEGSTSVSYDLFDAQGYPD--TLRIYRNKNTINSENHLIALY 229

Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKVWDSKDVKIEV 233

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

RESULT 42

US-09-314-235-26

;; Sequence 26, Application US/09314235

;; Patent No. 6338845

;; GENERAL INFORMATION:

;; APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

;; FILE REFERENCE: 09629/005004

;; CURRENT APPLICATION NUMBER: US/09/314,235

;; CURRENT FILING DATE: 1999-05-18

;; EARLIER APPLICATION NUMBER: 08/896,933

;; EARLIER FILING DATE: 1997-07-18

```

; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match      23.9%; Score 296.5; DB 4; Length 239;
Best Local Similarity 34.9%; Pred. No. 1.3e-22;
Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
DB 1 ESQDPKPDELHKSCKFTG-LMENMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTKL 58

QY 62 PWNDDLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GNYDNVRVEFKNLADKYKVDVFGANYYYQCYSFKTKTNDINSHQTDKRTCMYGGV 118

QY 112 TLHNNRLTEEEKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
DB 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAGELDLVTLRHYLVKKNKLYE 176

QY 172 SDSFGGKVQRLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRDNKTINSNHLIALY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFQSKYLMYNDNKNWDSKDVKIEV 233

QY 230 L 230
DB 234 L 234

RESULT 43
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Artzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match      23.9%; Score 296.5; DB 4; Length 266;
Best Local Similarity 34.0%; Pred. No. 1.5e-22;
Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 27 AESQDPKPDELHKSCKFTG-LMENMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTK 84

```

```

QY 61 HPWYNDDLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGNYDNVRVEFKNLADKYKVDVFGANYYYQCYSFKTKTNDINSHQTDKRTCMYGG 144

QY 111 VTLDHNNRLTEEEKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAGELDLVTLRHYLVKKNKLY 202

QY 171 NSDSFGGKVQRLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRDNKTINSNHLIAL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFQSKYLMYNDNKNWDSKDVKIEV 259

QY 229 YLYT 232
DB 260 YLYT 263

RESULT 44
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match      23.9%; Score 296.5; DB 4; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.5e-22;
Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 27 AESQDPKPDELHKSCKFTG-LMEDMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTK 84

```

Qy		61	HPWYNDLLVDLGSKOATNKYKCKKYDLYGAYGYQC-----AGGTNPNTACWYGG	110
Dd		85	LGYDNRVVEFNKKDLADKYDKYDVDFGANYYCYCFSKKTNDINSHQTDRKTCWYGG	144
Qy		111	VTLHDNNRLTEEEKVPINLWDGKQTTVPIDKVTSKEVTVOELDAQAHYLHGFGFLY	170
Dd		145	VTEHNGNQLDKYSRIVTRVPEDGK-NLLSFP-VOTNKKVKTAQELDYLTHRYLVGNKKLY	202
Qy		171	NDSDFGKGQORGLLIVFHSEGSTVSVDLFDAQGQ--YPDITLLIRYRNKNTINSNLHAL	228
Dd		203	EFTN--SPIETGYIKFIENENS-FWYDMPPAGPKFAQQSKYLMYINDNRKWSDSKVIEV	259
Qy		229	YLYT 232	
Dd		260	YLT 263	

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999

```

Query Match 23.5%; Score 291.5; DB 4; Length 239;
Best Local Similarity 35.0%; Pred. No. 4.2e-22;
Matches 82; Conservative 42; Mismatches 91; Indels 19; Gaps 8

QY 11 DIRKSELQTALGNLKIYYINEKALTENKESDQFLENTLLFKGFFTHPWYNDLVD 70
: : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : :

Db 10 ELHKSFTG-LMENMKVLYDDNHVSAT-NVKSIDQFRYFDLIYSGIKDTKLGYNDRVE 67
 Qy 71 LGSXDAATNKYKKGVLDLYGAYGYQCAGG-----TPNKATCMYGGVTLHDNNRLT 120
 Db 68 FKNFDLADKPKYKVDVFGANAYTQCAFSKKTNDINSHQTDKRKTCMYGGVTEHNGQLD 127
 Qy 121 BEKVPINLWIDGKOTTPIDIKVTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQ 180
 Db 128 KYRITVRFEGK-NLUSFD-VQTNKKKVAQAQLDYLTRHVLVKNKKLYEFNN--SPYE 183
 Qy 181 RGLIVFHSSEGTSVYDLFDAGQGYD--TLIRIYRDNKTINSENHLIALYLT 232
 Db 184 TGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMVYNDKNKWDSDKVIEVLYTT 236

RESULT 46
 US-09-144-776B-8
 ; Sequence 8, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army NRCM -504 Scott Street
 ; MCMR-UA (Charles H. Harris-Patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 286
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-144-776B-8

Query Match 23.1%; Score 286.5; DB 4; Length 266;
 Best Local Similarity 33.6%; Pred. No. 1.6e-21;
 Matches 82; Conservative 44; Mismatches 99; Indels 19; Gaps 81

Qy 1 SEXSEBINEKDLRKSELOQTALGNLKQIYYNYEKAITENKESDDQLENTLLFKGPTG 60
 Db 27 AESQPKPKDELHKSFKFTG-LMENMKVLYDDNHVSAT-NVKSIDQFRYFDLIYSIKDTK 84
 Qy 61 HPWYNDLLVLDGSKDATNKYKGKKVLDLYGAYGYQCAGG-----TPNKATCMYGG 110

Db 85 LGYNDVRVEFKKDLADKYKDYVDFGANAYYQCAFSKTKTNDINSHQTDKRTCTMYGG 144
Qy 111 VTHDNRRLTEKKVVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGY 170
Db 145 VTHNGQLDKYSITVRFEEDGK-NLLSPD-VOYNKKKVTQAGELDYLRHLYVKNKKLY 202
Qy 171 NSDSFGKVGQGLIVFHSSSGSVSYDLFDQAQOYPD--TLRIYRDNKTINSENHLIAL 228
Db 203 EFN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMWYNDNKMWDVKVIEV 259
Qy 229 YLYT 232
Db 260 YLYT 263

RESULT 47
US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match 23.0%; Score 284.5; DB 3; Length 221;
Best Local Similarity 35.1%; Pred. No. 2e-21;
Matches 79; Conservative 41; Mismatches 86; Indels 19; Gaps 10;
Qy 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVDLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLKTLEK 63
Qy 73 SKDATNKYKGGKVDLYGAYGYQC-AGTPTNKATCMYGGVTLHDNNRLTEKKVVPINLWI 131
Db 64 NOEMATLFDKKNVDIYGYVEYHLCVLCENASERSACIYGGVTNHEGHNLEIPKIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSS 191
Db 124 DGIO-SLSFD-IEYNKQMTAQELDYKVRKYLTDNKNQLYNGP--SKYETGYIKFIPKN 179
Qy 192 STVSVDLFD---AQOYPDTLRIYRDNKTINSENHLIALYLT 232
Db 180 ESFWDLPEPEFTQSKY----LMYKDNELDNTSQTIEVLYTT 220

RESULT 48
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02

; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-08-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 23.0%; Score 284.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 2e-21;
Matches 79; Conservative 41; Mismatches 86; Indels 19; Gaps 10;
Qy 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVDLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLKTLEK 63
Qy 73 SKDATNKYKGGKVDLYGAYGYQC-AGTPTNKATCMYGGVTLHDNNRLTEKKVVPINLWI 131
Db 64 NOEMATLFDKKNVDIYGYVEYHLCVLCENASERSACIYGGVTNHEGHNLEIPKIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSS 191
Db 124 DGIO-SLSFD-IEYNKQMTAQELDYKVRKYLTDNKNQLYNGP--SKYETGYIKFIPKN 179
Qy 192 STVSVDLFD---AQOYPDTLRIYRDNKTINSENHLIALYLT 232
Db 180 ESFWDLPEPEFTQSKY----LMYKDNELDNTSQTIEVLYTT 220

RESULT 49
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggliant, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 22.8%; Score 282.5; DB 4; Length 251;
Best Local Similarity 33.8%; Pred. No. 3.9e-21;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;
Qy 4 SBEINEKDLRKSELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SEVFAQQDPDPSQLERSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VS 81
Qy 61 HPWYNDLLVDLGSKQATNKYKGGKVDLYGAYGYQC-AGGTENKTACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTLEKNQEMATLFDKKNVDIYGYVEYHLCVLCENASERSACIYGGVTNHEGHN 141

QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVKVSIDGQ-SLSFD-IEINKKQVTAQELDYKVKYLTNDKQLYTNGP--SKY 197
QY 180 ORGLIVPHSSEGSTVSVDLPD---AQGVPTDLLRIYRDNKTINSENLHIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250

RESULT 50
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stroehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 500.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 22.6%; Score 279.5; DB 4; Length 221;
Best Local Similarity 34.7%; Pred. No. 6.6e-21;
Matches 78; Conservative 41; Mismatches 87; Indels 19; Gaps 10;
QY 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVDLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHLIYN---VSGPNYDKLKTLEK 63
QY 73 SKDATNKYKGVLDYAGAYGYQC-AGGTPNKATACMYGGVTLHDNRLTEKKVPINLWI 131
Db 64 NQEMATLFDKKNVDIYGVYHLCYLCLCENASACIYGGVTNHEGNHLEIPKIVKVS 123
QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQORGLIVPHSSEG 191
Db 124 DGIO-SLSFD-IEINKKQVTAQELDYKVKYLTNDKQLYTNGP--SKYETGYIKFIPKNK 179
QY 192 STVSVDLPD---AQGVPTDLLRIYRDNKTINSENLHIALYLT 232
Db 180 ESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220

RESULT 51
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; CITY: FORT DETRICK
; MCM3-JA (Charles H. Harris-Patent
; Atty)

STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

Query Match 22.4%; Score 277.5; DB 4; Length 251;
Best Local Similarity 33.3%; Pred. No. 1.3e-20;
Matches 79; Conservative 44; Mismatches 95; Indels 19; Gaps 10;
QY 4 SEINEKDLRKKSELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SQEFAQQDPDPSOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHLIYN---VS 81
QY 61 HPWYNDLLVDLGSKDANKYKGVLDYAGAYGYQC-AGGTPNKATACMYGGVTLHDNRL 119
Db 82 GPNYDKLKTLEKQEMATLFDKKNVDIYGVYHLCYLCLCENASACIYGGVTNHEGNH 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVKVSIDGQ-SLSFD-IEINKKQVTAQELDYKVKYLTNDKQLYTNGP--SKY 197
QY 180 ORGLIVPHSSEGSTVSVDLPD---AQGVPTDLLRIYRDNKTINSENLHIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250

RESULT 52
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Query Match 21.9%; Score 271.5; DB 3; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHASKFTG-LMENMKVLYDDHYVSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYNYNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNVLRVY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176

QY 173 DSFGGKVGRLIVPHSSEGSTVSYDLFDAQGOYPD--TLRIYRDNKTINSENHLIALYL 230
 DB 177 NS--SPYETGYIKFIENNGNTFWYDLMPAPGDRFDQSKYLMYNDNKTVDKSKVLEVHL 234

QY 231 YT 232
 DB 235 TT 236

RESULT 54
 US-08-896-933-21
 ; Sequence 21, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-08-896-933-21

Query Match 21.4%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 32.7%; Pred. No. 2.6e-19;
 Matches 80; Conservative 47; Mismatches 95; Indels 23; Gaps 11;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHASKFTG-LMENVK-VLYNDHVSAINVKSINEFFDLIYLSIKDTKL 58

QY 62 PWNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGG 110
 DB 59 GNYDNVRVEFKKDLADKYKDYVDVFGANY-YOCYFSKKTNNIDSHENTKRTK-CMYGG 116

QY 111 VTLHNNRLTEE-EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFG 169
 DB 117 VTEHGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTABOLDLTHYLKVKKL 174

QY 170 YNSDGFSGKVGRLIVPHSSEGSTVSYDLFDAQGOYPD--TLRIYRDNKTINSENHLIA 227
 DB 175 YEFNN--SPYETGYIKFIENENS-FWYDMWPAFGNKPDQSKYLMYNNNDKWDKDKVIE 231

QY 228 LYLTT 232
 DB 232 VYLTT 236

RESULT 55
 US-09-314-235-21
 ; Sequence 21, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342

Query Match 21.9%; Score 271.5; DB 4; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHASKFTG-LMENMKVLYDDHYVSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYNYNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNVLRVY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176

QY 173 DSFGGKVGRLIVPHSSEGSTVSYDLFDAQGOYPD--TLRIYRDNKTINSENHLIALYL 230
 DB 177 NS--SPYETGYIKFIENNGNTFWYDLMPAPGDRFDQSKYLMYNDNKTVDKSKVLEVHL 234

QY 231 YT 232
 DB 235 TT 236

RESULT 53
 US-09-314-235-27
 ; Sequence 27, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-314-235-27

Query Match 21.9%; Score 271.5; DB 4; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHASKFTG-LMENMKVLYDDHYVSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYNYNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNVLRVY-ENKENTISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176


```

Db      122 SIDGIQSLSDIEQIKNG-----NCSRISYTVRKYLTDNKKQLYTNGP--SKYETGYIKFIP 175
      QY      189 SEGSTVSVDLFD-----AQGQYPTDLLRIYRDNKTINSENHLIALYLT 232
      Db      176 KNKESWFDFPPEFTQSKI-----LMIYKDNETLDSNTSQIEVILTT 219

RESULT 58
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match      18.9%; Score 234; DB 4; Length 220;
Best Local Similarity 30.3%; Pred. No. 3,3e-16;
Matches 69; Conservative 41; Mismatches 96; Indels 22; Gaps 9

QY      14 KKSELGQTALGNLKQIYYNEKA--IT-ENKESDDQFLENTLLPKGFTGHPWYNDLLVD 70
Db      5 KPSQLQRSLVTKFKIYIFFMFVTLTHTENKVSVDQLSHDLIYN--VSGPNYDKLKE 61
QY      71 LGSKDATNYKGGKVDLYGAYGYOC-AGGTPNTACNYGGVTLHDNNRLTEKKVPINL 129
Db      62 LKQEQMATUFLKQNDVIYGVYTHLCYLCENASRACLYGGVTNHEGNHLEIPKKIVKV 121
QY      130 WIDGKQT-TPVIDKVTSKKEVTVOELDQARHYLHGKFGLYNDSFGCKVQVORGLIVFHS 188
Db      122 SIDGIQSLSDIEQIKNG-----NCSRISYTVRKYLTDNKKQLYTNGP--SKYETGYIKFIP 175
QY      189 SEGSTVSVDLFD-----AQGQYPTDLLRIYRDNKTINSENHLIALYLT 232
Db      176 KNKESWFDFPPEFTQSKI-----LMIYKDNETLDSNTSQIEVILTT 219

RESULT 59
US-09-144-776B-18
; Sequence 18, Application US/09144776B
; Patent No. 639332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris

```

```
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UFI26.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-220-378-1

Query Match 17.2%; Score 213; DB 1; Length 45;
Best Local Similarity 95.6%; Pred. No. 4.9e-15;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESHD 45

RESULT 61
US-08-696-012-1
/ Sequence 1, Application US/08696012
/ Patent No. 5859207
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Portzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ TITLE OF INVENTION: Peptides
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/696,012
/ FILING DATE: 12-AUG-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UFI26.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-696-012-1

Query Match 17.2%; Score 213; DB 2; Length 45;
Best Local Similarity 95.8%; Pred. No. 4.9e-15;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESHD 45

RESULT 62
US-08-896-933-30
/ Sequence 30, Application US/08896933
/ Patent No. 6221351
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005002
/ CURRENT APPLICATION NUMBER: US/08/896,933
/ EARLIER FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 30
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Streptococcus pyogenes
US-08-896-933-30

Query Match 14.0%; Score 173.5; DB 3; Length 208;
Best Local Similarity 26.7%; Pred. No. 5.4e-10;
Matches 59; Conservative 41; Mismatches 76; Indels 45; Gaps 11;

QY 40 NKESDDQFLENTLLFKGFETGHPW-YNDLLVDLGSKDA-----TNKYKGK----- 83
Db 1 DSKKDISNVKSDLLYA--YTITPYDYKCRVNFSTHTLTNIDTQYRGDKYVVISSEMSYE 58
QY 84 -----KVDLYGAYGYQCAGGTPNKTACWYGVTLDNNRLTEKKVFPINLWIDGK 134
Db 59 ASQKFKRDDHVDVFGLFYILNSHTG-----EVIYGGITPAQNNKYNH--KLLGNLFISGE 111
QY 135 QTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGKVQKGLIVFHSSEGS 192
Db 112 SQQLANKKIILEKDIVTFOEIDFKIRKYLMDNYKIYDATSPYVSGRIEIG-----TKDGK 166
QY 193 TVSYDLFDA--QGQYPTTLRIYRDNKTINSENL-HIALYL 230
Db 167 HEQIDLFDSFNEGTRSDIFAK-YKDNRIINMKNFHFSDIYL 206

RESULT 63
US-09-314-235-30
/ Sequence 30, Application US/09314235
/ Patent No. 6338845
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005004
/ CURRENT APPLICATION NUMBER: US/09/314,235
/ EARLIER FILING DATE: 1999-05-18
/ EARLIER APPLICATION NUMBER: 08/896,933
/ EARLIER FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
```

EARLIER APPLICATION NUMBER: 07/891,718
 EARLIER FILING DATE: 1992-06-01
 EARLIER APPLICATION NUMBER: US91/00342
 EARLIER FILING DATE: 1991-01-17
 EARLIER APPLICATION NUMBER: 07/466,577
 EARLIER FILING DATE: 1990-01-17
 EARLIER APPLICATION NUMBER: 07/416,530
 EARLIER FILING DATE: 1989-10-03
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 30
 LENGTH: 208
 TYPE: PR1
 ORGANISM: Streptococcus pyogenes
 US-09-314-235-30

Query Match 14.0%; Score 173.5; DB 4; Length 208;
 Best Local Similarity 26.7%; Pred. No. 5.4e-10;
 Matches 59; Conservative 41; Mismatches 76; Indels 45; Gaps 11;
 QY 40 NKESDQFLENTLLFKGFTGHPW-YNDLLVGLSKDA-----TNKYKKGK----- 83
 Db 1 DSKKDISNVKSDLLYA-YTITPDYKQCRVNFSTHTLINDTQYRGKDYVISSEMSYE 58
 QY 84 -----KVDLYGAYGVQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPIINLWIDGK 134
 Db 59 ASOKFKRDDHVDVFGULYILNSHTG-----EYIGGITPAQNNKVNH--KLLGNLFISGE 111
 QY 135 QTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFLYNSDS--FGGKVQGLIVFHSSSGS 192
 Db 112 SQQLNKKILERDITVFQSIDPKIRKYLMDNYKIYDATSPYVSGRIEIG-----TKDGK 166
 QY 193 TVSYDLPDA--QQQYPTLLRIYRDKNTINSENL-HIALYL 230
 Db 167 HEQIDLFDSPNEGTRSDIFAK-YKONRIINKNKFNHSHFDIYL 206

RESULT 64
 US-09-144-776B-20
 Sequence 20, Application US/09144776B
 Patent No. 6399332
 GENERAL INFORMATION:
 APPLICANT: Robert G. Ulrich,
 Mark A. Olson
 Sina Bavari
 TITLE OF INVENTION: Bacterial Superantigen
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Charles H. Harris
 STREET: US Army MRC -504 Scott Street
 MCMR-JA (Charles H. Harris-Patent
 Acty)
 CITY: FORT DETRICK
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 21702-5012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Apple Macintosh
 OPERATING SYSTEM: Macintosh 7.5
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,776B
 FILING DATE: 01-Sep-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/882,431
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles H. Harris
 REGISTRATION NUMBER: 34,616
 REFERENCE/DOCKET NUMBER: <Unknown>

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 619-2065
 TELEFAX: (301) 619-7714
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 89
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 20:
 US-09-144-776B-20

Query Match 11.1%; Score 137.5; DB 4; Length 89;
 Best Local Similarity 39.1%; Pred. No. 8.4e-07;
 Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;
 QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDQATNKYKGVLYGAYGYQC----- 96
 Db 1 SIDQFLYDLYISIKDKLGNVDNRVFEKNKDLADKYDKYVDVFGANY-YQCYFSKKT 59
 QY 97 ----AGGTPNKTACMYGGVTLHDNNRL 119
 Db 60 NDINSHQTDKRTKTCMYGGVTEHNGNQL 86

RESULT 65
 US-08-896-933-34
 Sequence 34, Application US/08896933
 Patent No. 6221351
 GENERAL INFORMATION:
 APPLICANT: Terman, David S.
 TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 FILE REFERENCE: 09629/005002
 CURRENT APPLICATION NUMBER: US/08/896,933
 CURRENT FILING DATE: 1997-07-18
 EARLIER APPLICATION NUMBER: 08/252,978
 EARLIER FILING DATE: 1994-06-02
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 34
 LENGTH: 27
 TYPE: PR1
 ORGANISM: Staphylococcal
 US-08-896-933-34

Query Match 10.6%; Score 131; DB 3; Length 27;
 Best Local Similarity 100.0%; Pred. No. 7e-07;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLKKKSELQGTALGNLK 27
 Db 1 SEKSEINEKDLKKKSELQGTALGNLK 27

RESULT 66
 US-09-314-235-34
 Sequence 34, Application US/09314235
 Patent No. 6338845
 GENERAL INFORMATION:
 APPLICANT: Terman, David S.
 TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 FILE REFERENCE: 09629/005004
 CURRENT APPLICATION NUMBER: US/09/314,235
 CURRENT FILING DATE: 1999-05-18
 EARLIER APPLICATION NUMBER: 08/896,933
 EARLIER FILING DATE: 1997-07-18
 EARLIER APPLICATION NUMBER: 08/252,978
 EARLIER FILING DATE: 1994-06-02
 EARLIER APPLICATION NUMBER: 07/891,718
 EARLIER FILING DATE: 1992-06-01

EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466, 577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416, 530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34
LENGTH: 27
TYPE: PRT
ORGANISM: Staphylococcal
US-09-314-235-34

Query Match 10.4%; Score 131; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLK 27
DB 1 SEKSEINEKDLRKXSELQGTALGNLK 27

RESULT 67

US-08-220-378-2
Sequence 2, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE: 08-SEP-1992

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 10.4%; Score 129; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 1.2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 39 ENKESDDQLENTLLFKGFTGHPWYND 66
DB 1 ENKESDDQLENTLLFKGFTGHPWYND 28

RESULT 68

US-08-696-012-2
Sequence 2, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-2

Query Match 10.4%; Score 129; DB 2; Length 28;
Best Local Similarity 78.6%; Pred. No. 1.2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 39 ENKESDDQLENTLLFKGFTGHPWYND 66
DB 1 ENKESDDQLENTLLFKGFTGHPWYND 28

RESULT 69

US-08-838-413A-22
Sequence 22, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22

Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 KKEVTQVQLDQARHYLHGKGLY 170
DB 1 KKEVTQVQLDQARHYLHGKGLY 24

RESULT 70
US-08-220-378-5
Sequence 5, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22
Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 147 KKEVTQVQLDQARHYLHGKGLY 170
DB 1 KKEVTQVQLDQARHYLHGKGLY 24
RESULT 70
US-08-220-378-5
Sequence 5, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US/07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22
Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 147 KKEVTQVQLDQARHYLHGKGLY 170
DB 1 KKEVTQVQLDQARHYLHGKGLY 24
RESULT 70
US-08-220-378-5
Sequence 5, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US/07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22
Query Match 10.2%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 NKTACMYGGVTLHDNNRLTEKK 124
DB 1 NKTACMYGGVTLHDNNRLTEKK 23
RESULT 71
US-08-696-012-5
Sequence 5, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US/07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22
Query Match 10.2%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 102 NKTACMYGGVTLHDNNRLTEKK 124
DB 1 NKTACMYGGVTLHDNNRLTEKK 23

```



```
; MOLECULE TYPE: peptide
US-08-696-012-5
Query Match      10.2%; Score 126; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      102 NKTACMYGGVTLHDNNRLTEKK 124
Db      1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 72
US-08-220-378-6
; Sequence 6, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; NUMBER OF SEQUENCES: 10
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-596-012-6
Query Match      10.0%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 4.1e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      121 EEKVPINLWDGKQTVPIDKVTKSK 148
Db      1 EEKVPINLWDGKQTVPIETVKTKK 28

RESULT 74
US-09-144-776B-24
; Sequence 24, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 79
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 3.6e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;
QY 43 SDQFLNTLLFKGFTGHEWYNDLVLSGDATNKYKGVLDLYGAYGYQC-AGGTP 101
Db 1 SVQQLSHDIYN--VSGENYDKLTSLKQEMATLFRKKNVDIYGVYHLCLVCNA 57
QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 75
US-08-220-378-4
Sequence 4, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: Uf126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-4

Query Match 9.7%; Score 120; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 83 KKVDLYGAYGYQCAGGTPNKT 104
Db 1 KKVDKYGAYGYQCAGGTPNKT 22

Search completed: August 12, 2004, 13:34:05
Job time : 11.2135 secs